MOLECULAR HEPATOTOXICOLOGY MODELING

RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Applications 60/364,045 filed on March 15, 2002, 60/364,055 filed on March 15, 2002, and 60/436,643 filed on December 30, 2002, and is a continuation-in-part of pending U.S. Application 10/060,087 filed January 31, 2002. In addition, this application is related to U.S. Provisional Applications 60/222,040, 60/244,880, 60/290,029, 60/290,645, 60/292,336, 60/295,798, 60/297,457, 60/298,884, 60/303,459, and 60/331,273, as well as to pending U.S. Application 09/917,800, filed July 31, 2001, all of which are herein incorporated by reference in their entirety.

SEQUENCE LISTING SUBMISSION ON COMPACT DISC

[0002] The Sequence Listing submitted concurrently herewith on compact disc is herein incorporated by reference in its entirety. Four copies of the Sequence Listing, one on each of four compact discs are provided. Copies 1, 2, and 3 are identical. Copies 1, 2, and 3 are also identical to the CRF. Each electronic copy of the Sequence Listing was created on January 30, 2003 with a file size of 5795 KB. The file names are as follows: Copy 1- gl5038us01.txt; Copy 2- gl5038us01.txt; Copy 3- gl5038us01.txt; and CRF-gl5038us01.txt.

BACKGROUND OF THE INVENTION

[0003] The need for methods of assessing the toxic impact of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism has led to the development of procedures which utilize living organisms as biological monitors. The simplest and most convenient of these systems utilize unicellular microorganisms such as yeast and bacteria, since they are most easily maintained and manipulated. Unicellular screening systems also often use easily detectable changes in phenotype to monitor the effect of test compounds on the cell. Unicellular organisms, however, are inadequate models for estimating the potential effects of many compounds on complex multicellular animals, as they do not have the ability to carry out biotransformations to the extent or at levels found in higher organisms.



[0004] The biotransformation of chemical compounds by multicellular organisms is a significant factor in determining the overall toxicity of agents to which they are exposed. Accordingly, multicellular screening systems may be preferred or required to detect the toxic effects of compounds. The use of multicellular organisms as toxicology screening tools has been significantly hampered, however, by the lack of convenient screening mechanisms or endpoints, such as those available in yeast or bacterial systems. In addition, previous attempts to produce toxicology prediction systems have failed to provide the necessary modeling data and statistical information to accurately predict toxic responses (e.g., WO 00/12760, WO 00/47761, WO 00/63435, WO 01/32928 and WO 01/38579).

SUMMARY OF THE INVENTION

[0005] The present invention is based on the elucidation of the global changes in gene expression in tissues or cells exposed to known toxins, in particular hepatotoxins, as compared to unexposed tissues or cells as well as the identification of individual genes that are differentially expressed upon toxin exposure.

[0006] In various aspects, the invention includes methods of predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, and predicting the hepatoxicity of a compound. The invention also includes methods of identifying agents that modulate the onset or progression of a toxic response. Also provided are methods of predicting the cellular pathways that a compound modulates in a cell. The invention includes methods of identifying agents that modulate protein activities.

[0007] In a further aspect, the invention provides probes comprising sequences that specifically hybridize to genes in Tables 1-5WWW. Also provided are solid supports comprising at least two of the previously mentioned probes. The invention also includes a computer system that has a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes in Tables 1-5WWW.

[0008] The invention further provides a core set of genes in Tables 5A-5WWW from which probes can be made and attached to solid supports. These core genes serve as a preferred set of markers of liver toxicity and can be used with the methods of the

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invention to predict or monitor a toxic effect of a compound or to modulate the onset or progression of a toxic response.

DETAILED DESCRIPTION

[0009] Many biological functions are accomplished by altering the expression of various genes through transcriptional (e.g. through control of initiation, provision of RNA precursors, RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death are often characterized by the variations in the expression levels of groups of genes.

[0010] Changes in gene expression are also associated with the effects of various chemicals, drugs, toxins, pharmaceutical agents and pollutants on an organism or cells. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression of oncogene/protooncogenes after exposure to an agent could lead to tumorgenesis or hyperplastic growth of cells (Marshall (1991) Cell 64: 313-326; Weinberg (1991) Science 254:1138-1146). Thus, changes in the expression levels of particular genes (e.g. oncogenes or tumor suppressors) may serve as signposts for the presence and progression of toxicity or other cellular responses to exposure to a particular compound.

[0011] Monitoring changes in gene expression may also provide certain advantages during drug screening and development. Often drugs are screened for the ability to interact with a major target without regard to other effects the drugs have on cells. These cellular effects may cause toxicity in the whole animal, which prevents the development and clinical use of the potential drug.

[0012] The present inventors have examined tissue from animals exposed to the known hepatotoxins which induce detrimental liver effects, to identify global changes in gene expression induced by these compounds. These global changes in gene expression, which can be detected by the production of gene expression profiles, provide useful toxicity markers that can be used to monitor toxicity and/or toxicity progression by a test compound. Some of these markers may also be used to monitor or detect various disease or physiological states, disease progression, drug efficacy and drug metabolism.

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Identification of Toxicity Markers

[0013] To evaluate and identify gene expression changes that are predictive of toxicity, studies using selected compounds with well characterized toxicity have been conducted by the present inventors to catalogue altered gene expression during exposure *in vivo*. In the present study, acetominophen, 2-acetylaminofluorene (2-AAF), acyclovir, ANIT, AY-25329, BI liver toxin, chloroform, bicalutamide, carbon tetrachloride, chloroform, CI-1000, clofibrate, colchicine, CPA, diclofenac, diflunisal, dimethylnitrosamine (DMN), dioxin, 17α-ethinylestradiol, gemfibrozil, hydrazine, indomethacin, LPS, menadione, phenobarbital, tacrine, thioacetamide, valproate, Wy-14643, and zileuton were selected as known hepatotoxins.

[0014] Aromatic and aliphatic isothiocyanates are commonly used soil fumigants and pesticides (Shaaya et al. (1995) Pesticide Science 44(3):249-253; Cairns et al. (1988) J Assoc Official Analytical Chemists 71(3):547-550). These compounds are also environmental hazards, because they remain as toxic residues in plants (Cerny et al. (1996) J Agricultural and Food Chemistry 44(12):3835-3839) and because they are released from the soil into the surrounding air (Gan et al. (1998) J Agricultural and Food Chemistry 46(3):986-990).

[0015] Exposure to α-naphthylisothiocyanate (ANIT) has been shown to increase serum levels of total bilirubin, alkaline phosphatase, serum glutamic oxaloacetic transaminase and serum glutamic pyruvic transaminase, while total bile flow was reduced, all of which are indications of severe biliary dysfunction. ANIT also induces jaundice and cholestatis (the condition caused by failure to secrete bile, resulting in plasma accumulation of bile substances, liver cell necrosis and bile duct obstruction) (Tanaka et al. (1993) Clinical and Experimental Pharmacology and Physiology 20:543-547). ANIT fails to produce extensive necrosis, but was found to produce inflammation and edema in the portal tract of the liver (Maziasa et al.(1991) Toxicol Appl Pharmacol 110:365-373). ANIT-induced hepatotoxicity may also characterized by cholangiolitic hepatitis and bile duct damage. Acute hepatotoxicity caused by ANIT in rats is manifested as neutrophil-dependent necrosis of bile duct epithelial cells (BDECs) and hepatic parenchymal cells. These changes mirror the cholangiolitic hepatitis found in humans (Hill (1999) Toxicol Sci 47:118-125).

[0016] Histological changes include an infiltration of polymorphonuclear neutrophils and elevated number of apoptotic hepatocytes (Calvo et al. (2001) J Cell Biochem

80(4):461-470). Other known hepatotoxic effects of exposure to ANIT include a damaged antioxidant defense system, decreased activities of superoxide dismutase and catalase (Ohta et al. (1999) Toxicology 139(3):265-275), and the release of proteases from the infiltrated neutrophils, alanine aminotransferase, cathepsin G, elastase, which mediate hepatocyte killing (Hill et al. (1998) Toxicol Appl Pharmacol 148(1):169-175). [0017] The effects of the model compound 2-acetylaminofluorene (2-AAF), a strong carcinogen and liver tumor inducer, have been studied in rat livers. 2-AAF has been shown to cause changes in the mitochondria which trigger apoptosis and regenerative cell proliferation. These in turn, cause cirrhosis-like changes in the liver. Exposure to 2-AAF also produces elevated levels of ALT and AST, hemoglobin adducts and foci containing the placental form of glutathione S-transferase. Chromosome aberrations, micronuclei and sister-chromatid exchanges have also been observed (Bitsch et al. (2000) Toxicol Sci 55(1):44-51; Lorenzini et al. (1996) Carcinogenesis 17:1323-1329; Sawada et al. (1991) Mutat Res 251(1):59-69).

[0018] Acyclovir (9-[(2-hydroxyethyl) methyl] guanine, Zovirax®), an anti-viral guanosine analogue, is used to treat herpes simplex virus (HSV), varicella zoster virus (VZV) and Epstein-Barr virus (EBV) infections. The most common adverse effect of acyclovir treatment is damage to various parts of the kidney, particularly the renal tubules, although the drug can also cause damage to the liver and nervous system. Crystalluria, or the precipitation of crystals of acyclovir in the lumina of the renal tubules can occur (Fogazzi (1996) Nephrol Dial Transplant 11(2):379-387). If the drug crystallizes in the renal collecting tubules, obstructive nephropathy and tubular necrosis can result (Richardson (2000) Vet Hum Toxicol 42(6):370-371). Examination of biopsy tissues from affected patients showed dilation of the proximal and distal renal tubules, with loss of the brush border, flattening of the lining cells and focal nuclear loss (Becker et al. (1993) Am J Kidney Dis 22(4):611-615).

[0019] Liver damage in patients taking acyclovir is indicated clinically by abnormal liver function tests (http://www.hopkins-aids.edu/publications/book/ch6_acyclovir.html).

Adverse effects in the liver include hepatitis, hyperbilirubinemia and jaundice

(Physicians' Desk Reference, 56th ed., p. 1707, Medical Economics Co. Inc., Montvale,

NJ, 2002), although findings of hepatotoxicity in animals have not yet been published.

Studies by the present inventors on rats treated with acyclovir have found elevated serum levels of BUN and creatinine. Decreased levels of ALT, AST and triglycerides

(indicators of liver function) have also been found, but these may be attributed to kidney damage as well as to liver damage. While classic signs of hepatotoxicity in rats due to acyclovir administration have not been published, gene expression changes can be used to predict that the drug will be a liver toxin in humans.

[0020] Acetominophen (APAP) is a widely used analgesic and antipyretic agent that is an effective substitute for aspirin. Although acetaminophen does not have anti-inflammatory properties, it is preferably given to patients with ulcers or patients in whom prolonged clotting times would not be desirable. It also preferably taken by people who do not tolerate aspirin well.

[0021] Acetominophen is metabolized to *N*-acetyl-*p*-benzoquinoneimine (NAPQI) by N-hydroxylation in a cytochrome P450-mediated process. This highly reactive intermediate, which reacts with sulfhydryl groups in glutathione, and in other liver proteins following the depletion of glutathione, can cause centrilobular hepatic necrosis (particularly in zone 3), renal tubular necrosis, and hepatic and renal failure (Goodman and Gilman's The Pharmacological Basis of Therapeutics, Ninth Ed., Hardman *et al.*, eds., pp. 631-633, McGraw-Hill, New York, 1996; Chanda *et al.* (1995) *Hepatology* 21(2):477-486). Less serious side effects include skin rashes (erythemas and urticarias) and allergic reactions.

[0022] Upon treatment of rats with acetaminophen, hepatotoxicity can be observed 24 hours after dosing, as determined by statistically significant elevations of ALT and AST in the serum and by hepatocellular necrosis visualized at the light microscopic level (Hessel et al. (1996) Braz J Med Biol Res 29(6):793-796; Bruck et al. (1999) Dig Dis Sci 44(6):1228-1235). High, but non-lethal, doses of acetaminophen given to rats also produced elevated levels of genes involved in hepatic acute phase response and liver cell maintenance and repair: arginase, beta-fibrinogen, alpha 1-acid glycoprotein, alphatubulin, histone 3, TGF beta and cyclin d. Expression levels of genes regulated by the cell cycle were decreased (Tygstrup et al. (1996) J Hepatol 25(2):183-190; Tygstrup et al. (1997) J Hepatol 27(1):156-162). In mice, expression levels of genes that encode growth arrest and cell cycle regulatory proteins were increased, along with expression levels of stress-induced genes, transcription factor LRG-21, SOCS-2 (cytokine signaling repressor) and PAI-1 (plasminogen activator inhibitor-1) (Reilly et al. (2001) Biochem Biophys Res Comm 282(1):321-328).

[0023] AY-25329, a proprietary compound, is a phenothiazine that has been shown to be toxic in liver and in kidney tissue, where it can cause nephrosis. Phenothiazines are a class of psychoactive drugs that are used to treat schizophrenia, paranoia, mania, hyperactivity in children, some forms of senility, and anxiety (http://www.encyclopedia.com/articlesnew/ 36591.html). Side effects associated with prolonged use of these drugs are reduced blood pressure, Parkinsonism, reduction of motor activity, and visual impairment.

[0024] The present inventors have noted indications of liver and renal effects of AY-25329 by changes in serum chemistry. As early as 6 hours after the first dose, statistically significant increases in serum levels of creatinine, BUN, ALT, triglycerides and cholesterol were observed. Most of these markers of renal and liver dysfunction remained altered throughout the 14 day study period. Light microscopic analysis revealed effects in the liver as early as 6 and 24 hours, as evidenced by an increased number of hepatocytic mitotic figures and decreased glycogen content. Following 14 days of repeated dosing, nephrosis and alterations in the peripheral lobes of the liver and in the cytoplasm of hepatocytes were evident in rats dosed with 250 mg/kg/day of AY-25329.

[0025] BI liver toxin, a model compound, produces cardiac changes (QT_C prolongation) in dogs and liver and cardiac changes in rats. Liver samples collected from rats over a four-week period showed that this compound induces sedation, lowers body weight, increases liver weight, and slightly increases serum levels of AST, ALP and BUN. Over a three-month period, cardiovascular effects are observed as well.

[0026] The toxicological profile of bicalutamide, a drug for treating prostate-cancer, is closely associated with the drug's non-steroidal anti-androgenic activity. Bicalutamide produces typical effects of an anti-androgen, including atrophy of the prostate, testis and seminal vesicles and Leydig cell hyperplasia resulting from inhibition of pituitary feedback by testosterone. Benign Leydig cell tumors and elevated levels of CYP3A1 were seen in rats, but not in humans, although liver toxicity in humans has been observed. Bicalutamide causes liver enlargement and is a mixed function oxidase inducer in rodents and dogs. These effects lead to thyroid hypertrophy and adenoma in the rat and hepatocellular carcinoma in the male mouse (Iswaran et al. (1997) J Toxicol Sci 22(2):75-88; Oh et al. (2002) Urology 60(3 Suppl 1):87-93; McKillop et al. (1998) Xenobiotica 28(5):465-478). In prostate cancer patients treated with bicalutamide,

elevated levels of the liver enzymes glutamic-oxalacetic transaminase (GOT), glutamic-pyruvic transaminase (GPT), alkaliphosphatase (AL-P) and gamma guanosine 5'-triphosphate (gamma-GTP) have been noted, along with breast pain, gynecomastia and hot flashes (Kotake et al. (1996) Hinyokika Kiyo 42(2):143-153).

[0027] The pathogenesis of acute carbon tetrachloride (CCl₄)-induced hepatotoxicity follows a well-characterized course in humans and experimental animals resulting in centrilobular necrosis and steatosis, followed by hepatic regeneration and tissue repair. Severity of the hepatocellular injury is also dose-dependent and may be affected by species, age, gender and diet.

[0028] Differences in susceptibility to CCl₄ hepatotoxicity are primarily related to the ability of the animal model to metabolize CCl₄ to reactive intermediates. CCl₄-induced hepatotoxicity is dependent on CCl₄ bioactivation to trichloromethyl free radicals by cytochrome P450 enzymes (CYP2E1), localized primarily in centrizonal hepatocytes. Formation of the free radicals leads to membrane lipid peroxidation and protein denaturation resulting in hepatocellular damage or death.

[0029] The onset of hepatic injury is rapid following acute administration of CCl₄ to male rats. Morphologic studies have shown cytoplasmic accumulation of lipids in hepatocytes within 1 to 3 hours of dosing, and by 5 to 6 hours, focal necrosis and hydropic swelling of hepatocytes are evident. Centrilobular necrosis and inflammatory infiltration peak by 24 to 48 hours post dose. The onset of recovery is also evident within this time frame by increased DNA synthesis and the appearance of mitotic figures. Removal of necrotic debris begins by 48 hours and is usually completed by one week, with full restoration of the liver by 14 days.

[0030] Increases in serum transaminase levels also parallel CCl₄-induced hepatic histopathology. In male Sprague Dawley (SD) rats, alanine aminotrasferase (ALT) and aspartate aminotransferase (AST) levels increase within 3 hours of CCl₄ administration (0.1, 1,2, 3, 4 mL/kg, ip; 2.5 mL/kg, po) and reach peak levels (approximately 5-10 fold increases) within 48 hours post dose. Significant increases in serum α -glutathione stransferase (α -GST) levels have also been detected as early as 2 hours after CCl₄ administration (25 μ L/kg, po) to male SD rats.

[0031] At the molecular level, induction of the growth-related proto-oncogenes, c-fos and c-jun, is reportedly the earliest event detected in an acute model of CCl₄-induced

hepatotoxicity (Schiaffonato et al. (1997) Liver 17:183-191). Expression of these early-immediate response genes has been detected within 30 minutes of a single dose of CCl₄ to mice (0.05 -1.5 mL/kg, ip) and by 1 to 2 hours post dose in rats (2 mL/kg, po; 5 mL/kg,po) (Schiaffonato et al., supra, and Hong et al.(1997) Yonsei Medical J 38:167-177). Similarly, hepatic c-myc gene expression is increased by 1 hour following an acute dose of CCl₄ to male SD rats (5 mL/kg, po) (Hong et al., supra). Expression of these genes following exposure to CCl₄ is rapid and transient. Peak hepatic mRNA levels for c-fos, c-jun, and c-myc, after acute administration of CCl₄ have been reported at 1 to 2 hours, 3 hours, and 1 hour post dose, respectively.

[0032] The expression of tumor necrosis factor- α (TNF- α) is also increased in the livers of rodents exposed to CCl₄, and TNF-α has been implicated in initiation of the hepatic repair process. Pre-treatment with anti-TNF-α antibodies has been shown to prevent CCl₄-mediated increases in c-jun and c-fos gene expression, whereas administration of TNF-α induced rapid expression of these genes (Bruccoleri et al. (1997) Hepatol 25:133-141). Up-regulation of transforming growth factor- β (TGF-β) and transforming growth factor receptors (TBRI-III) later in the repair process (24 and 48 hours after CCl₄ administration) suggests that TGF-β may play a role in limiting the regenerative response by induction of apoptosis (Grasl-Kraupp et al. (1998) Hepatol 28:717-7126). [0033] Chloroform (CHCl₃) is an obsolete anesthetic that was abandoned due to its hepatotoxicity. The pathogenesis of acute CHCl₃ - induced hepatotoxicity follows a well-characterized course in humans and experimental animals resulting in centrilobular necrosis and steatosis, followed by hepatic regeneration and tissue repair. Severity of the hepatocellular injury is dose-dependent and may be affected by the animal species, strain, age, gender, diet, vehicle and/or route of administration (Lilly et al. (1997) Fund Appl Toxicol 40:101-110 and Raymond et al. (1997) J Toxicol Environ Health 52:463-476).

[0034] Differences in susceptibility to CHCl₃ toxicity are considered related to differential metabolism. CHCl₃- induced hepatotoxicity is primarily mediated by formation of reactive species, such as phosgene and trichloromethyl free radicals, by cytochrome P450 enzymes (CYP2E1). CHCl₃ hepatotoxicity is also increased by exposure to agents that induce cytochrome P450 (*i.e.*, ethanol, phenobarbital), and

deplete hepatic glutathione (GSH). Formation of the free radicals leads to membrane lipid peroxidation and protein denaturation resulting in hepatocellular damage or death. [0035] Chronic administration of CHCl₃ to rodents induces an increased incidence of hepatic and renal carcinomas by a nongenotoxic-cytotoxic mode of action. Carcinogenicity of CHCl₃ is considered secondary to chemically-induced cytotoxicity with subsequent compensatory cell proliferation, rather than to direct interaction of CHCl₃ or its metabolites with DNA.

[0036] The onset of hepatic toxicity is rapid following acute administration of CHCl₃ to male rats. Morphologic studies have shown cytoplasmic accumulation of lipids in hepatocytes within 1 to 3 hours of dosing, and by 5 to 6 hours, focal necrosis and hydropic swelling of hepatocytes are evident. Centrilobular necrosis and inflammatory infiltration peak by 24 to 48 hours post dose. The onset of recovery is also evident within this time frame by increased DNA synthesis and the appearance of mitotic figures. Removal of necrotic debris begins by 48 hours and is usually completed by one week, with full restoration of the liver by 14 days.

[0037] In studies on rats and mice, significant changes in clinical parameters included increased levels of BUN and serum creatinine and decreased levels of phosphatidylethanolamine and tissue glutathione (GSH). There is a strong correlation between the formation of the phospholipid adducts, GSH depletion and liver toxicity (Di Consiglio et al. (2001) Toxicology 159(1-2):43-53). Experiments on mice have shown that exposure to chloroform also increases the liver weight:body weight ratio and the proliferating cell nuclear antigen-labeling index. Decreased levels of 5-methylcytosine and of the methylated c-myc gene (associated with increased carcinogenic activity) were also found (Coffin et al. (2000) Toxicol Sci 58(2):243-252). Other studies on mice have noted that elevated levels of the P450 cytochromes, such as P450 2E1 and CYP2A5, are involved in cytotoxic metabolic conversions (Constan et al. (1999) Toxicol Appl Pharmacol 160(2):120-126; Camus-Randon et al. (1996) Toxicol Appl Pharmacol 138(1):140-148). [0038] Studies of chloroform poisoning in humans have noted hepatocellular necrosis characterized by decreased levels of serum biomarkers (AST, ALT, alkaline phosphatase and lactate dehydrogenase) and increased levels of markers of hepatocellular regeneration (alpha-fetoprotein, retinol-binding protein, gamma-glutamyl transferase and des-gamma-carboxyprothrombin) (Horn et al. (1999) Am J Clin Pathol 112(3):351-357).

[0039] At the molecular level, CHCl₃-induced changes in mRNA levels of 2 known genes, MUSTI21(a mouse primary response gene induced by growth factors and tumor promoters) and MUSMRNAH (a gene highly homologous to a gene isolated from a prostate carcinoma cell line), and 2 novel genes (MUSFRA and MUSFRB) have been identified by differential display in regenerating mouse liver (Kegelmeyer *et al.* (1997) *Molecul Carcin* 20:288-297). These genes have been postulated to play a role in hepatic regeneration or possibly CHCl₃- induced hepatocarcinogenesis.

[0040] CI-1000 (4H-pyrrolo:3,2-d:pyrimidin-4-one, 2-amino-3,5-dihydro-7-(3-thienylmethyl)-monohydrochloride monohydrate) is a compound with anti-inflammatory properties. After treatment with CI-1000, increased serum ALT levels, a standard marker of liver toxicity, were observed in dogs.

[0041] Clofibrate, a halogenated phenoxypropanoic acid derivative (ethyl ester of clofibric acid), is an antilipemic agent. The exact mechanism by which clofibrate lowers serum concentrations of triglycerides and low-density lipoprotein (LDL) cholesterol, as well as raising high-density lipoprotein (HDL) cholesterol is uncertain. The drug has several antilipidemic actions, including activating lipoprotein lipase, which enhances the clearance of triglycerides and very-low-density lipoprotein (VLDL) cholesterol, inhibition of cholesterol and triglyceride biosynthesis, mobilization of cholesterol from tissues, increasing fecal excretion of neutral steroids, decreasing hepatic lipoprotein synthesis and secretion, and decreasing free fatty acid release.

[0042] Clofibrate has a number of effects on the rat liver, including hepatocellular hypertrophy, cellular proliferation, hepatomegaly, induction of CYP450 isozymes, and induction of palmitoyl CoA oxidation. Long term administration of clofibrate causes increased incidence of hepatocellular carcinoma, benign testicular Leydig cell tumors, and pancreatic acinar adenomas in rats. Clofibrate induces proliferation of peroxisomes in rodents and this effect, rather than genotoxic damage, is believed to be the causative event in rodent carcinogenesis (AHFS Drug Information Handbook 2001, McEvoy, ed., pp.1735-1738; Electronic Physicians' Desk Reference- Atromid-S (clofibrate) at www.pdr.net; Brown and Goldstein, "Drugs used in the treatment of hyperliproteinemias," in Goodman and Gilman's The Pharmacological Basis of Therapeutics, Eighth ed., Goodman et al., eds., pp. 874-896, Pergamon Press, New York, 1990).

[0043] Clofibrate also increases hepatic lipid content and alters its normal composition by significantly increasing levels of phosphatidylcholine and phosphatidyl-ethanolamine (Adinehzadeh et al. (1998) Chem Res Toxicol 11(5):428-440). A rat study of liver hyperplasia and liver tumors induced by peroxisome proliferators revealed that administration of clofibrate increased levels of copper and altered copper-related gene expression in the neoplastic liver tissues. Down-regulation of the ceruloplasmin gene and of the Wilson's Disease gene (which encodes P-type ATPase), along with upregulation of the metallothionein gene, were noted in these tissues (Eagon et al. (1999) Carcinogenesis 20(6):1091-1096). Clofibrate-induced peroxisome proliferation and carcinogenicity are believed to be rodent-specific, and have not been demonstrated in humans.

[0044] Colchicine, an alkoloid of Colchicum autumale, is an antiinflammatory agent used in the treatment of gouty arthritis (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th ed., p. 647, J.G. Hardman et al., Eds., McGraw Hill, New York, 1996). An antimitotic agent, colchicine binds to tubulin which leads to depolymerization and disappearance of the fibrillar microtubules in granulocytes and other motile cells. As a result, the migration of granulocytes into the inflamed area is inhibited, thereby suppressing the inflammatory response.

[0045] Some common, mild side effects associated with colchicine treatment are gastrointestinal disturbances, loss of appetite and hair loss. More serious side effects include hepatotoxicity, nausea, vomiting, and severe diarrhea and/or abdominal pain. Colchicine overdose can induce convulsions, coma, and multiorgan failure with a high incidence of mortality. Renal failure is multifactorial and related to prolonged hypotension, hypoxemia, sepsis, and rhabdomyolysis. In rats, less dramatic doses have been shown to inhibit the secretion of many endogenous proteins such as insulin and parathyroid hormone. Signs of liver damage are leakage of marker compounds, such as lactate dehydrogenase and albumin, into plasma and bile (Dvorak et al. (2002) Toxicol In Vitro 16(3):219-227; Crocenzi et al. (1997) Toxicology 121(2):127-142).

[0046] Cyproterone acetate (CPA) is a potent androgen antagonist and has been used to treat acne, male pattern baldness, precocious puberty, and prostatic hyperplasia and carcinoma (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th ed., p. 1453, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). Additionally, CPA has been used clinically in hormone replacement therapy to protect the endometrium and

decrease menopausal symptoms and the risk of osteoporotic fracture (Schneider, "The role of antiandrogens in hormone replacement therapy," *Climacteric* 3 (Suppl. 2): 21-27 (2000)).

[0047] In experiments with rats, CPA was shown to induce unscheduled DNA synthesis in vitro. After a single oral dose, continuous DNA repair activity was observed after 16 hours. CPA also increased the occurrence of S phase cells, which corroborated the mitogenic potential of CPA in rat liver (Kasper et al. (1996) Carcinogenesis 17(10): 2271-2274). CPA has also been shown to produce cirrhosis in humans (Garty et al. (1999) Eur J Pediatr 158(5): 367-370).

[0048] Diclofenac, a non-steroidal anti-inflammatory drug, has been frequently administered to patients suffering from rheumatoid arthritis, osteoarthritis, and ankylosing spondylitis. Following oral administration, diclofenac is rapidly absorbed and then metabolized in the liver by cytochrome P450 isozyme of the CYC2C subfamily (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th ed., p. 637, J.G. Hardman et al., eds., McGraw Hill, New York, 1996). In addition, diclofenac has been applied topically to treat pain due to corneal damage (Jayamanne et al., (1997) Eye 11(Pt. 1): 79-83; Dornic et al. (1998) Am J Ophthalmol 125(5): 719-721). [0049] Although diclofenac has numerous clinical applications, adverse side-effects have been associated with the drug, such as corneal complications, including corneal melts, ulceration, and severe keratopathy (Guidera et al. (2001) Ophthalmology 108(5): 936-944). Another study investigated 180 cases of patients who had reported adverse reactions to diclofenac to the Food and Drug Administration (Banks et al. (1995) Hepatology 22(3): 820-827). Of the 180 reported cases, the most common symptom was jaundice (75% of the symptomatic patients). Liver sections were taken and analyzed, and hepatic injury was apparent one month after drug treatment. An additional report showed that a patient developed severe hepatitis five weeks after beginning diclofenac treatment for osteoarthritis (Bhogaraju et al. (1999) South Med J 92(7): 711-713). [0050] In one study on diclofenac-treated Wistar rats (Ebong et al. (1998) Afr J Med Sci 27(3-4): 243-246), diclofenac treatment induced an increase in serum chemistry levels of alanine aminotransferase, aspartate aminotransferase, methaemoglobin, and total and conjugated bilirubin. Additionally, diclofenac enhanced the activity of alkaline phosphatase and 5'nucleotidase. A study on humans revealed elevated levels of hepatic

transaminases and serum creatine when compared to the control group (McKenna et al. (2001) Scand J Rheumatol 30(1): 11-18).

[0051] Diffunisal, a non-steroidal anti-inflammatory drug (NSAID), is a difluorophenyl derivative of salicylic acid (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th ed., p. 631, J.G. Hardman et al., Eds., McGraw Hill, New York, 1996). It is most frequently used in the treatment of osteoarthritis and musculoskeletal strains. NSAIDs have analgesic, antipyretic and anti-inflammatory actions, however, hepatotoxicity is known to be an adverse side effect of NSAID treatment (Masubuchi et al. (1998) J Pharmacol Exp Ther 287:208-213). Diflunisal has been shown to be less toxic than other NSAIDs, but it can eventually have deleterious effects on platelet or kidney function (Bergamo et al. (1989) Am J Nephrol 9:460-463). Other side effects that have been associated with diflunisal treatment are diarrhea, dizziness, drowsiness, gas or heartburn, headache, nausea, vomiting, and insomnia (http://arthritisinsight.com/medical/meds/dolobid.html).

[0052] In a comparative hepatotoxicity study of 18 acidic NSAIDs, diflunisal was shown to increase LDH leakage in rat hepatocytes, a marker for cell injury, when compared to control samples. Additionally, treatment with diflunisal led to decreased intracellular ATP concentrations. In a study comparing the effects of diflunisal and ibuprofen, (Muncie and Nasrallah (1989) Clin Ther 11:539-544) both drugs appeared to cause abdominal cramping, even during short-term usage. Because the toxic dosages were selected to be below the level at which gastric ulceration occurs, more severe gastrointestinal effects were not detected. But, increased serum levels of creatinine, a sign of renal injury, were also observed (Muncie et al. (1989) Clin Ther 11:539-544). [0053] Dioxin, an environmental and workplace toxin, is the name given to a class of compounds that are bi-products in the manufacture of chlorinated herbicides, pesticides and plastics. The most toxic and carcinogenic of these is 2,3,7,8-tetrachlorodibenzo-pdioxin (2,3,7,8-TCDD). Exposure to dioxin increases expression of the aromatic hydrocarbon (Ah) receptor and also increases the production of reactive oxygen species in the mitochondria. Dioxin also increases mitochondrial levels of CYP1A1, CYP1A2 and glutathione, as well as hepatocyte levels of SOD and enzymes associated with oxidative stress (Senft et al. (2002) Free Radic Biol Med 33: 1268-1278; Kern et al. (2002) Toxicology 171: 117-1125.

[0054] Another model compound, dimethylnitrosamine (DMN), is a known carcinogen and inducer of liver fibrosis and lipid peroxidation. DMN causes oxidative stress in liver cells, which may be the link between chronic liver damage and liver fibrosis. Rats treated with DMN showed diffuse fibronectin deposition, elevated hydroxyproline levels (an indicator of fibrosis), increased levels of collagens, fibrous septa, and impaired oxidative balance. Serum levels of ALT and malondialdehyde (MDA) were increased, while serum levels of SOD were decreased (Vendemiale et al. (2001) Toxicol Appl Pharmacol 175: 130-139; Liu et al. (2001) Zhonghua Gan Zang Bing Za Zhi 9 Suppl:18-20). Other studies in rats have noted severe centrilobular congestion and haemorrhagic necrosis several days after a three-day period of DMN administration. Following additional periods of DMN treatment, the rats developed centrilobular necrosis and intense neutrophilic infiltration, which progressed to severe centrilobular necrosis, fiber deposition, focal fatty deposits, bile duct proliferation, bridging necrosis and fibrosis around the central veins (cirrhosis-like symptoms). A decrease in total protein and increase in DNA were also observed (George et al. (2001) Toxicology 156: 129-138). [0055] 17α -ethinylestradiol, a synthetic estrogen, is a component of oral contraceptives, often combined with the progestational compound norethindrone. It is also used in postmenopausal estrogen replacement therapy (PDR 47th Ed., pp. 2415-2420, Medical Economics Co., Inc., Montvale, NJ, 1993; Goodman & Gilman's The Pharmalogical Basis of Therapeutics 9th Ed., pp. 1419-1422, J.G. Hardman et al. Eds., McGraw Hill, New York, 1996).

[0056] The most frequent adverse effects of 17α -ethinylestradiol usage are increased risks of cardiovascular disease: myocardial infarction, thromboembolism, vascular disease and high blood pressure, and of changes in carbohydrate metabolism, in particular, glucose intolerance and impaired insulin secretion. There is also an increased risk of developing benign hepatic neoplasia. Because this drug decreases the rate of liver metabolism, it is cleared slowly from the liver, and carcinogenic effects, such as tumor growth, may result.

[0057] 17α -ethinylestradiol has been shown to cause a reversible intrahepatic cholestasis in male rats, mainly by reducing the bile-salt-independent fraction of bile flow (BSIF) (Koopen *et al.* (1998) *Hepatology* 27: 537-545). Plasma levels of bilirubin, bile salts, aspartate aminotransferase (AST) and alanine aminotransferase (ALT) in this study were not changed. This study also showed that 17α -ethinylestradiol produced a decrease in

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plasma cholesterol and plasma triglyceride levels, but an increase in the weight of the liver after 3 days of drug administration, along with a decrease in bile flow. Further results from this study are as follows. The activities of the liver enzymes leucine aminopeptidase and alkaline phosphatase initially showed significant increases, but enzyme levels decreased after 3 days. Bilirubin output increased, although glutathione (GSH) output decreased. The increased secretion of bilirubin into the bile without affecting the plasma level suggests that the increased bilirubin production must be related to an increased degradation of heme from heme-containing proteins. Similar results were obtained in another experiment (Bouchard et al., (1993) Liver 13: 193-202) in which the livers were also examined by light and electron microscopy. Daily doses of 17α-ethinylestradiol have been shown to cause cholestasis as well, although, following drug treatment, bile flow rates gradually returned to normal (Hamada et al. (1995) Hepatology 21: 1455-1464). Liver hyperplasia, possibly in response to the effects of tumor promoters, has also been observed (Mayol (1992) Carcinogenesis 13: 2381-2388). [0058] The lipid-lowering drug gemfibrozil is a know peroxisome proliferator in liver tissue, causing both hyperplasia and enlargement of liver cells. Upon exposure to gemfibrozil, hepatocarcinogenesis has been observed in rats and mice, and a decrease in alpha-tocopherol and an increase in DT-diaphorase activity have been observed in rats and hamsters (impaired antioxidant capability). Peroxisome proliferators increase the activities of enzymes involved in peroxisomal beta-oxidation and omega-hydroxylation of fatty acids, which results in oxidative stress (O'Brien et al. (2001) Toxicol Sci 60: 271-278; Carthew et al. (1997) J Appl Toxicol 17: 47-51).

[0059] Hydrazine (NH₂=NH₂), is a component of many industrial chemicals, such as aerospace and airplane fuels, corrosion inhibitors, dyes and photographic chemicals. Its derivatives are used in pharmaceuticals such as hydrazine sulphate, used to treat cachexia in cancer patients, isoniazid, an anti-tuberculosis drug, and hydralazine, an anti-hypertensive. These drugs are metabolized *in vivo* to produce hydrazine, among other by-products. Consequently, exposure to hydrazine is by direct contact, *e.g.*, among military and airline personnel, or the result of its production in the body, *e.g.*, in patients with cancer or high blood pressure.

[0060] Studies on rat hepatocytes have shown that hydrazine causes a dose-dependent loss of viability, leakage of LDH, depletion of GSH and ATP and a decreased rate of protein synthesis (Delaney et al. (1995) Xenobiotica 25: 1399-1410). When

administered to rats, hepatotoxic changes, characterized by GSH and ATP depletion and induction of fatty liver (increases in liver weight and triglycerides, with the appearance of fatty droplets, swelling of mitochondria and appearance of microbodies) were also found to be dose-dependent (Jenner et al. (1994) Arch Toxicol 68: 349-357; Scales et al. (1982) J Toxicol Environ Health 10: 941-953). The hepatoxicity, as well as renal toxicity, associated with hydrazine exposure has been linked to free radical damage resulting from oxidative metabolism by cytochrome P4502E1 (CYP2E1), which catalyzes the conjugation of free radicals with reduced glutathione. Although exposure to hydrazine and several hydrazine derivatives increased enzyme levels in kidney tissue, increased enzyme levels were not detected in liver tissue (Runge-Morris et al. (1996) Drug Metab Dispos 24: 734-737).

[0061] The mutagenic and hepatocarcinogenic effects of hydrazine were examined in hamster livers. *In vivo*, hydrazine reacts with formaldehyde to form formaldehyde hydrazone (CH₂=N-NH₂), an alkylating intermediate that methylates guanine in DNA. Upon treatment with hydrazine, liver DNA showed the presence of methylated guanine, DNA adducts and the impairment of maintenance methylation (impaired methylation of deoxycytosine). Hepatic adenomas and carcinomas also developed in a dose-dependent manner and could be correlated with decreased maintenance methylation (FitzGerald *et al.* (1996) *Carcinogenesis* 17: 2703-2709).

[0062] Indomethacin is a non-steroidal antiinflammatory, antipyretic and analgesic drug commonly used to treat rheumatoid arthritis, osteoarthritis, ankylosing spondylitis, gout and a type of severe, chronic cluster headache characterized by many daily occurrences and jabbing pain. This drug acts as a potent inhibitor of prostaglandin synthesis; it inhibits the cyclooxygenase enzyme necessary for the conversion of arachidonic acid to prostaglandins (PDR 47th Ed., Medical Economics Co., Inc., Montvale, NJ, 1993; Goodman & Gilman's The Pharmalogical Basis of Therapeutics 9th Ed., J.G. Hardman et al. eds., pp. 1074-1075, 1089-1095, McGraw Hill, New York, 1996; Cecil Textbook of Medicine, 20th Ed., part XII, pp. 772-773, 805-808, J. C. Bennett and F. Plum Eds., W. B. Saunders Co., Philadelphia, 1996).

[0063] The most frequent adverse effects of indomethacin treatment are gastrointestinal disturbances, usually mild dyspepsia, although more severe conditions, such as bleeding, ulcers and perforations can occur. Hepatic involvement is uncommon, although some fatal cases of hepatitis and jaundice have been reported. Renal toxicity can also result,

[0064] In rats, although indomethacin produces more adverse effects in the

particularly after long-term administration. Renal papillary necrosis has been observed in rats, and interstitial nephritis with hematuria, proteinuria and nephrotic syndrome have been reported in humans. Patients suffering from renal dysfunction risk developing a reduction in renal blood flow, because renal prostaglandins play an important role in renal perfusion.

gastrointestinal tract than in the liver, it has been shown to induce changes in hepatocytic cytochrome P450. In one study, no widespread changes in the liver were observed, but a mild, focal, centrilobular response was noted. Serum levels of albumin and total protein were significantly reduced, while the serum level of urea was increased. No changes in creatinine or aspartate aminotransferase (AST) levels were observed (Falzon et al. (1985) Br J exp Path 66: 527-534). In another rat study, a single dose of indomethacin was shown to reduce liver and renal microsomal enzymes, including CYP450, and cause lesions in the GI tract (Fracasso et al. (1990) Agents Actions 31: 313-316). [0065] Menadione (vitamin K₃) is a fat-soluble vitamin precursor that is converted into menaquinone in the liver. The primary known function of vitamin K is to assist in normal blood clotting, but it may also play a role in bone calcificaton. Menadione is a quinone compound that induces oxidative stress. It has been used as an anticancer agent and radiosensitizer and can produce toxicity in the kidney, lung, heart, and liver. In the kidney, signs of toxicity are dose-dependent, ranging from minor degranulation of tubular cells at lower doses to tubular dilatation, formation of protein casts in the renal tubules, calcium mineralization, vacuolization in the proximal and distal renal tubules, granular degeneration in the cortex and necrosis and apoptosis (Chiou et al. (1997) Toxicology 124: 193-202). Toxic effects in the liver include depletion of glutathione, increased levels of Ca²⁺, increased lipid peroxidation and protein thiol oxidation, DNA strand breaks, and plasma membrane protrusions (blebs), which lead to cell degeneration. Oxidative stress induced by menadione also causes cytoskeletal abnormalities, which are related to the surface blebs (Chiou et al. (1998) Proc Natl Sci

[0066] Phenobarbital is used as an anti-epileptic, sedative or hypnotic drug and can also be used to treat neuroses with related tension states, such as hypertension, coronary artery disease, gastrointestinal disturbances and preoperative apprehension.

Counc Repub China B 22: 13-21; Mirabelli et al. (1988) Arch Biochem Biophys 264:

261-269).

Phenobarbital is also found in medications to treat insomnia and headaches (Remington: The Science and Practice of Pharmacy, 19th Ed., A. R. Gennaro ed., pp. 1164-1165, Mack Publishing Co., Easton, Pennsylvania, 1995). Although liver toxicity is not a common side effect, the drug produces elevated levels of CYP2B1, and incidences of cholestasis and hepatocellular injury have been found (Selim et al. (1999) Hepatology 29: 1347-1351; Gut et al. (1996) Environ Health Perspect 104: 1211-1218). [0067] Tacrine (1,2,3,4-tetrahydro-9-aminoacridine-hydrochloride), a strong acetylcholinesterase (AChE) inhibitor, is used in the treatment of mild to moderate cases Alzheimer's dimentias. Alzheimer's patients have synaptic loss, neuronal atrophy and degeneration of cholinergic nuclei in the forebrain, which are associated with reduced oxidative metabolism of glucose and decreased levels of ATP and acetyl CoA. Administration of AChE inhibitors, such as tacrine, is designed to increase cholinergic activity to combat this loss (Weinstock (1995) Neurodegeneration 4: 349-356). The effect seen in the patients is a reversal of the cognitive and functional decline, but the drug does not appear to change the neurodegenerative process (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th Ed., Hardman et al. eds., p. 174, McGraw Hill, New York, 1996).

[0068] Hepatotoxicty caused by tacrine is typically reversible, although cases of severe hepatotoxicity have been seen (Blackard et al. (1998) J Clin Gastroenterol 26: 57-59). The toxicity is characterized by decreased levels of protein synthesis and the release of lactate dehydrogenase, as well as by increased transaminase levels and decreased levels of ATP, glycogen and glutathione. The decrease in protein synthesis may represent a signal leading to cell death (Lagadic-Gossmann et al. (1998) Cell Biol Toxicol 14: 361-373).

[0069] Preclinical studies have failed to detect adverse hepatic events, although tacrine displayed cytotoxicity to human hepatoma cell lines and primary rat hepatocytes (Viau et al. (1993) Drug Chem Toxicol 16: 227-239). While hepatotoxicity has been found in humans, in vivo rat studies have not shown a correlation between tacrine exposure and hepatotoxicity, and the mechanism of action is not completely understood. An in vitro study comparing the reaction of human and rat liver microsomal preparations to tacrine (Woolf et al. (1993) Drug Metab Dispos 21: 874-882) showed that the two species reacted differently to the drug, suggesting that the rat may not be the best model for

monitoring tacrine-induced elevations in liver marker enzymes (Woolf et al. (1993) Drug Metab Dispos 21: 874-882).

[0070] While tacrine does not reveal classic signs of hepatotoxicity in rats, gene expression changes due to tacrine administration can be used to predict that the drug will be a liver toxin in humans. This suggests that toxicogenomics might be able to detect drugs that prove to be toxic in the clinic even when classical but more crude measures in preclinical screening fail to detect toxicity.

[0071] Thioacetamide's only significant commercial use is as a replacement for hydrogen sulfide in qualitative analyses (IARC, Vol. 7, 1974). It has also been used as a fungicide, an organic solvent in the leather, textile and paper industries, as an accelerator in the vulcanization of buna rubber, and as a stabilizer of motor fuel. The primary routes of human exposure are inhalation and skin contact with products in which thioacetamide was used as a solvent (9th Report on Carcinogens, U.S. Dept. of Health and Human Services, Public Health Service, National Toxicology Program,

http://ehp.niehs.nih.gov/roc/toc9.html). Thioacetamide is metabolized to a nonionic electrophile, leading to oxidative stress and other injurious events; both cytochrome P4502E1 and the flavin-containing monooxygenase system have been implicated in this bioactivation (R. Snyder & L. S. Andrews, Toxic Effects of Solvents and Vapors, in Casarett & Doull's Toxicology: The Basic Science of Poisons, Klaasen, ed., p. 737, McGraw-Hill, New York, 1996; Smith et al. (1983) Toxicol Appl Pharmacol 70: 467-479; Jurima-Romet et al. (1993) Biochem Pharmacol 14:46(12):2163-2170).

[0072] In exposed rats, thioacetamide was shown to accumulate in the liver and kidney, resulting in elevated levels of serum total bilirubin, aspartate aminotransferase, alanine aminotransferase, BUN, creatinine and TNFα. Impaired clearance of the toxin and increased secretion of TNFα are related to the progression of toxic effects in the liver and kidney (Nakatani et al. (2001) Liver 21(1):64-70). Additional histological changes in kidney tissue include glomerular tuft collapse and interstitial haemorrhage (Caballero et al. (2001) Gut 48: 34-40).

[0073] In the liver, low acute doses of thioacetamide induce apoptosis, while high acute doses induce necrosis (Casarett & Doull's Toxicology, supra). Long term exposure induces cirrhosis and tumors (Risteli et al. (1976) Biochem J 158: 361-367). The acute liver injury is characterized by severe perivenous necrosis, immediately followed by hepatocellular regeneration and this necrosis. Nitric oxide synthase activity and nitric

oxide release are thought to play a role in the pathophysiological mechanisms that trigger liver regeneration following thioacetamide exposure (Ala-Kokko et al. (1987) Biochem J 244: 75-79). Exposure to thioacetamide also decreases levels of antioxidants, such as SOD, glutathione peroxidase and uric acid. It also increases apoptosis, along with caspase-3 activity, and has been observed to affect hepatic nitrogen metabolism. Rates of urea production and excretion were decreased, as well as glutamate dehydrogenase activity and glutamine synthetase activity. Mitogenic activity and DNA synthesis, however, were observed to increase (Abul et al. (2002) Anat Histo Embryol 31: 66-71; Hayami et al. (1999) Biochem Pharmacol 58: 1941-1943; Masumi et al. (1999) Toxicology 135: 21-31; Maier et al. (1991) Arch Toxicol 65: 454-464). 100741 Valproate (n-dipropylacetic acid, Depakene[®]) is routinely used to treat several types of epileptic seizures- absence seizures, myoclonic seizures and tonic-clonic seizures. Most other anti-epileptics are effective against only one type. Valproate acts on neurons to inhibit the sustained repetitive firing caused by depolarization of cortical or spinal cord neurons, and a prolonged recovery of inactivated voltage-activated Na channels follows. The drug also acts by reducing the low-threshold Ca²⁺ current and its multiple mechanisms contribute to its use in multiple types of seizures. Although valproate does not affect neuronal responses to GABA, it does increase the activity of the GABA synthetic enzyme, glutamic acid decarboxylase, and it inhibits enzymes that degrade GABA, GABA transaminase and succinic semialdehyde dehydrogenase (Goodman and Gilman's The Pharmacological Basis of Therapeutics, 9th Ed., Hardman et al., eds., pp. 462, 476 and 477, McGraw-Hill, New York, 1996). [0075] The most common side effects are gastrointestinal symptoms, including anorexia, nausea and vomiting. Effects on the CNS include sedation, ataxia and tremor. Rash, hair loss, increased appetite and teratogenic effects have also been observed (Briggs et al., A Reference Guide to Fetal and Neonatal Risk. Drugs in Pregnancy and Lactation, 4th ed., p. 869, Williams & Wilkins, Baltimore, 1994). With respect to liver toxicity, valproate produces elevated levels of hepatic enzymes in about 40% of patients, which may be an asymptomatic condition, and elevated levels of hepatic lipids. Fulminant hepatitis, microvesicular steatosis (fatty degeneration), hepatocyte necrosis and hepatic failure can also result. It is believed that hepatoxicity is caused by an accumulation of unsaturated metabolites of valproate, in particular 4-en-valproate, which is structurally

similar to two known hepatotoxins, 4-en-pentanoate and methylenecyclopropylacetic acid (Eadie et al. (1988) Med Toxicol Adverse Drug Exp 3: 85-106).

acid (Eadie et al. (1988) Med Toxicol Adverse Drug Exp 3: 85-106).

[0076] In a study on rats, microvesicular steatosis caused by valproate was found to be accompanied by myeloid bodies, lipid vacuoles and mitochondrial abnormalities (Kesterson et al. (1984) Hepatology 4: 1143-1152). Experiments on cultured rat hepatocytes have shown that valproate produces a dose-dependent leakage of lactic acid dehydrogenase and increased amounts of acyl-CoA esters, compounds that interfere with the beta-oxidation of fatty acids (Vance et al. (1994) Epilepsia 35: 1016-1022).

Administration of valproate to rats has also been shown to cause enhanced excretion of dicarboxylic acids, a sign of impaired mitochondrial beta-oxidation. Other metabolic effects include hypoglycemia, hyperammonemia, decreased levels of beta-hydroxybutyrate and carnitine and decreased activities of acyl-CoA dehydrogenases, enzymes involved in fatty acid oxidation. mRNA levels of genes involved in fatty acid oxidation, however, such as the short-, medium- and long-chain acyl-CoA dehydrogenases, were found to have increased (Kibayashi et al. (1999) Pediatr Int 41: 52-60).

[0077] Wy-14643, a tumor-inducing compound that acts in the liver, has been used to study the genetic profile of cells during the various stages of carcinogenic development, with a view toward developing strategies for detecting, diagnosing and treating cancers (Rockett et al. (2000) Toxicology 144(1-3):13-29). In contrast to other carcinogens, Wy-14643 does not mutate DNA directly. Instead, it acts on the peroxisome proliferator activated receptor-alpha (PPARalpha), as well as on other signaling pathways that regulate growth (Johnson et al. (2001) J Steroid Biochem Mol Biol 77(1):59-71). The effect is elevated and sustained cell replication, accompanied by a decrease in apoptosis (Rusyn et al. (2000) Carcinogenesis 21(12):2141-2145). These authors (Rusyn et al.) noted an increase in the expression of enzymes that repair DNA by base excision, but no increased expression of enzymes that do not repair oxidative damage to DNA. In a study on rodents, Johnson et al. noted that Wy-14643 inhibited liver-X-receptor-mediated transcription in a dose-dependent manner, as well as de novo sterol synthesis. [0078] In experiments with mouse liver cells (Peters et al. (1998) Carcinogenesis 19(11):1989-1994), exposure to Wy-14643 produced increased levels of acyl CoA oxidase and proteins involved in cell proliferation: CDK-1, 2 and 4, PCNA and c-myc. Elevated levels may be caused by accelerated transcription that is mediated directly or

indirectly by PPARalpha. It is likely that the carcinogenic properties of peroxisome proliferators are due to the PPARalpha-dependent changes in levels of cell cycle regulatory proteins.

[0079] Another study on rodents (Keller et al. (1992) Biochim Biophys Acta 1102(2):237-244) showed that Wy-14643 was capable of uncoupling oxidative phosphorylation in rat liver mitochondria. Rates of urea synthesis from ammonia and bile flow, two energy-dependent processes, were reduced, indicating that the energy supply for these processes was disrupted as a result of cellular exposure to the toxin. Wy-14643 has also been shown to activate nuclear factor kappaB, NADPH oxidase and superoxide production in Kupffer cells (Rusyn et al. (2000) Cancer Res 60(17):4798-4803). NADPH oxidase is known to induce mitogens, which cause proliferation of liver cells.

[0080] The anti-asthma drug zileuton is a 5-lipoxygenase inhibitior and leukotriene synthesis inhibitor and is given to asthma patients to counter the negative effects of leukotrienes- exacerbation of the harmful effects of the inflammatory process and bronchoconstriction. Zileuton has, however, been reported to cause hepatomegaly and elevated levels of liver peroxisomal palmitoyl CoA oxidase and microsomal cytochromes P450 2B and P450 4A. The monooxygenase activities of these cytochromes was also seen to increase (Rodrigues et al. (1996) Toxicol Appl Pharmacol 137(2):193-201; Sorkness (1997) Pharmacotherapy 17(1 Pt 2):50S-54S).

[0081] LPS (lipopolysaccharide) is an endotoxin released by gram-negative bacteria upon breakage or rupture of the cells that induces an acute inflammatory response in mammals and that can cause septic shock. LPS is also a research tool used to initiate liver injury in rats through an inflammatory mechanism. Typically, the membrane components of LPS are lipid-A, KDO (2-keto-3-deoxy-octulosonic acid), core polysaccharides and O-antigen polysaccharides, the polysaccharide units differing from one bacterium to another (Zinsser Microbiology 20th Ed., Joklik et al., eds., pp. 82-87, Appleton & Lange, Norwalk, CT, 1992).

[0082] Primary rat hepatocytes derived from liver parenchymal cells and sinusoidal cells of rats that have been exposed to LPS in vivo can directly respond to LPS in cell culture. Numerous effects of LPS-induced endotoxemia can be detected, including elevated levels of nitric oxide synthetase (NOS) with increased nitric oxide and nitrite production, cellular hypertrophy, vacuolization, chromosomal emargination, cytoplasmic DNA

fragmentation and necrosis (Pittner et al. (1992) Biochem Biophys Res Commun

185(1):430-435; Laskin et al., (1995) Hepatology 22(1):223-234; Wang et al. (1995) Am J Physiol 269(2 Pt 1):G297-304). Other studies have indicated that the presence of Kupffer cells with primary rat hepatocytes is essential for the induction of hepatocyte apoptosis by LPS (Hamada et al. (1999) J Hepatol 30(5):807-818). [0083] Exposure of rats or primary hepatocytes to LPS induces the expression of a number of acute-phase proteins in the liver. Recent evidence has indicated that rat hepatocytes express soluble CD14 protein, and LPS is capable of markedly increasing levels of CD14 at both the gene expression and protein expression levels (Liu et al. (1998) Infect Immun 66(11):5089-5098). Soluble CD14 is believed to be a critical LPS recognition protein required for the activation of a variety of cells to toxic levels of LPS, even in endothelial and epithelial cells (Pugin et al. (1993) Proc Natl Acad Sci USA 90(7):2744-2748). Another key component of the LPS recognition system is lipopolysaccharide-binding protein (LBP), which binds to LPS. The LPS-LBP complex interacts with the CD14 receptor, inducing LPS sensitive genes. LBP can be induced in hepatocytes isolated from rats that have not been primed with LPS, indicating that this key regulatory pathway is intact in primary rat hepatocytes (Wan et al. (1995) Infect Immun 63(7):2435-2442).

Toxicity Prediction and Modeling

[0084] The genes and gene expression information, as well as the portfolios and subsets of the genes provided in Tables 1-5WWW, such as the core toxicity markers in Tables 5A-5WWW, may be used to predict at least one toxic effect, including the hepatotoxicity of a test or unknown compound. As used, herein, at least one toxic effect includes, but is not limited to, a detrimental change in the physiological status of a cell or organism. The response may be, but is not required to be, associated with a particular pathology, such as tissue necrosis. Accordingly, the toxic effect includes effects at the molecular and cellular level. Hepatotoxicity is an effect as used herein and includes but is not limited to the pathologies of liver necrosis, hepatitis, steatosis (fatty degeneration of the liver), carcinogenesis, cholestasis, liver enlargement, inflammation and peroxisome proliferation.

[0085] In general, assays to predict the toxicity or hepatotoxicity of a test agent (or compound or multi-component composition) comprise the steps of exposing a cell

population to the test compound, assaying or measuring the level of relative or absolute gene expression of one or more of the genes in Tables 1-5WWW and comparing the identified expression level(s) to the expression levels disclosed in the Tables and database(s) disclosed herein. Assays may include the measurement of the expression levels of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 50, 75, 100 or more genes from Tables 1-5WWW to create multi-gene expression profiles. In some instances, expression levels are assayed and compared for and to all or substantially all the genes in the tables. [0086] In the methods of the invention, the gene expression level for a gene or genes induced by the test agent, compound or compositions may be comparable to the levels found in the Tables or databases disclosed herein if the expression level varies within a factor of about 2, about 1.5 or about 1.0 fold. In some cases, the expression levels are comparable if the agent induces a change in the expression of a gene in the same direction (e.g., up or down) as a reference toxin.

[0087] The cell population that is exposed to the test agent, compound or composition may be exposed in vitro or in vivo. For instance, cultured or freshly isolated hepatocytes, in particular rat hepatocytes, may be exposed to the agent under standard laboratory and cell culture conditions. In another assay format, in vivo exposure may be accomplished by administration of the agent to a living animal, for instance a laboratory rat. [0088] Procedures for designing and conducting toxicity tests in in vitro and in vivo systems are well known, and are described in many texts on the subject, such as Loomis et al., Loomis's Esstentials of Toxicology, 4th Ed., Academic Press, New York, 1996; Echobichon, The Basics of Toxicity Testing, CRC Press, Boca Raton, 1992; Frazier, editor, *In Vitro* Toxicity Testing, Marcel Dekker, New York, 1992; and the like. [0089] In in vitro toxicity testing, two groups of test organisms are usually employed. One group serves as a control and the other group receives the test compound in a single dose (for acute toxicity tests) or a regimen of doses (for prolonged or chronic toxicity tests). Because, in some cases, the extraction of tissue as called for in the methods of the invention requires sacrificing the test animal, both the control group and the group receiving compound must be large enough to permit removal of animals for sampling tissues, if it is desired to observe the dynamics of gene expression through the duration of an experiment.

[0090] In setting up a toxicity study, extensive guidance is provided in the literature for selecting the appropriate test organism for the compound being tested, route of

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administration. dose ranges, and the like. Water or physiological saline (0.9% NaCl in water) is the solute of choice for the test compound since these solvents permit administration by a variety of routes. When this is not possible because of solubility limitations, vegetable oils such as corn oil or organic solvents such as propylene glycol may be used.

[0091] Regardless of the route of administration, the volume required to administer a given dose is limited by the size of the animal that is used. It is desirable to keep the volume of each dose uniform within and between groups of animals. When rats or mice are used, the volume administered by the oral route generally should not exceed about 0.005 ml per gram of animal. Even when aqueous or physiological saline solutions are used for parenteral injection the volumes that are tolerated are limited, although such solutions are ordinarily thought of as being innocuous. The intravenous LD₅₀ of distilled water in the mouse is approximately 0.044 ml per gram and that of isotonic saline is 0.068 ml per gram of mouse. In some instances, the route of administration to the test animal should be the same as, or as similar as possible to, the route of administration of the compound to man for therapeutic purposes.

[0092] When a compound is to be administered by inhalation, special techniques for generating test atmospheres are necessary. The methods usually involve aerosolization or nebulization of fluids containing the compound. If the agent to be tested is a fluid that has an appreciable vapor pressure, it may be administered by passing air through the solution under controlled temperature conditions. Under these conditions, dose is estimated from the volume of air inhaled per unit time, the temperature of the solution, and the vapor pressure of the agent involved. Gases are metered from reservoirs. When particles of a solution are to be administered, unless the particle size is less than about 2 µm the particles will not reach the terminal alveolar sacs in the lungs. A variety of apparatuses and chambers are available to perform studies for detecting effects of irritant or other toxic endpoints when they are administered by inhalation. The preferred method of administering an agent to animals is via the oral route, either by intubation or by incorporating the agent in the feed.

[0093] When the agent is exposed to cells *in vitro* or in cell culture, the cell population to be exposed to the agent may be divided into two or more subpopulations, for instance, by dividing the population into two or more identical aliquots. In some preferred embodiments of the methods of the invention, the cells to be exposed to the agent are

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derived from liver tissue. For instance, cultured or freshly isolated rat hepatocytes may be used.

[0094] The methods of the invention may be used to generally predict at least one toxic response, and as described in the Examples, may be used to predict the likelihood that a compound or test agent will induce various specific liver pathologies such as liver necrosis, fatty liver disease, protein adduct formation, hepatitis or other pathologies associated with at least one of the toxins herein described. The methods of the invention may also be used to determine the similarity of a toxic response to one or more individual compounds. In addition, the methods of the invention may be used to predict or elucidate the potential cellular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin (see Tables 5A-5WWW).

Diagnostic Uses for the Toxicity Markers

[0095] As described above, the genes and gene expression information or portfolios of the genes with their expression information as provided in Tables 1-5WWW may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or to identify or predict the toxic effects of a compound or agent. For instance, a tissue sample such as a sample of peripheral blood cells or some other easily obtainable tissue sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-5WWW may be compared to the expression levels found in tissues or cells exposed to the toxins described herein. These methods may result in the diagnosis of a physiological state in the cell or may be used to identify the potential toxicity of a compound, for instance a new or unknown compound or agent. The comparison of expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described below.

[0096] In another format, the levels of a gene(s) of Tables 1-5WWW, its encoded protein(s), or any metabolite produced by the encoded protein may be monitored or detected in a sample, such as a bodily tissue or fluid sample to identify or diagnose a physiological state of an organism. Such samples may include any tissue or fluid

sample, including urine, blood and easily obtainable cells such as peripheral lymphocytes.

Use of the Markers for Monitoring Toxicity Progression

[0097] As described above, the genes and gene expression information provided in Tables 1-5WWW may also be used as markers for the monitoring of toxicity progression, such as that found after initial exposure to a drug, drug candidate, toxin, pollutant, etc. For instance, a tissue or cell sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-5WWW may be compared to the expression levels found in tissue or cells exposed to the hepatotoxins described herein. The comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases.

Use of the Toxicity Markers for Drug Screening

[0098] According to the present invention, the genes identified in Tables 1-5WWW may be used as markers or drug targets to evaluate the effects of a candidate drug, chemical compound or other agent on a cell or tissue sample. The genes may also be used as drug targets to screen for agents that modulate their expression and/or activity. In various formats, a candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or markers or to down-regulate or counteract the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of a drug's effects by looking at the number of markers which the drug induces and comparing them. More specific drugs will have less transcriptional targets. Similar sets of markers identified for two drugs may indicate a similarity of effects.

[0099] Assays to monitor the expression of a marker or markers as defined in Tables 1-5WWW may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

[0100] In one assay format, gene chips containing probes to one, two or more genes from Tables 1-5WWW may be used to directly monitor or detect changes in gene expression in the treated or exposed cell. Cell lines, tissues or other samples are first

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exposed to a test agent and in some instances, a known toxin, and the detected expression levels of one or more, or preferably 2 or more of the genes of Tables 1-5WWW are compared to the expression levels of those same genes exposed to a known toxin alone. Compounds that modulate the expression patterns of the known toxin(s) would be expected to modulate potential toxic physiological effects *in vivo*. The genes in Tables 1-5WWW are particularly appropriate marks in these assays as they are differentially expressed in cells upon exposure to a known hepatotoxin.

[0101] In another format, cell lines that contain reporter gene fusions between the open reading frame and/or the transcriptional regulatory regions of a gene in Tables 1-5WWW and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam et al. (1990) Anal Biochem 188:245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

[0102] Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a gene identified in Tables 1-5WWW. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.* (Molecular Cloning: A Laboratory Manual, Third Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2001).

[0103] In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically. Cell and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (e.g., a plasmid or viral vector) construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the gene products of Tables 1-5WWW fused to one or more antigenic fragments or other detectable

markers, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct or other detectable tag. Such a process is well known in the art (see Sambrook et al., supra).

[0104] Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and/or serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells are disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (e.g., ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agentcontacted" sample is then compared with the control samples (no exposure and exposure to a known toxin) where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control is used to distinguish the effectiveness and/or toxic effects of the agent.

[0105] Another embodiment of the present invention provides methods for identifying agents that modulate at least one activity of a protein(s) encoded by the genes in Tables 1-5WWW. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

[0106] In one format, the relative amounts of a protein (Tables 1-5WWW) between a cell population that has been exposed to the agent to be tested compared to an unexposed control cell population and a cell population exposed to a known toxin may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control,

unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

[0107] Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism. [0108] As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site. [0109] The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNAs encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see G.A. Grant in: Molecular Biology and Biotechnology, Meyers, ed., pp. 659-664, VCH Publishers, New York, 1995). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Nucleic Acid Assay Formats

[0110] The genes identified as being differentially expressed upon exposure to a known hepatotoxin (Tables 1-5WWW) may be used in a variety of nucleic acid detection assays to detect or quantititate the expression level of a gene or multiple genes in a given sample. The genes described in Tables 1-5WWW may also be used in combination with one or more additional genes whose differential expression is associate with toxicity in a cell or tissue. In preferred embodiments, the genes in Tables 1-5WWW may be combined with one or more of the genes described in related U.S. applications

60/222,040, 60/244,880, 60/290,029, 60/290,645, 60/292,336, 60/295,798, 60/297,457, 60/298,884, 60/303,459, 60/331,273, 60/364,045, 60/364,055, 60/436,643, 09/917,800 and 10/060,087, all of which are herein incorporated by reference.

[0111] Any assay format to detect gene expression may be used. For example, traditional Northern blotting, dot or slot blot, nuclease protection, primer directed amplification, RT- PCR, semi- or quantitative PCR, branched-chain DNA and differential display methods may be used for detecting gene expression levels. Those methods are useful for some embodiments of the invention. In cases where smaller numbers of genes are detected, high throughput amplification-based assays may be most efficient. Methods and assays of the invention, however, may be most efficiently designed with hybridization-based methods for detecting the expression of a large number of genes.

[0112] Any hybridization assay format may be used, including solution-based and solid support-based assay formats. Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, particles, beads, microparticles or silicon or glass based chips, etc. Such chips, wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755).

[0113] Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, from 2, 10, 100, 1000 to 10,000, 100,000 or 400,000 or more of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of about a square centimeter. Probes corresponding to the genes of Tables 1-5WWW or from the related applications described above may be attached to single or multiple solid support structures, e.g., the probes may be attached to a single chip or to multiple chips to comprise a chip set.

[0114] Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart *et al.* (1996) *Nat Biotechnol* 14: 1675-1680; McGall *et al.* (1996) *Proc Nat Acad Sci* USA 93: 13555-

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13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described in Tables 1-5WWW. For instance, such arrays may contain oligonucleotides that are complementary or hybridize to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70, 100 or more the genes described herein. Preferred arrays contain all, substantially all, or nearly all of the genes listed in Tables 1-5WWW, or individually, the gene sets of Tables 5A-5WWW. In another preferred embodiment, arrays are constructed that contain oligonucleotides to detect all or nearly all of the genes in any one of or all of Tables 1-5WWW on a single solid support substrate, such as a chip.

[0115] The sequences of the expression marker genes of Tables 1-5WWW are in the

public databases. Table 1 provides the GenBank Accession Number for each of the sequences (see www.ncbi.nlm.nih.gov/). The sequences of the genes in GenBank are expressly herein incorporated by reference in their entirety as of the filing date of this application, as are related sequences, for instance, sequences from the same gene of different lengths, variant sequences, polymorphic sequences, genomic sequences of the genes and related sequences from different species, including the human counterparts, where appropriate (see Table 3). These sequences may be used in the methods of the invention or may be used to produce the probes and arrays of the invention. In some embodiments, the genes in Tables 1-5WWW that correspond to the genes or fragments previously associated with a toxic response may be excluded from the Tables. [0116] As described above, in addition to the sequences of the GenBank Accessions Numbers disclosed in the Tables 1-5WWW, sequences such as naturally occurring variant or polymorphic sequences may be used in the methods and compositions of the invention. For instance, expression levels of various allelic or homologous forms of a gene disclosed in the Tables 1-5WWW may be assayed. Any and all nucleotide variations that do not alter the functional activity of a gene listed in the Tables 1-5WWW, including all naturally occurring allelic variants of the genes herein disclosed, may be used in the methods and to make the compositions (e.g., arrays) of the invention. [0117] Probes based on the sequences of the genes described above may be prepared by any commonly available method. Oligonucleotide probes for screening or assaying a tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes

will be at least about 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases, longer probes of at least 30, 40, or 50 nucleotides will be desirable.

[0118]. As used herein, oligonucleotide sequences that are complementary to one or more of the genes described in Tables 1-5WWW refer to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequences of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

[0119] "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

[0120] The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (e.g., the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (e.g. probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all. [0121] The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or

sequences under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA.

[0122] Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 100,000 or 1,000,000 or more different nucleic acid hybridizations.

[0123] As used herein a "probe" is defined as a nucleic acid, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

[0124] The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe."

[0125] The terms "mismatch control" or "mismatch probe" refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence. For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.

[0126] While the mismatch(s) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

[0127] The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other

sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH.

[0128] Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M Na⁺ ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

[0129] The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical submit (e.g. nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

Probe design

[0130] One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of test probes that specifically hybridize to the sequences of interest. Probes may be produced from any region of the genes identified in the Tables and the attached representative sequence listing. In instances where the gene reference in the Tables is an EST, probes may be designed from that sequence or from other regions of the corresponding full-length transcript that may be available in any of the sequence databases, such as those herein described. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, any available software may be used to

produce specific probe sequences, including, for instance, software available from Molecular Biology Insights, Olympus Optical Co. and Biosoft International. In a preferred embodiment, the array will also include one or more control probes. [0131] High density array chips of the invention include "test probes." Test probes may be oligonucleotides that range from about 5 to about 500, or about 7 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 35 nucleotides in length. In other particularly preferred embodiments, the probes are about 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using native nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect. [0132] In addition to test probes that bind the target nucleic acid(s) of interest, the high density array can contain a number of control probes. The control probes may fall into three categories referred to herein as 1) normalization controls; 2) expression level

[0133] Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample to be screened. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (e.g., fluorescence intensity) read from all other probes in the array are divided by the signal (e.g., fluorescence intensity) from the control probes thereby normalizing the measurements.

controls; and 3) mismatch controls.

[0134] Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only

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one or a few probes are used and they are selected such that they hybridize well (i.e., no secondary structure) and do not match any target-specific probes.

[0135] Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typically expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

[0136] Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (e.g., stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent) Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a 20 mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (e.g., substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

[0137] Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. For example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation, for instance, a mutation of a gene in the accompanying Tables 1-5WWW. The difference in intensity between the perfect match and the mismatch probe provides a good measure of the concentration of the hybridized material.

Nucleic Acid Samples

[0138] Cell or tissue samples may be exposed to the test agent in vitro or in vivo. When cultured cells or tissues are used, appropriate mammalian liver extracts may also be added with the test agent to evaluate agents that may require biotransformation to exhibit toxicity. In a preferred format, primary isolates of animal or human hepatocytes which already express the appropriate complement of drug-metabolizing enzymes may be exposed to the test agent without the addition of mammalian liver extracts. [0139] The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may be cloned or not. The genes may be amplified or not. The cloning and/or amplification do not appear to bias the representation of genes within a population. In some assays, it may be preferable, however, to use polyA+RNA as a source, as it can be used with less processing steps. [0140] As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process. Methods of isolating total mRNA are well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 24, Hybridization With Nucleic Acid Probes: Theory and Nucleic Acid Probes, P. Tijssen, Ed., Elsevier Press, New York, 1993. Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates are used.

[0141] Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised *in vitro*, such as cell lines and tissue culture cells. Frequently the sample will be a tissue or cell sample that has been exposed to a compound, agent, drug, pharmaceutical composition, potential environmental pollutant or other composition. In some formats, the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical samples include, but are not limited to, sputum, blood, blood cells (*e.g.*, white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom.

[0142] Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

Forming High Density Arrays

[0143] Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a single or on multiple solid substrates by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling (see Pirrung, U.S. Patent No. 5,143,854).

[0144] In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing a functional group, e.g., a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithogaphic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents. [0145] In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in PCT Publication Nos. WO 93/09668 and WO 01/23614. High density nucleic acid arrays can also be fabricated by depositing pre-made or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

Hybridization

[0146] Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. See WO 99/32660. The

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nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (e.g., low temperature and/or high salt) hybrid duplexes (e.g., DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus, specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (e.g., higher temperature or lower salt) successful hybridization tolerates fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency.

[0147] In a preferred embodiment, hybridization is performed at low stringency, in this case in 6X SSPET at 37°C (0.005% Triton X-100), to ensure hybridization and then subsequent washes are performed at higher stringency (e.g., I X SSPET at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (e.g., down to as low as 0.25 X SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (e.g., expression level control, normalization control, mismatch controls, etc.).

[0148] In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

Signal Detection

[0149] The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art. See WO 99/32660.

Databases

[0150] The present invention includes relational databases containing sequence information, for instance, for the genes of Tables 1-5WWW, as well as gene expression information from tissue or cells exposed to various standard toxins, such as those herein described (see Tables 5A-5WWW). Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information (see Table 1), or descriptive information concerning the clinical status of the tissue sample, or the animal from which the sample was derived. The database may be designed to include different parts, for instance a sequence database and a gene expression database. Methods for the configuration and construction of such databases and computer-readable media to which such databases are saved are widely available, for instance, see U.S. Patent No. 5,953,727, which is herein incorporated by reference in its entirety.

[0151] The databases of the invention may be linked to an outside or external database such as GenBank (www.ncbi.nlm.nih.gov/entrez.index.html); KEGG (www.genome.ad.jp/kegg); SPAD (www.grt.kyushu-u.ac.jp/spad/index.html); HUGO (www.gene.ucl.ac.uk/hugo); Swiss-Prot (www.expasy.ch.sprot); Prosite (www.expasy.ch/tools/scnpsit1.html); OMIM (www.ncbi.nlm.nih.gov/omim); and GDB (www.gdb.org). In a preferred embodiment, as described in Tables 1-3, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI) (www.ncbi.nlm.nih.gov).

[0152] Any appropriate computer platform, user interface, etc. may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or information provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such has those available from Silicon Graphics. Client/server environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

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[0153] The databases of the invention may be used to produce, among other things, electronic Northerns that allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell.

[0154] The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising one or more of the genes in Tables 1-5WWW, comprising the step of comparing the expression level of at least one gene in Tables 1-5WWW in a cell or tissue exposed to a test agent to the level of expression of the gene in the database. Such methods may be used to predict the toxic potential of a given compound by comparing the level of expression of a gene or genes in Tables 1-5WWW from a tissue or cell sample exposed to the test agent to the expression levels found in a control tissue or cell samples exposed to a standard toxin or hepatotoxin such as those herein described. Such methods may also be used in the drug or agent screening assays as described herein.

Kits

[0155] The invention further includes kits combining, in different combinations, high-density oligonucleotide arrays, reagents for use with the arrays, protein reagents encoded by the genes of the Tables, signal detection and array-processing instruments, gene expression databases and analysis and database management software described above. The kits may be used, for example, to predict or model the toxic response of a test compound, to monitor the progression of hepatic disease states, to identify genes that show promise as new drug targets and to screen known and newly designed drugs as discussed above.

[0156] The databases packaged with the kits are a compilation of expression patterns from human or laboratory animal genes and gene fragments (corresponding to the genes of Tables 1-5WWW). In particular, the database software and packaged information that may contain the databases saved to a computer-readable medium include the expression results of Tables 1-5WWW that can be used to predict toxicity of a test agent by comparing the expression levels of the genes of Tables 1-5WWW induced by the test agent to the expression levels presented in Tables 1-5WWW. In another format, database and software information may be provided in a remote electronic format, such as a website, the address of which may be packaged in the kit.

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[0157] The kits may used in the pharmaceutical industry, where the need for early drug testing is strong due to the high costs associated with drug development, but where bioinformatics, in particular gene expression informatics, is still lacking. These kits will reduce the costs, time and risks associated with traditional new drug screening using cell cultures and laboratory animals. The results of large-scale drug screening of pre-grouped patient populations, pharmacogenomics testing, can also be applied to select drugs with greater efficacy and fewer side-effects. The kits may also be used by smaller biotechnology companies and research institutes who do not have the facilities for performing such large-scale testing themselves.

[0158] Databases and software designed for use with use with microarrays are discussed in Balaban et al., U.S. Patent Nos. 6,229,911, a computer-implemented method for managing information, stored as indexed tables and collected from small or large numbers of microarrays, and 6,185,561, a computer-based method with data mining capability for collecting gene expression level data, adding additional attributes and reformatting the data to produce answers to various queries. Chee et al., U.S. Patent No. 5,974,164, discloses a software-based method for identifying mutations in a nucleic acid sequence based on differences in probe fluorescence intensities between wild type and mutant sequences that hybridize to reference sequences.

[0159] Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

EXAMPLES

Example 1: Identification of Toxicity Markers

[0160] The hepatotoxins 2-acetylaminofluorene (2-AAF), BI liver toxin, chloroform, CI-1000, dimethylnitrosamine (DMN), gemfibrozil, menadione, thioacetamide, acyclovir, AY-25329, bicalutamide, clofibrate, colchicine, diflunisal, dioxin, hydrazine, phenobarbital, valproate, zileuton and LPS were administered to male Sprague-Dawley rats at various time points using administration diluents, protocols and dosing regimes as indicated in Table 6. The hepatotoxins ANIT, acetominophen, carbon tetrachloride, chloroform, CPA, diclofenac, 17α-ethinylestradiol, indomethacin, tacrine and Wy-14643 were administered to male Sprague-Dawley rats at various time points using administration diluents, protocols and dosing regimes as previously described in the art and previously described in the related applications discussed above.

[0161] After adminstration, the dosed animals were observed and tissues were collected as described below:

OBSERVATION OF ANIMALS

- [0162] 1. Clinical Observations- Twice daily: mortality and moribundity check.
- [0163] Cage Side Observations skin and fur, eyes and mucous membrane, respiratory system, circulatory system, autonomic and central nervous system, somatomotor pattern, and behavior pattern.
- [0164] Potential signs of toxicity, including tremors, convulsions, salivation, diarrhea, lethargy, coma or other atypical behavior or appearance, were recorded as they occurred and included a time of onset, degree, and duration.
- [0165] 2. Physical Examinations- Prior to randomization, prior to initial treatment, and prior to sacrifice.
- [0166] 3. Body Weights- Prior to randomization, prior to initial treatment, and prior to sacrifice.

CLINICAL PATHOLOGY

[0167] 1. Frequency Prior to necropsy.

[0168] 2. Number of animals All surviving animals.

[0169] 3. Bleeding Procedure Blood was obtained by puncture of the orbital sinus while under 70% CO₂/ 30% O₂ anesthesia.

[0170] 4. Collection of Blood Samples- Approximately 0.5 mL of blood was collected into EDTA tubes for evaluation of hematology parameters. Approximately 1 mL of blood was collected into serum separator tubes for clinical chemistry analysis. Approximately 200 uL of plasma was obtained and frozen at ~-80°C for test compound/metabolite estimation. An additional ~2 mL of blood was collected into a 15 mL conical polypropylene vial to which ~3 mL of Trizol was immediately added. The contents were immediately mixed with a vortex and by repeated inversion. The tubes were frozen in liquid nitrogen and stored at approximately -80° C.

TERMINATION PROCEDURES

Terminal Sacrifice

[0171] At the sampling times indicated in Table 6 for each hepatotoxin, and as previously described in the related applications mentioned above, rats were weighed, physically examined, sacrificed by decapitation, and exsanguinated. The animals were necropsied within approximately five minutes of sacrifice. Separate sterile, disposable instruments were used for each animal, with the exception of bone cutters, which were used to open the skull cap. The bone cutters were dipped in disinfectant solution between animals.

[0172] Necropsies were conducted on each animal following procedures approved by board-certified pathologists.

[0173] Animals not surviving until terminal sacrifice were discarded without necropsy (following euthanasia by carbon dioxide asphyxiation, if moribund). The approximate time of death for moribund or found dead animals was recorded.

Postmortem Procedures

[0174] Fresh and sterile disposable instruments were used to collect tissues. Gloves were worn at all times when handling tissues or vials. All tissues were collected and frozen within approximately 7 minutes of the animal's death. The liver sections were frozen within approximately 2 minutes of the animal's death. The time of euthanasia, an interim time point at freezing of liver sections and kidneys, and time at completion of necropsy were recorded. Tissues were stored at approximately -80°C or preserved in 10% neutral buffered formalin.

Tissue Collection and Processing

Liver

[0175] 1. Right medial lobe – snap frozen in liquid nitrogen and stored at ~-80°C.

[0176] 2. Left medial lobe - Preserved in 10% neutral-buffered formalin (NBF) and evaluated for gross and microscopic pathology.

[0177] 3. Left lateral lobe – snap frozen in liquid nitrogen and stored at ~-80°C.

Heart

[0178] A sagittal cross-section containing portions of the two atria and of the two ventricles was preserved in 10% NBF. The remaining heart was frozen in liquid nitrogen and stored at \sim -80°C.

Kidneys (both)

[0179] 1. Left – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at \sim -80°C.

[0180] 2. Right – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at ~ -80°C.

Testes (both)

[0181] A sagittal cross-section of each testis was preserved in 10% NBF. The remaining testes were frozen together in liquid nitrogen and stored at ~-80°C.

Brain (whole)

[0182] A cross-section of the cerebral hemispheres and of the diencephalon was preserved in 10% NBF, and the rest of the brain was frozen in liquid nitrogen and stored at \sim -80°C.

Bone marrow

[0183] Bone marrow was flushed from each femur using a syringe and fresh, cold RPMI (~1 mL of RPMI x 3 washes per femur) into two separate 15 mL conical vials, labeled to distinguish right from left femur samples. The vials were gently inverted several times after collection and maintained on wet ice.

[0184] Microarray sample preparation was conducted with minor modifications, following the protocols set forth in the Affymetrix GeneChip Expression Analysis

Manual. Frozen tissue was ground to a powder using a Spex Certiprep 6800 Freezer

Mill. Total RNA was extracted with Trizol (GibcoBRL) utilizing the manufacturer's protocol. The total RNA yield for each sample was 200-500 µg per 300 mg tissue weight. mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen) followed by ethanol precipitation. Double stranded cDNA was generated from mRNA using the SuperScript Choice system (GibcoBRL). First strand cDNA synthesis was primed with a T7-(dT24) oligonucleotide. The cDNA was phenol-chloroform extracted and ethanol precipitated to a final concentration of 1 µg/ml. From 2 µg of cDNA, cRNA was synthesized using Ambion's T7 MegaScript in vitro Transcription Kit. [0185] To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. Following a 37°C incubation for six hours, impurities were removed from the labeled cRNA following the RNeasy Mini kit protocol (Qiagen). cRNA was fragmented (fragmentation buffer consisting of 200 mM Trisacetate, pH 8.1, 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C. Following the Affymetrix protocol, 55 µg of fragmented cRNA was hybridized on the Affymetrix rat array set for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between. Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Data was analyzed using Affymetrix GeneChip® version 3.0 and Expression Data Mining (EDMT) software (version 1.0), GeneExpress2000, and S-Plus.

[0186] Table 1 discloses a set of genes that are differentially expressed upon exposure to the named toxins and their corresponding GenBank Accession and Sequence Identification numbers, the gene names if known, and the sequence cluster titles (core set and alternate set gene fragments). The human homologues of the rat genes in Table 1 are indicated in Table 3. The identities of the metabolic pathways in which the genes of Table 1 function are indicated in Table 2. The model codes in Tables 1-3 represent the various toxicity or liver pathology states that differential expression of each gene is able to identify, as well as the individual toxin or toxin type associated with differential

expression of each gene. The model codes are defined in Table 4. The GLGC ID is the internal Gene Logic identification number.

[0187] Tables 5A-5WWW disclose a core or alternate set of genes, along with the summary statistics for each of the comparisons performed as indicated in these tablesi.e., expression levels of a particular gene in toxicity group samples compared to nontoxicity group samples in response to exposure to a particular toxin, or as measured in a particular disease state. Each of these tables contains a set of predictive genes and creates a model for predicting the hepatoxicity of an unknown, i.e., untested compound. Each gene is identified by its Gene Logic identification number and can be crossreferenced to a gene name and representative SEQ ID NO. in Table 1 or in one more related applications, as mentioned on page 1. For each comparison of gene expression levels between samples in the toxicity group (samples affected by exposure to a toxin) and samples in the non-toxicity group (samples not affected by exposure to a toxin), the tox mean (for toxicity group samples) is the mean signal intensity, as normalized for the various chip parameters that are being assayed. The non-tox mean represents the mean signal intensity, as normalized for the various chip parameters that are being assayed, in non-toxicity group samples. For individual genes, an increase in the tox mean compared to the non-tox mean indicates up-regulation upon exposure to a toxin, while a decrease in the group mean compared to the non-group mean indicates down-regulation.

[0188] The mean values are derived from Average Difference (AveDiff) values for a particular gene, averaged across the corresponding samples. Each individual Average Difference value is calculated by integrating the intensity information from multiple probe pairs that are tiled for a particular fragment. The normalization multiplies each expression intensity for a given experiment (chip) by a global scaling factor. The intent of this normalization is to make comparisons of individual genes between chips possible. The scaling factor is calculated as follows:

- 1. From all the unnormalized expression values in the experiment, delete the largest 2% and smallest 2% of the values. That is, if the experiment yields 10,000 expression values, order the values and delete the smallest 200 and largest 200.
- 2. Compute the trimmed mean, which is equal to the mean of the remaining values.
- 3. Compute the scale factor SF = 100/(trimmed mean)

[0189] The value of 100 used here is the standard target valued used.

Values greater than 2.0* SD noise are assumed to come from expressors. For 101901 these values, the standard deviation SD log (signal) of the logarithms is calculated. The logarithms are then multiplied by a scale factor proportional to 1/SD log (signal) and exponentiated. The resulting values are then multiplied by another scale factor, chosen so there will be no discontinuity in the normalized values from unscaled values on either side of 2.0* SD noise. Some AveDiff values may be negative due to the general noise involved in nucleic acid hybridization experiments. Although many conclusions can be made corresponding to a negative value on the GeneChip platform, it is difficult to assess the meaning behind the negative value for individual fragments. Our observations show that, although negative values are observed at times within the predictive gene set, these values reflect a real biological phenomenon that is highly reproducible across all the samples from which the measurement was taken. For this reason, those genes that exhibit a negative value are included in the predictive set. It should be noted that other platforms of gene expression measurement may be able to resolve the negative numbers for the corresponding genes. The predictive ability of each of those genes should extend across platforms, however. Each mean value is accompanied by the standard deviation for the mean. The linear discriminant analysis score (discriminant score, or LDA), as disclosed in the tables, measures the ability of each gene to predict whether or not a sample is toxic. The discriminant score is calculated by the following steps:

Calculation of a discriminant score

[0191] Let X_i represent the AveDiff values for a given gene across the Group 1 samples, i=1...n.

[0192] Let Y_i represent the AveDiff values for a given gene across the Group 2 samples, i=1...t.

[0193] The calculations proceed as follows:

[0194] Calculate mean and standard deviation for X_i 's and Y_i 's, and denote these by m_X , m_Y , s_X , s_Y .

[0195] For all X_i 's and Y_i 's, evaluate the function $f(z) = ((1/s_Y) * \exp(-.5*((z-m_Y)/s_Y)^2)) / (((1/s_Y) * \exp(-.5*((z-m_Y)/s_Y)^2)) + ((1/s_X) * \exp(-.5*((z-m_X)/s_X)^2))).$

[0196] The number of correct predictions, say P, is then the number of Y_i 's such that $f(Y_i) > .5$ plus the number of X_i 's such that $f(X_i) < .5$.

[0197] The discriminant score is then P/(n+t).

[0198] Linear discriminant analysis (LDA) uses both the individual measurements of each gene and the calculated measurements of all combinations of genes to classify samples. For each gene a weight is derived from the mean and standard deviation of the tox and nontox groups. Every gene is multiplied by a weight and the sum of these values results in a collective discriminate score. This discriminant score is then compared against collective centroids of the tox and nontox groups. These centroids are the average of all tox and nontox samples respectively. Therefore, each gene contributes to the overall prediction. This contribution is dependent on weights that are large positive or negative numbers if the relative distances between the tox and nontox samples for that gene are large and small numbers if the relative distances are small. The discriminant score for each unknown sample and centroid values can be used to calculate a probability between zero and one as to the group in which the unknown sample belongs.

Example 2: General Toxicity Modeling

[0199] Samples were selected for grouping into tox-responding and non-tox-responding groups by examining each study individually with Principal Components Analysis (PCA) to determine which treatments had an observable response. Only groups where confidence of their tox-responding and non-tox-responding status was established were included in building a general tox model.

[0200] Linear discriminant models were generated to describe toxic and non-toxic samples. The top discriminant genes and/or EST's were used to determine toxicity by calculating each gene's contribution with homo and heteroscedastic treatment of variance and inclusion or exclusion of mutual information between genes. Prediction of samples within the database exceeded 80% true positives with a false positive rate of less than 5%. It was determined that combinations of genes and/or EST's generally provided a better predictive ability than individual genes and that the more genes and/or EST used the better predictive ability. Although the preferred embodiment includes fifty or more genes, many pairings or greater combinations of genes and/or EST can work better than individual genes. All combinations of two or more genes from the selected list could be used to predict toxicity. These combinations could be selected by pairing in an agglomerate, divisive, or random approach. Further, as yet undetermined genes and/or EST's could be combined with individual or combination of genes and/or EST's

described here to increase predictive ability. However, the genes and/or EST's described here would contribute most of the predictive ability of any such undetermined combinations.

[0201] Other variations on the above method can provide adequate predictive ability. These include selective inclusion of components via agglomerate, divisive, or random approaches or extraction of loading and combining them in agglomerate, divisive, or random approaches. Also the use of composite variables in logistic regression to determine classification of samples can also be accomplished with linear discriminate analysis, neural or Bayesian networks, or other forms of regression and classification based on categorical or continual dependent and independent variables.

Example 3: Modeling with Core Gene Set

[0202] As described in Examples 1 and 2, above, the data collected from microarray hybridization experiments were analyzed by LDA and by PCA. The genes in Tables 5A, 5C, 5D, 5E, 5F, 5G, 5I, 5K, 5L, 5M, 5N, 5O, 5Q, 5S, 5T, 5U, 5V, 5W, 5X, 5Z, 5BB, 5DD, 5FF, 5GG, 5HH, 5II, 5JJ, 5LL, 5MM, 5NN, 5PP, 5RR, 5SS, 5TT, 5UU, 5VV, 5WW, 5XX, 5ZZ, 5BBB, 5DDD, 5EEE, 5FFF, 5GGG, 5HHH, 5III, 5KKK, 5LLL, 5MMM, 5NNN, 5OOO, 5PPP, 5RRR, 5SSS, 5TTT, 5UUU and 5VVV constitute a core set of markers for predicting the hepatotoxicity of a compound. The genes in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW constitute an alternate set of markers which may also be used in the methods of the invention, although the core marker sets of Tables 5A, 5C, 5D, 5E, 5F, 5G, 5I, 5K, 5L, 5M, 5N, 5O, 5Q, 5S, 5T, 5U, 5V, 5W, 5X, 5Z, 5BB, 5DD, 5FF, 5GG, 5HH, 5II, 5JJ, 5LL, 5MM, 5NN, 5PP, 5RR, 5SS, 5TT, 5UU, 5VV, 5WW, 5XX, 5ZZ, 5BBB, 5DDD, 5EEE, 5FFF, 5GGG, 5HHH, 5III, 5KKK, 5LLL, 5MMM, 5NNN, 5OOO, 5PPP, 5RRR, 5SSS, 5TTT, 5UUU and 5VVV may be preferred in some embodiments of the invention because the core sets contain additional predictive genes. Each gene fragment in Tables 1-5WWW is assigned an LDA score, and those gene fragments in the core set are those with the highest LDA scores. The gene fragments in Tables 5A-5WWW were determined to give greater than 80% true positive results and less than 5% false positive results. Gene expression profiles prepared from expression data for these genes, in the presence and absence of toxin treatment, can be used a controls in assays of compounds whose toxic properties have not been examined. Comparison of data from

test compound-exposed and test compound-unexposed animals with the data in Tables 5A-5WWW, or with data from the core gene set controls, allows the prediction of toxic effects- or no toxic effects- upon exposure to the test compound. Thus, with a smaller gene set than in Table 1 and as described in Example 1, the core gene set can be used to examine the biological effects of a compound whose toxic properties following exposure are not known and to predict the toxicity in liver tissue of this compound.

Example 4: Modeling Methods

[0203] The above modeling methods provide broad approaches of combining the expression of genes to predict sample toxicity. One method uses each variable individually and weights them; the other combines variables as a composite measure and adds weights to them after combination into a new variable. One could also provide no weight in a simple voting method or determine weights in a supervised or unsupervised method using agglomerate, divisive, or random approaches. All or selected combinations of genes may be combined in ordered, agglomerate, or divisive, supervised or unsupervised clustering algorithms with unknown samples for classification. Any form of correlation matrix may also be used to classify unknown samples. The spread of the group distribution and discriminate score alone provide enough information to enable a skilled person to generate all of the above types of models with accuracy that can exceed discriminate ability of individual genes. Some examples of methods that could be used individually or in combination after transformation of data types include but are not limited to: Discriminant Analysis, Multiple Discriminant Analysis, logistic regression, multiple regression analysis, linear regression analysis, conjoint analysis, canonical correlation, hierarchical cluster analysis, k-means cluster analysis, selforganizing maps, multidimensional scaling, structural equation modeling, support vector machine determined boundaries, factor analysis, neural networks, bayesian classifications, and resampling methods.

Example 5: Grouping of Individual compound and Pathology Classes

[0204] Samples were grouped into individual pathology classes based on known toxicological responses and observed clinical chemical and pathology measurements or into early and late phases of observable toxicity within a compound (Tables 1-5WWW). The top 10, 25, 50, 100 genes based on individual discriminate scores were used in a model to ensure that combination of genes provided a better prediction than individual

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genes. As described above, all combinations of two or more genes from this list could potentially provide better prediction than individual genes when selected in any order or by ordered, agglomerate, divisive, or random approaches. In addition, combining these genes with other genes could provide better predictive ability, but most of this predictive ability would come from the genes listed herein.

[0205] Samples may be considered toxic if they score positive in any pathological or individual compound class represented here or in any modeling method mentioned under general toxicology models based on combination of individual time and dose grouping of individual toxic compounds obtainable from the data. The pathological groupings and early and late phase models are preferred examples of all obtainable combinations of sample time and dose points. Most logical groupings with one or more genes and one or more sample dose and time points should produce better predictions of general toxicity, pathological specific toxicity, or similarity to known toxicant than individual genes.

[0206] Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, patent applications and publications referred to in this application are herein incorporated by reference in their entirety.

TABL	E 1		torney Docket 44921-5038-01WO Document No. 1935828.1		
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
20	16901	AA799479	FF	HHs:NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	ESTs, Highly similar to NUIM_HUMAN NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (Complex I-23KD) (CI-23KD) (TYKY subunit) [H.sapiens] ESTs, Highly similar to
153	16756	AA818089	G, Н	HHs:glycyl-tRNA synthetase	SYG_HUMAN Glycyl-tRNA synthetase (GlycinetRNA ligase) (GlyRS) [H.sapiens]
727	22847	AA923982	ввв, ссс	HHs:succinate-CoA ligase, ADP-forming, beta subunit	ESTs, Moderately similar to T12480 hypothetical protein DKFZp564P2062.1 - human (fragment) [H.sapiens]
905	22283	AA945172	LL	HHs:leucine aminopeptidase 3	ESTs, Highly similar to AMPL_HUMAN Cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Proline aminopeptidase) (Prolyl aminopeptidase) [H.sapiens]
1161	16625	AA998062	A, B, N	HHs:Alg5, S. cerevisiae, homolog of	ESTs, Highly similar to T51776 dolichyl-phosphate beta- glucosyltransferase (EC 2.4.1.117) [imported] - human [H.sapiens]
1196	3082	AA999172	C, UU, General Alternate	HHs:guanine monphosphate synthetase	ESTs, Highly similar to GUAA_HUMAN GMP synthase [glutamine-hydrolyzing] (Glutamine amidotransferase) (GMP synthetase) [H.sapiens]
4266	22050	A10000050		HHs:ubiquinol- cytochrome c reductase hinge	ESTs, Moderately similar to UCRH_HUMAN Ubiquinol-cytochrome C reductase complex 11 kDa protein, mitochondrial precursor (Mitochondrial hinge protein) (Cytochrome C1, nonheme 11 kDa protein) (Complex III subunit VIII)
1266	22056	AI008066	F	protein HHs:partner of RAC1	[H.sapiens] ESTs, Highly similar to S71627 Rac1-interacting protein por1 -
1600 2066	17027	AI170679	BBB, CCC, RRR	(arfaptin 2) HHs:UDP-glucose pyrophosphorylase 2	human [H.sapiens] ESTs, Highly similar to UDP- glucose pyrophosphorylase 2; UTP-glucose-1-phosphate uridyltransferase; UDP-glucose diphosphorylase; UGPase 2 [Homo sapiens]

TABL	E 1	100 分 200 分 大 中		A	iomey Dockei 44921-5033-01WC Document No. 1935328.1
509 _, ID.::	(ID) (NO) (GTGC)	Consent Acc or Reference	Modal Code	Known Cene Name	Unigene Sequence Cluster Title
				HHs:NADH	
				dehydrogenase	ESTs, Moderately similar to
				(ubiquinone) Fe-S	S17854 NADH dehydrogenase
				protein 1 (75kD)	(ubiquinone) (EC 1.6.5.3) 75K
2000	4420	A1474262	000	(NADH-coenzyme Q	chain precursor - human
2090	4428	AI171362	ccc	reductase) HHs:NADH	[H.sapiens]
				1	ESTs, Moderately similar to
	•			dehydrogenase (ubiquinone) Fe-S	NADH dehydrogenase (ubiquinone) Fe-S protein 3
			1	protein 3 (30kD)	(30kD) (NADH-coenzyme Q
1				(NADH-coenzyme Q	reductase) [Homo sapiens]
2471	3099	AI229680	RRR	reductase)	[H.sapiens]
-	10000	A1223000	13137	neurexophilin 4	ESTs, Highly similar to
			1	(Nxph4), mRNA.	SYA_HUMAN Alanyl-tRNA
				11/2002 Length =	synthetase (AlaninetRNA ligase)
3429	23424	NM 021680	E	1265	(AlaRS) [H.sapiens]
				heterogeneous	(riidi to) [riidapidio]
				nuclear	heterogeneous nuclear
789	16944	AA925541	sss	ribonucleoprotein L	ribonucleoprotein L
— ——				heterogeneous	
			C, BBB,	nuclear	heterogeneous nuclear
789	16945	AA925541	ннн	ribonucleoprotein L	ribonucleoprotein L
				succinate	
1	i	1	v v.	dehydrogenase	succinate dehydrogenase
1			General	complex, subunit A,	complex, subunit A, flavoprotein
791	17514	AA925554	Alternate	flavoprotein (Fp)	(Fp)
3097	20589	NM 012618	O, W, VV, EEE, MMM	S100 calcium-binding protein A4 (S100a4), mRNA. 10/2002 Length = 487	S100 calcium-binding protein A4
	 			Interleukin 6 receptor	у година
1	[DD, EE,	(II6r), mRNA.	
		}	ss, ww,	11/2002 Length =	
3253	6598	NM_017020	บบบ	4614	Interleukin 6 receptor
				solute carrier family	
ł				14, member 2	
i		j		(Slc14a2), mRNA.	
				11/2002 Length =	
3398	235	NM_019347	RR	3974	Urea transporter
				5-hydroxytryptamine	
				(serotonin) receptor	
		\	Z, AA,	3a (Htr3a), mRNA.	
2550	2220	NINA 004004	MM, WW,	11/2002 Length =	5-Hydroxytryptamine (serotonin)
3556	22282	NM_024394	TTT	2230	receptor 3A
				Retinoic acid	
				receptor, alpha	
				(Rara), mRNA. 11/2002 Length =	l l
3638	12996	NM_031528	C, RR	2130 Length =	Retinoic acid receptor, alpha
3030	12330	14141_021250	U, KK	2100	reunoic acid receptor, aipha

TABL	E 1	······································		At	torney Docket 44921-5038-01WO Document No. 1935828.1
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3683	13185	NM 021755	CC DD	carcinoembryonic antigen-related cell adhesion molecule 1 (Ceacam1), mRNA. 11/2002 Length =	carcinoembryonic antigen-related cell adhesion molecule
3083	13163	NM_031755	GG, RR	carcinoembryonic antigen-related cell adhesion molecule 1 (Ceacam1), mRNA. 11/2002 Length =	carcinoembryonic antigen-related
3683	13186	NM_031755 NM_031755	L, RR GG, OO	1481 carcinoembryonic antigen-related cell adhesion molecule 1 (Ceacam1), mRNA. 11/2002 Length =	cell adhesion molecule carcinoembryonic antigen-related cell adhesion molecule
3745	5175		O, P, NN, OO, VV, EEE,	Pyruvate kinase, muscle (Pkm2), mRNA. 11/2002	
3921	17512	NM_053297	S, General Alternate	Length = 1973 succinate dehydrogenase complex, subunit A, flavoprotein (Fp) (Sdha), mRNA. 1/2002 Length =	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
3999	15380	NM_139083	F	ribosomal protein L41 (Rpl41), mRNA. 11/2002 Length = 357	ribosomal protein L41
4173	1359	U78977	XX, YY . E, I, J,	ATPase, Class II, type 9A	ATPase, Class II, type 9A
1000		750050	BB, JJ, EEE, GGG, III, JJJ, MMM,	Complement component 4 binding	Complement component 4
4290 7	1561 16950	Z50052 AA686164	SSS S, VV, PPP, QQQ	protein, beta	binding protein, beta ESTs, Highly similar to dendritic cell protein [Homo sapiens] [H.sapiens]
9	21815	AA686423	RRR, UUU	-	ESTs, Highly similar to T46390 hypothetical protein DKFZp434C1920.1 - human (fragment) [H.sapiens]

TABL	E1 .				iomey Docket 44921-5058-01WO
Seq. 1D :≟	id No.	Consini Ace or Reference	Gogo Mogaj	Known Cone Name	Unigene Sequence Cluster Title
14	18299	AA799369	N, General Alternate		ESTs, Weakly similar to 2113200F ribosomal protein S9 [Homo sapiens] [H.sapiens]
18	23293	AA799472	Z, AA		ESTs, Moderately similar to AD16_HUMAN Protein AD-016 (Protein CGI-116) (x0009) [H.sapiens]
		·			ESTs, Highly similar to hypothetical protein FLJ13725; KIAA1930 protein [Homo sapiens]
24	15303	AA799518	Q, R		[H.sapiens] ESTs, Highly similar to hypothetical protein FLJ13725;
36	16576	AA799570	Q, R		KIAA1930 protein [Homo sapiens] [H.sapiens] ESTs, Moderately similar to
					PTTG_HUMAN Pituitary tumor- transforming gene 1 protein- interacting protein (Pituitary tumor- transforming gene protein binding factor) (PTTG-binding factor)
44	19472	AA799616	c, uu		(PBF) [H.sapiens]
45	20980	AA799633	ввв, ссс		ESTs, Moderately similar to hypothetical protein MGC13016 [Homo sapiens] [H.sapiens]
63	16730	AA799766	L, FFF, HHH, OOO		ESTs, Moderately similar to JTV1; hypothetical protein PRO0992 [Homo sapiens] [H.sapiens]
75	20811	AA799899	RR		ESTs, Highly similar to R5RT18 ribosomal protein L18a, cytosolic [validated] - rat [R.norvegicus]
82	, 3915	AA800029	N		ESTs, Highly similar to T14792 hypothetical protein DKFZp586G0322.1 - human (fragment) [H.sapiens]
93	22918	AA800243	LL, PPP, QQQ, RRR, UUU		ESTs, Highly similar to CIDA_MOUSE Cell death activator CIDE-A (Cell death- inducing DFFA-like effector A) [M.musculus]
95	17206	AA800296	Z, AA		ESTs, Highly similar to PAP_HUMAN Poly(A) polymerase alpha (PAP) (Polynucleotide adenylyltransferase alpha) [H.sapiens]

TABL	፪ ୩ ∴		-	A	iomey Docket 44921-5033-0100 Document No. 1985323.1
Seq : [D	10 Kg.	Acc or Acc or Acc ol posicial	Model .	Known Cene Name	Unigene Sequence Cluster Title
	معبات حدا	i consession in		baneann eenne acenne	
		1			ESTs, Highly similar to
1			XX, YY,		peroxisomal farnesylated protein;
96	17187	AA800315	BBB, CCC		Housekeeping gene, 33kD [Homo
30	17 107	74000313	1555, CCC		sapiens] [H.sapiens] ESTs, Moderately similar to
					A54854 Ras GTPase activating
1			General		,
107	17997	AA800671	Alternate		protein-related protein - human [H.sapiens]
107	17337	7~000071	Alternate		ESTs, ESTs, Highly similar to
	1				
1		ļ			MLF2_MOUSE Myeloid leukemia
120	10320	AA800855	DD CC		factor 2 (Myelodysplasia-myeloid
120	10320	AA600655	вв, сс		leukemia factor 2) [M.musculus]
1	Ì				ESTs, Highly similar to
					transcriptional adaptor 3-like,
1464	2700	1 4040400			isoform a [Homo sapiens]
161	3709	AA818192	UU		[H.sapiens]
					ESTs, Highly similar to
1	j				S3A3_MOUSE Splicing factor 3A
		1			subunit 3 (Spliceosome
1					associated protein 61) (SAP 61)
176	6234	AA818612	F		(SF3a60) [M.musculus]
İ	1	•			ESTs, Highly similar to T47140
	l				hypothetical protein
			_		DKFZp761K1115.1 - human
211	7208	AA819337	F		(fragment) [H.sapiens]
					ESTs, Weakly similar to JC5707
			U, SSS,		HYA22 protein - human
219	6281	AA819517	บบบ		[H.sapiens]
					ESTs, Highly similar to
					SNX4_HUMAN Sorting nexin 4
222	15117	AA819623	00		[H.sapiens]
1	İ				EST, Highly similar to T08750
Ì					hypothetical protein
l			PPP,		DKFZp586E1519.1 - human
231	20668	AA819749	QQQ		(fragment) [H.sapiens]
1					ESTs, Weakly similar to T46904
			CC, PP,		hypothetical protein
			UU, III,		DKFZp761D081.1 - human
263	19412	AA849222	KKK, NNN		[H.sapiens]
			\exists		ESTs, Moderately similar to
					T08727 probable H+-transporting
		İ			ATP synthase (EC 3.6.1.34)
270	14024	AA849619	ccc		chain g - human [H.sapiens]
					ESTs, Highly similar to HLA-B
]			ļ		associated transcript-5; BAT5
			}	•	protein [Homo sapiens]
275	14608	AA849805	U		[H.sapiens]

TABL	E1 -				tomey Docker 44921-5083-0100 Document No. 1985323.1
. : Seq (D	ELEC (D No.:	CON-EML Ace or RefSeq ID +	Modd Codo	Known Cene Name	Unigana Saquanca Cluster Title
			S, JJ, KK, FFF, GGG, General		
296	1867	AA850940	Alternate	ribosomal protein L4	ribosomal protein L4
				•	ESTs, Highly similar to S26846 modifier protein 2 - mouse
311	19211	AA851329	КК, ННН		[M.musculus]
318	4941	AA851650	CCC	rap7a	EST, rap7a
					ESTs, Highly similar to
1	1				eukaryotic translation initiation
					factor 3, subunit 8 (110kD) [Homo
320	19269	AA851785	S		sapiens] [H.sapiens]
]			ESTs, Moderately similar to
l					T12501 hypothetical protein
					DKFZp434O171.1 - human
326	19158	AA851953	F		(fragment) [H.sapiens]
					ESTs, Weakly similar to solute carrier family 16 (monocarboxylic acid transporters), member 6; monocarboxylate transporter 6
328	6676	AA851967	С		[Homo sapiens] [H.sapiens]
		·			ESTs, Highly similar to I54388
342	10517	AA858600	KKK, NNN		LZTR-1 - human [H.sapiens]
					ESTs, Highly similar to CD81
	1				partner 3 [Homo sapiens]
348	12729	AA858677	XX		[H.sapiens]
			XX, YY,		ESTs, Moderately similar to mitochondrial ribosomal protein S33; mitochondrial 28S ribosomal protein S33 [Homo sapiens]
349	12829	AA858695	ccc		[H.sapiens]
					ESTs, Moderately similar to
	1		ļ .		T46317 hypothetical protein
				,	DKFZp434A0612.1 - human
369	18140	AA859240	JJ, KK		[H.sapiens]
					ESTs, Moderately similar to
	!				RP38 HUMAN Ribonuclease P
					protein subunit p38 (RNaseP
374	15160	AA859346	s		protein p38) [H.sapiens]
					ESTs, Highly similar to
					NICA MOUSE Nicastrin
376	4267	AA859412	V		precursor [M.musculus]
					ESTs, Highly similar to JC6127
]	•	[RNA-binding protein type 1 -
379	23340	AA859519	ввв, ссс		human [H.sapiens]
					ESTs, Highly similar to JC6127
			1		RNA-binding protein type 1 -
379	23341	AA859519	ccc		human [H.sapiens]

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TABL	3 1			, AS	tomey Doctet 44921-5133-011110 Document No. 1985323.1
509 ID.	GLGG ID No	TIME INDEX TO SEA TO DESIGN	Model Code	Known Cono Namo	Unigene Sequence Ciuster Title
			V, W, BB,		ESTs, Highly similar to SNX4_HUMAN Sorting nexin 4
427	15115	AA874928	cc		[H.sapiens]
			NN, PP,		ESTs, Highly similar to
			QQ, ZZ,		SNX4_HUMAN Sorting nexin 4
427	15116	AA874928	AAA		[H.sapiens]
					ESTs, Highly similar to protein translocation complex beta;
	1				protein transport protein SEC61
	1				beta subunit [Homo sapiens]
431	16215	AA874999	I, FF		[H.sapiens]
					ESTs, Weakly similar to T45062
]		! ·		hypothetical protein c316G12.3
442	15339	AA875171	UU		[imported] - human [H.sapiens]
ł					ESTs, Weakly similar to T45062
	45040				hypothetical protein c316G12.3
442	15340	AA875171	XX, YY		[imported] - human [H.sapiens] ESTs, Highly similar to
	1		N, MM,		IF39 HUMAN Eukaryotic
1	l		TTT,		translation initiation factor 3
ļ			General		subunit 9 (elF-3 eta) (elF3 p116)
444	15371	AA875205	Alternate		(eIF3 p110) [H.sapiens]
			A, B,		
1			FFF,		
		1	General		ESTs, Highly similar to
1	1	ł	Core Tox		IF39_HUMAN Eukaryotic
1		İ	Markers,		translation initiation factor 3
444	15372	AA875205	General Alternate		subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) [H.sapiens]
-	13372	AA013203	Alternate		ESTs, Highly similar to
ł	t				NUKM HUMAN NADH-
}]				ubiquinone oxidoreductase 20
l					kDa subunit, mitochondrial
			,		precursor (Complex I-20KD) (CI-
ļ					20KD) (PSST subunit)
450	15410	AA875268	III, JJJ		[H.sapiens]
					ESTs, Highly similar to A Chain A,
1	1				The Sh3 Domain Of Eps8 Exists As A Novel Intertwined Dimer
462	11889	AA875641	SS		[M.musculus]
 	1	7 3 3 3 3 3 3 4 1			ESTs, Weakly similar to protein
1]		UU, ZZ,		predicted by clone 23733 [Homo
477	21952	AA891537	AAA	·	sapiens] [H.sapiens]
					ESTs, Weakly similar to
	.	·	<u></u>		F22G12.5.p [Caenorhabditis
	1		L, BB,		elegans] [C.elegans], ESTs,
l	}		CC, NNN,		Weakly similar to IPYR_HUMAN
l		j	OOO,		Inorganic pyrophosphatase
501	11966	AA891800	General Alternate		(Pyrophosphate phosphohydrolase) (PPase) [H.sapiens]
1 <u>20 1</u>	11300	LANO3 1000	Altemate	L	inyurulase) (rrase) [ri.sapiens]

		2 (6)			Horney Docket 44921-5099-01WC Document No. 1935323.1
50g D	id ko.	Constant Acc or Reference	moce ;	Known Gone Name	Unigene Sequence Cluster Tille
	J 4000	500,000,0 <u>00</u> , <u>00</u>			ESTs, Weakly similar to
					IPYR_HUMAN Inorganic
			000,		pyrophosphatase (Pyrophosphate
			General		phospho-hydrolase) (PPase)
501	18128	AA891800	Alternate		[H.sapiens]
					ESTs, Moderately similar to
1			Q, R,		A47488 aminoacylase (EC
515	17779	AA891914	NNN		3.5.1.14) - human [H.sapiens]
					ESTs, Moderately similar to
			İ	!	uncharacterized hematopoietic
					stem/progenitor cells protein
]		MDS032 [Homo sapiens]
537	15576	AA892132	DDD		[H.sapiens]
					ESTs, Moderately similar to
1	ł	į į	A, B, X,		microsomal glutathione S-
	ł		Y, GG,	·	transferase 3; microsomal
			NN, 00,		glutathione S-transferase III
541	8317	AA892234	GGG		[Homo sapiens] [H.sapiens]
	1				ESTs, Highly similar to
	1				SYK_HUMAN Lysyl-tRNA
545	22903	A A 902250	P, VV		synthetase (LysinetRNA ligase)
345	22903	AA892250	P, VV		(LysRS) [H.sapiens] ESTs, Highly similar to T08783
	1				hypothetical protein
					DKFZp586O0120.1 - human
552	4373	AA892310	т		(fragment) [H.sapiens]
1002	1,0,0	7 4 1002010	<u> </u>		ESTs, Moderately similar to beta-
					tubulin cofactor E [Homo sapiens]
553	17405	AA892313	G, H		[H.sapiens]
			III, JJJ,		
l			KKK,		
			000,		
			General		
1			Core Tox		
	1		Markers,		ESTs, Moderately similar to
			General		hypothetical protein FLJ22353
555	22867	AA892353	Alternate		[Homo sapiens] [H.sapiens]
		0			ESTs, Highly similar to
					LCB1_MOUSE Serine
					palmitoyltransferase 1 (Long
					chain base biosynthesis protein
		İ			1) (LCB 1) (Serine-palmitoyl-CoA
EE0	0450	A A A A A A A A A A A A A	_		transferase 1) (SPT 1) (SPT1)
559	8159	AA892380	F		[M.musculus]
					ESTs, Moderately similar to Y054 HUMAN Hypothetical
566	9074	AA892465	Z, AA		protein KIAA0054 [H.sapiens]
550	30/4	~~U32400	۷, ۳۸		ESTs, Moderately similar to
				_	hypothetical protein FLJ20917
599	17923	AA892843	н	·	[Homo sapiens] [H.sapiens]
	1	. 3 .002070			[o.no outronal [rautrena]

TABL		1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	- 1		iomey Docket 44921-5088-01WC Document No. 1985328.1
Sog	©L@C	Centent Accor	Modol, ·;	72	
(D)	ווח ואסיי:	reneed in the	Receip : 1/4/2	KNOWN GOUG KRINGS	Uniciano Sequence Cluster Tille
					ESTs, Moderately similar to
			l		T00335 hypothetical protein
			N, U,		KIAA0564 - human (fragment)
614	3439	AA893000	BBB		[H.sapiens]
	1	<u> </u>			ESTs, Moderately similar to
626	3879	AA893237	T 000		hypothetical protein MBC3205 [Homo sapiens] [H.sapiens]
020	3079	AA693231	T, DDD		ESTs, Weakly similar to T46904
	1	1			hypothetical protein
1	ļ		PP, UU,		DKFZp761D081.1 - human
648	19410	AA893667	III, KKK		[H.sapiens]
1040	13410	74033007	E, BB,		[i i.sapieris]
ŀ	1		NN, PP,		
	l		QQ, EEE,		
	1		III, JJJ,		ESTs, Weakly similar to T46904
1			KKK,		hypothetical protein
]		ммм,		DKFZp761D081.1 - human
648	19411	AA893667	NNN		[H.sapiens]
					EST, Weakly similar to
	1				PDA2_HUMAN Protein disulfide
					isomerase A2 precursor (PDIp)
652	4554	AA893749	บบ		[H.sapiens]
			C, ZZ,		
1			AAA,		ESTs, Highly similar to
			General		hypothetical protein MGC17552
661	2192	AA894086	Alternate		[Homo sapiens] [H.sapiens]
					ESTs, Highly similar to
}					SYW_MOUSE Tryptophanyl-
			NN, 00,		tRNA synthetase (Tryptophan
007	4000		EEE,		tRNA ligase) (TrpRS)
687	4636	AA899491	MMM		[M.musculus]
			General		
			Core Tox Markers,		ESTo Highly similar to HI MSD2
			General		ESTs, Highly similar to HLMSP3 poliovirus receptor homolog
705	10555	AA900198	Alternate		precursor - mouse [M.musculus]
1703	10333	AA300130	Alternate		ESTs, Weakly similar to
1	1		General		Y193_HUMAN Hypothetical
733	4917	AA924140	Alternate		protein KIAA0193 [H.sapiens]
	 				ESTs, Weakly similar to
1	l				UBC3_HUMAN Ubiquitin-
	1				conjugating enzyme E2-32 kDa
}					complementing (Ubiquitin-protein
1			General		ligase) (Ubiquitin carrier protein)
740	20797	AA924310	Alternate		(E2-CDC34) [H.sapiens]
					ESTs, Weakly similar to T43481
]					probable mucin
					DKFZp434C196.1 - human
743	4942	AA924396	Q, R		(fragment) [H.sapiens]

TABL	eq.			A	tomey Decket 44921-5033-011W0
Seq .	elec elec	Constant Accor Rosson (D)		Known Cene Name	Unigene Sequence Cluster Tille
					ESTs, Highly similar to
					CSL4_HUMAN 3'-5'
754	11533	AA924716	MM, TTT	•	exoribonuclease CSL4 homolog
754	11000	77324710	IVIIVI, I I I		(CGI-108) [H.sapiens] ESTs, Highly similar to T17237
1					hypothetical protein
•					DKFZp434P106.1 - human
755	5009	AA924737	κ		(fragment) [H.sapiens]
1.00		70.027701			ESTs, Weakly similar to T03030
ŀ		ĺ	General		hypothetical protein KIAA0365 -
762	23440	AA924881	Alternate		human (fragment) [H.sapiens]
1.52		1.02.00.	ratornato		ESTs, Highly similar to T08747
ļ]			hypothetical protein
1					DKFZp586B0519.1 - human
774	22851	AA925204	FF		[H.sapiens]
					ESTs, Highly similar to T46399
					hypothetical protein
l					DKFZp434N2420.1 - human
781	5140	AA925391	บบบ		(fragment) [H.sapiens]
					ESTs, Moderately similar to
					T08732 hypothetical protein
					DKFZp566B0846.1 - human
784	12386	AA925450	LLL		(fragment) [H.sapiens]
					ESTs, Moderately similar to
]					mitochondrial ribosomal protein
812	20866	AA926098	D		L53 [Homo sapiens] [H.sapiens]
					ESTs, Moderately similar to
1					T43493 hypothetical protein
					DKFZp434C119.1 - human
821	21798	AA926365	X, DDD		[H.sapiens]
					ESTs, Highly similar to
					hypothetical protein MGC3133
824	9942	AA942697	SS		[Homo sapiens] [H.sapiens]
					ESTs, Weakly similar to T00084
					hypothetical protein KIAA0512 -
839	21993	AA943149	A, B		human [H.sapiens]
					ESTs, Highly similar to A41784
					tumor necrosis factor-alpha-
	7.00			·	induced protein B12 - human
842	7426	AA943494	MM, TTT		[H.sapiens]
			1		ESTs, Highly similar to T08795
			l		hypothetical protein
0.40	04044				DKFZp586J1822.1 - human
848	21911	AA943610	JJ, KK		(fragment) [H.sapiens]
					ESTs, Moderately similar to
					SR68_HUMAN Signal recognition
004	.4500		EEE,		particle 68 kDa protein (SRP68)
881	21522	AA944449	MMM		[H.sapiens]

TABL	3 1	-17.4	· 4 4	. A	torney Docket 44921-5088-01WO
	_ ·				Document No. 1985323.1
899 . D: ₍	ELEC	Constant Accor Reference	Model :	Known Cene Name	Unigene Sequence Cluster Title
					ESTs, Weakly similar to JC5511
	1		PPP,		TATA-binding protein-associated
886	22457	AA944572	QQQ		factor II 31 - rat [R.norvegicus]
			1		ESTs, Highly similar to T43483
					translation initiation factor IF-2
					homolog (similarity) - human
931	21974	AA945769	Q, R		(fragment) [H.sapiens]
					ESTs, Highly similar to S59641
			MM, UU,		transcription factor TFEB - mouse
952	18383	AA946421	TTT		(fragment) [M.musculus]
					ESTs, Moderately similar to
1		 			S78100 MAPK-activated protein
004	00504	44055477	_		kinase (EC 2.7.1) 2 - mouse
981	23561	AA955477	E		(fragment) [M.musculus]
					ESTs, Moderately similar to T08802 hypothetical protein
					DKFZp586D0623.1 - human
982	12407	AA955495	xx		(fragment) [H.sapiens]
902	12407	AA333433	^^		ESTs, Highly similar to T08683
1					hypothetical protein
					DKFZp564J2123.1 - human
994	12427	AA955771	Т		(fragment) [H.sapiens]
1004	12721	77.000111	<u>'</u>		ESTs, Moderately similar to
					down-regulated in lung cancer
995	23272	AA955819	x, y, ww		[Homo sapiens] [H.sapiens]
			000,	•	
ĺ	1		General		
			Core Tox		ESTs, Moderately similar to
	1		Markers,		T46373 hypothetical protein
			General		DKFZp434B2119.1 - human
1006	24366	AA956246	Alternate		(fragment) [H.sapiens]
					ESTs, Highly similar to
1	l				LSM5_HUMAN U6 snRNA-
			00, PP,		associated Sm-like protein LSm5
1009	23762	AA956431	QQ		[H.sapiens]
			i		ESTs, Weakly similar to
					C3X1_RAT CX3C CHEMOKINE
ŀ					RECEPTOR 1 (C-X3-C CKR-1)
					(CX3CR1) (FRACTALKINE
					RECEPTOR) (GPR13) (RBS11)
1017	23841	AA956693	K		[R.norvegicus]
l					COTa diable similard
					ESTs, Highly similar to
ŀ					IF3A_MOUSE EUKARYOTIC
			İ		TRANSLATION INITIATION
					FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EIF3 P167) (EIF3 P180)
			MM, WW,		(EIF3 P185) (P162 PROTEIN)
1022	5989	AA956907	TTT		(CENTROSOMIN) [M.musculus]
1022	10003	(V)300901			(CEITTICOCIVIII) [W.IIIO3CUIU3]

TABL	E1			A	tomey Docket 44921-5033-91WO
10 Seq	ELEC	CONSTRUCTION :: Reference :: : Reference :: :	Model Code	Known Cene Name	Unigaño Soquence Clustor Title
					ESTs, Highly similar to
					IF3A_MOUSE EUKARYOTIC
1	1		[TRANSLATION INITIATION
1					FACTOR 3 SUBUNIT 10 (EIF-3
					THETA) (EIF3 P167) (EIF3 P180)
Ī	ļ				(EIF3 P185) (P162 PROTEIN)
1022	5990	AA956907	L		(CENTROSOMIN) [M.musculus]
			 I, J, WW,	amino acid	
1			General	transporter system	
1046	5952	AA963102	Alternate	A2	amino acid transporter system A2
					ESTs, Moderately similar to
					T02345 hypothetical protein
					KIAA0324 - human (fragment)
1084	24166	AA964630	ww		[H.sapiens]
					ESTs, Weakly similar to
					SYW_MOUSE Tryptophanyl-
					tRNA synthetase (Tryptophan
					tRNA ligase) (TrpRS)
1095	2514	AA964944	UU, KKK	*****	[M.musculus]
					ESTs, Highly similar to T14795
		<u> </u>			hypothetical protein
1105	15885	AA965207	С		DKFZp434E171.1 - human (fragment) [H.sapiens]
1103	13003	AA303207	<u> </u>		ESTs, Moderately similar to
					JM11 protein [Homo sapiens]
1111	2809	AA996471	A, B, II		[H.sapiens]
			, -,		ESTs, Highly similar to S55370
1					RNA polymerase II chain hRPB17
1128	23930	AA997182	TT		- human [H.sapiens]
					ESTs, Highly similar to T46390
1					hypothetical protein
					DKFZp434C1920.1 - human
1142	21812	AA997588	ccc		(fragment) [H.sapiens]
	, i				ESTs, Moderately similar to
1					T17239 hypothetical protein
1440	0054	4 4 0 0 7 7 0 0	C, L, Z,		DKFZp434B027.1 - human
1148	2354	AA997763	GG, HH		(fragment) [H.sapiens]
					ESTs, Weakly similar to
1164	3367	AA998110	II, FFF		YCE3_HUMAN Hypothetical protein CGI-143 [H.sapiens]
1104	3307	~~330110	11, T I F		ESTs, Highly similar to 149668
1 1					binding protein - mouse
1176	26116	AA998471	D		[M.musculus]
					ESTs, Highly similar to I49668
			į		binding protein - mouse
1176	26117	AA998471	F, HH		[M.musculus]

TABU	3 1			, Ad	tomey Docket 44921-5033-011WO Document No. 1985323.1
Seq 10	GLEC ID No.	Consent Acc or Refseq ID	Modol Godo	Known Cene Name	Unizane Sequence Civeter Title
1177	23770	AA998488	SS		ESTs, Weakly similar to atrophin- 1 [Homo sapiens] [H.sapiens]
	<u> </u>				ESTs, Weakly similar to T51776 dolichyl-phosphate beta- glucosyltransferase (EC 2.4.1.117) [imported] - human
1180	26120	AA998619	D		[H.sapiens]
1192	3710	AA999064	Q, R		ESTs, Highly similar to T47142 hypothetical protein DKFZp761P0724.1 - human (fragment) [H.sapiens]
			B, S, GGG, PPP, ¬ QQQ, General	·	
1214	23417	AB022209	Alternate	ribonucleoprotein F	ribonucleoprotein F
1260	3148	Al007881	В		ESTs, Moderately similar to x 003 protein [Homo sapiens] [H.sapiens]
	47250	A1007004			ESTs, Moderately similar to UCRX_HUMAN Ubiquinol-cytochrome C reductase complex 7.2 kDa protein (Cytochrome C1, nonheme 7 kDa protein) (Complex III subunit X) (7.2 kDa cytochrome c1-associated protein
1264	17359	AI007981	GG		subunit) (HSPC119) [H.sapiens]
4000	3121	A10004C0	N, U, NN, OO, III, LLL, RRR,	·	ESTs, Moderately similar to T44603 hypothetical protein CGI-
1268	2193	Al008160 Al009062	DD, EE, WW		83 [imported] - human [H.sapiens] ESTs, Highly similar to hypothetical protein MGC17552 [Homo sapiens] [H.sapiens]
1315	19275	Al009460	O, P		ESTs, Moderately similar to A37098 gelation factor ABP-280, long form - human [H.sapiens]
1317	11322	A1009492	CC, UUU		ESTs, Highly similar to hypothetical protein [Homo sapiens] [H.sapiens]
1348	16035	Al010295	L		ESTs, Highly similar to hypothetical protein MGC13010 [Homo sapiens] [H.sapiens]

TABL	E1			AX	tomey Docket 44921-5063-011W0 Document No. 1665323.1
509 ID	id kie Gree	Consent Acc or Refeq ID	Model ; Code	Knewn Cene Name	Unigana Saquanca Cluster Title
					ESTs, Moderately similar to
					T00637 hypothetical protein
					H_GS541B18.1 - human
1376	24022	AI011474	DDD		(fragment) [H.sapiens]
	1				ESTs, Moderately similar to
	10000	1,,,,,,,,,	_		JC5707 HYA22 protein - human
1377	12629	Al011492	F		[H.sapiens]
					ESTs, Highly similar to T47183
	1	1			hypothetical protein DKFZp434K1822.1 - human
1379	7060	AI011547	ZZ, AAA		(fragment) [H.sapiens]
13/9	7000	AI011347	22, 200		ESTs, Moderately similar to
					S21977 Pm5 protein - human
1383	23768	AI011709	Υ		[H.sapiens]
1000	20.00	7.1011100	 		ESTs, Highly similar to T12468
l					hypothetical protein
					DKFZp564O123.1 - human
1391	18684	AI011812	ZZ, AAA		[H.sapiens]
					ESTs, Weakly similar to A61231
İ			JJ, QQ,		myosin heavy chain nonmuscle
1403	16783	AI012215	ннн		form A - human [H.sapiens]
					ESTs, Moderately similar to
					T02246 hypothetical protein
1432	11197	AI012937	UU		P1.11659_4 - human [H.sapiens]
Į.	į				CCTs Highly similar to
	}				ESTs, Highly similar to SRE1_RAT Sterol regulatory
Ì					element binding protein-1
			1		(SREBP-1) (Sterol regulatory
		1	I, J, III,		element-binding transcription
	l	,	JJJ, KKK,	\	factor 1) (Adipocyte determination
			General		and differentiation-dependent
1437	11191	AI013042	Alternate		factor 1) (ADD1) [R.norvegicus]
		1			ESTs, Highly similar to T12539
					hypothetical protein
					DKFZp434J154.1 - human
1448	12794	AI013442	R		[H.sapiens]
					ESTs, Moderately similar to
					BMP6_RAT BONE
					MORPHOGENETIC PROTEIN 6
		i			PRECURSOR (BMP-6) (VG-1-
					RELATED PROTEIN) (VGR-1)
1452	7274	AI013715	U		[R.norvegicus]
					ESTs, Moderately similar to
4450	00500	1040740	O, P,		S32567 A4 protein - human
1453	22592	AI013740	UUU		[H.sapiens]
]				ESTs, Highly similar to T46332
					hypothetical protein DKFZp434H0413.1 - human
1461	9885	AI013878	LL		(fragment) [H.sapiens]
1701	19000	MO 13010	<u> </u>		(mayment) [m.sapiens]

TABL	E1				iotney Decket 44921-5033-011WO Document No. 1995323.1
S09 10:	ELEC	CONSON ID	Model		Unijene Sequence Cluster Tille
1486	7420	Al029291	U		ESTs, Highly similar to CLPX_MOUSE ATP-dependent CLP protease ATP-binding subunit ClpX-like, mitochondrial precursor [M.musculus]
			E, DD, UU, III, JJJ, KKK, NNN, General		ESTs, Moderately similar to SYEP_HUMAN Bifunctional aminoacyl-tRNA synthetase [Includes: Glutamyl-tRNA synthetase (GlutamatetRNA ligase); Prolyl-tRNA synthetase (ProlinetRNA ligase)]
1518	23273	Al029450 Al030738	Alternate VV, WW		[H.sapiens] ESTs, Moderately similar to down-regulated in lung cancer [Homo sapiens] [H.sapiens]
1593	5877	Al045768	บบบ		ESTs, Moderately similar to T08692 hypothetical protein DKFZp564K112.1 - human (fragment) [H.sapiens]
1603	18172	AI058364	EE, WW		ESTs, Weakly similar to G02313 CDC37 homolog - human [H.sapiens] ESTs, Moderately similar to
1607	10069	AI058503	III, JJJ		Y247_HUMAN Hypothetical protein KIAA0247 [H.sapiens] ESTs, Highly similar to 2122208A
1636	8315	Al059389	SSS, UUU		adenylosuccinate synthetase:ISOTYPE=muscle [Mus musculus] [M.musculus]
1652	8132	Al060050	General Core Tox Markers, General Alternate		ESTs, Highly similar to NGP1_HUMAN Autoantigen NGP- 1 [H.sapiens]
1671	18	Al070195	RR		ESTs, Highly similar to T42648 hypothetical protein DKFZp434C1415.1 - human [H.sapiens]
1678	22684	Al070323	vv		ESTs, Highly similar to AR34_HUMAN ARP2/3 complex 34 kDa subunit (P34-ARC) (Actin- related protein 2/3 complex subunit 2) [H.sapiens]
1686	514	Al070584		matrix metalloproteinase 14, membrane-inserted	matrix metalloproteinase 14, membrane-inserted

TABL	E 1	Mark Market Street Barrier		A	tomey Doctet 44921-5033-011WO Document No. 1935323.1
Seq :	@ 7.0° ;;	Consink Accor Rasson ID	Model :	Control Concess	Unigene Sequence Cluster Tille
٠. ١.	UD 8000018	10000000 TE	4 eeee	nanemin erane indina	ESTs, Highly similar to
1					YC97_HUMAN Hypothetical
1687	8944	AI070597	υ	J '	protein CGI-97 [H.sapiens]
1007	10344	1070337	 		ESTs, Highly similar to S50852
1	1				cleavage stimulation factor 77K
1688	8950	AI070621	lu .	İ	chain - human [H.sapiens]
1000	0000	741070021	17		ESTs, Weakly similar to S16506
l					hypothetical protein - human
1698	11596	Al071194	вв		[H.sapiens]
1000	111000	7.1071134	150		ESTs, Weakly similar to
İ	1	İ			PSS1 HUMAN
	1				Phosphatidylserine synthase I
]				(Serine-exchange enzyme I)
1713	11125	AI071867	z		[H.sapiens]
	11120	1.007	 		EST, Moderately similar to I38937
			Ì		DNA/RNA-binding protein -
1715	17673	AI071895	RR		human (fragment) [H.sapiens]
 	1	7.1107 1000	1	<u> </u>	ESTs, Moderately similar to
}					S24B_HUMAN Protein transport
	1				protein Sec24B (SEC24-related
1778	13261	AI101465	R		protein B) [H.sapiens]
	1333				ESTs, Highly similar to
İ	1		1		hypothetical protein MGC10540
1789	21691	AI102027	T		[Homo sapiens] [H.sapiens]
			 		ESTs, Highly similar to
	1	İ			SSRB_HUMAN Translocon-
			ļ		associated protein, beta subunit
					precursor (TRAP-beta) (Signal
			EEE,		sequence receptor beta subunit)
1854	6823	Al103793	MMM		(SSR-beta) [H.sapiens]
					ESTs, Weakly similar to T46363
		}			hypothetical protein
					DKFZp434O0916.1 - human
1863	3259	AI104245	SS, TT		(fragment) [H.sapiens]
					ESTs, Highly similar to HSPC142
					protein [Homo sapiens]
1869	21922	AI104376	SS		[H.sapiens]
					ESTs, Weakly similar to NADH
					dehydrogenase (ubiquinone) 1
					beta subcomplex, 6 (17kD, B17)
1876	18509	Al104528	LL, RRR		[Homo sapiens] [H.sapiens]
					ESTs, Moderately similar to
		1			MEA6_HUMAN Meningioma-
			İ		expressed antigen 6/11 (MEA6)
1882	22957	AI104897	Q, R		(MEA11) [H.sapiens]

TABL	E1		* * * * * * * * * * * * * * * * * * *	A	tomey Docket 44921-5033-01000 Document No. 1935323.1
S09 ID ::		Centions Acc or Roseq ID	Model (Code)	Known Cene Name	Unigene Sequence Cheder Tide
			General		ESTs, Moderately similar to EBNA1 binding protein 2; nucleolar protein p40; homolog of yeast EBNA1-binding protein; nuclear FGF3 binding protein;
1004	24275	A1404070	Core Tox		EBNA1-binding protein 2 [Homo
1959	7414	Al104979 Al137586	Markers		sapiens] [H.sapiens] ESTs, Highly similar to IMB3_HUMAN Importin beta-3 subunit (Karyopherin beta-3 subunit) (Ran-binding protein 5) [H.sapiens]
1962	12654	Al137864	QQQ		ESTs, Highly similar to MG15_HUMAN Transcription factor-like protein MRG15 (MORF-related gene 15 protein) (MSL3-1 protein) (Protein HSPC008/HSPC061) [H.sapiens]
					ESTs, Moderately similar to hypothetical protein FLJ13222; likely ortholog of mouse testis expressed gene 27 [Homo
1967	11588	Al138121	V, AA III, JJJ, OOO, General Core Tox Markers, General		ESTs, Moderately similar to YCD1_HUMAN Hypothetical
1986	13167	AI145832	Alternate		protein CGI-131 [H.sapiens] ESTs, Moderately similar to
2014	20891	Al169337	А, В, ННН		CGB7_HUMAN Hypothetical protein CGI-117 (Protein HSPC111) [H.sapiens]
2023	23260	AI169617	мм, ттт		ESTs, Highly similar to Y124_HUMAN Hypothetical protein KIAA0124 [H.sapiens]
2025	18343	AI169648	ww		ESTs, Highly similar to RT25_MOUSE Mitochondrial 28S ribosomal protein S25 (MRP-S25) [M.musculus]
2026	24146	A1160669	D		ESTs, Weakly similar to ATP- binding cassette, sub-family F, member 2 [Homo sapiens]
2026	19884	AI169668 AI170501	R PP, QQ, YY		[H.sapiens] ESTs, Moderately similar to 0806162H protein URF3 [Mus musculus] [M.musculus]

TABL	E 1.	e – Frankja Polikija	Control of the Contro	#AM	tomey,Docket 44921-5033-011W0
509. D	ELEC. (CL)	Consons Acc or Reference	Model Code	Known Gene Name	Unigane Sequence Cluster Title
					ESTs, Moderately similar to COQ6_HUMAN Putative ubiquinone biosynthesis
2058	24048	AI170570	s		monooxgenase COQ6 (CGI-10) [H.sapiens]
2071	1923	Al170754	Q, R		ESTs, Highly similar to T50836 Yippee protein [imported] - human (fragment) [H.sapiens]
2081	5953	Al171231	C, I, MM,	amino acid transporter system A2	amino acid transporter system A2
2001				, u	ESTs, Highly similar to JC2472 brain and reproductive organ-
2085	3664	Al171289	GG		expressed protein - human [H.sapiens] ESTs, Moderately similar to
2093	22958	AI171374	Q, R, FF		MEA6_HUMAN Meningioma- expressed antigen 6/11 (MEA6) (MEA11) [H.sapiens]
2108	18994	Al171759	вв, сс		ESTs, Moderately similar to beta- tubulin cofactor E [Homo sapiens] [H.sapiens]
2.00	1000				ESTs, Highly similar to CGB0_HUMAN Hypothetical
2110	15109	AI171768	บบบ		protein CGI-110 (Protein HSPC175) [H.sapiens] ESTs, Highly similar to T08675
2115	3266	AI171948	FFF, General Alternate		hypothetical protein DKFZp564F0522.1 - human (fragment) [H.sapiens]
2117	18325	Al171953	Υ	glutamate receptor, ionotropic	glutamate receptor, ionotropic ESTs, Highly similar to T46333
2123	23422	AI172034	O, P, CC		hypothetical protein DKFZp434J1813.1 - human (fragment) [H.sapiens]
2130	6057	AI172102	E, DD, EE		ESTs, Highly similar to STXH_HUMAN Syntaxin 18 [H.sapiens]
					ESTs, Highly similar to mitochondrial ribosomal protein
2133	11416		S, EEE, MMM		L49; chromosome 11 open reading frame 4 [Homo sapiens] [H.sapiens]
2135	20867	Al172214	F		ESTs, Moderately similar to mitochondrial ribosomal protein L53 [Homo sapiens] [H.sapiens]

					M
TABL	1			A A	tomey Docket 44921-5033-91WO Document No. 1995323.1
		(Gen): ank	1		
Seq	@L@C	Accor.	Model :	· .	
(D)	(D) (100.=	RefSeq ID	Codo:	Known Cone Name	Unigene Sequence Cluster Title
					ESTs, Moderately similar to
	1		4		LPRC_HUMAN 130 kDa leucine-
1					rich protein (LRP 130) (GP130)
1			ccc,		(Leucine-rich PPR-motif
2140	11525	AI172286	RRR, SSS		containing protein) [H.sapiens]
					ESTs, Highly similar to DEAD/H
					(Asp-Glu-Ala-Asp/His) box
l					polypeptide 1; DEAD/H box-1
2143	15842	AI172325	FFF		[Homo sapiens] [H.sapiens]
l					ESTs, Highly similar to
1					PRLP_HUMAN Prolargin
1	ļ				precursor (Proline-arginine-rich end leucine-rich repeat protein)
2181	23311	AI176003	Z, AA		[H.sapiens]
2.01	20011	71170000	A, Y.		[i i.sapieris]
			GGG,		1
	1		QQQ,		ESTs, Moderately similar to
		İ	General		SCO2_HUMAN SCO2 protein
1			Core Tox		homolog, mitochondrial precursor
2195	19363	Al176247	Markers		[H.sapiens]
					ESTs, Moderately similar to
i					C560_HUMAN Succinate
•		}			dehydrogenase cytochrome B560
					subunit, mitochondrial precursor
					(QPS1) (CII-3) (Succinate
					dehydrogenase complex subunit
					C) (Succinate-ubiquinone
2203	20001	AI176396	LL		oxidoreductase cytochrome B large subunit) (CYBL) [H.sapiens]
2200	20001	A1170000			ESTs, Highly similar to S41115
					probable flavoprotein-ubiquinone
					oxidoreductase (EC 1.6.5) -
2205	17920	AI176422	lu l		human [H.sapiens]
					ESTs, Weakly similar to T00065
					hypothetical protein KIAA0442 -
2210	13678	Al176490	ww		human (fragment) [H.sapiens]
	\				
· ·			J, General		
			Core Tox		ESTs, Highly similar to
			Markers,		NSDL_MOUSE NAD(P)-
0057	40050	A1477455	General		dependent steroid
2257	12958	Al177155	Alternate		dehydrogenase [M.musculus]
					ESTs, Moderately similar to
					COQ6_HUMAN Putative
			к, ү,		ubiquinone biosynthesis monooxgenase COQ6 (CGI-10)
2264	24049	Al177341	DDD		[H.sapiens]
2204	27043	/W11/1041	000		[i i.sahisi is]

TABL				A	Normay Docket 44921-5033-01WO Document No. 1985323.1
809 D	GLEC		Modal (2)	Kinoxun Gened Klame	Unigene Sequence Cluster Title
					EST, Highly similar to T08750
1	1		1		hypothetical protein
					DKFZp586E1519.1 - human
l					(fragment) [H.sapiens], ESTs,
1					Highly similar to T08750
1	i	ļ	Ĭ		hypothetical protein
					DKFZp586E1519.1 - human
2273	20669	AI177590	GG		(fragment) [H.sapiens]
					ESTs, Weakly similar to S69890
	1				mitogen inducible gene mig-2 -
2274	6315	AI177645	VV		human [H.sapiens]
					ESTs, Highly similar to T14743
1	ł		i		hypothetical protein
			1		DKFZp586F1524.1 - human
2283	3834	AI177902	X, Y		(fragment) [H.sapiens]
					ESTs, Highly similar to T46366
			1		hypothetical protein
					DKFZp434C0118.1 - human
2288	16739	AI178151	C, HH		(fragment) [H.sapiens]
				phosphatidylinositol	phosphatidylinositol glycan, class
2293	1050	Al178219	V	glycan, class L	L
			ннн,		ESTs, Highly similar to T03842
	ì		General		fission yeast Skb1 protein
2322	11660	AI178944	Alternate		homolog - human [H.sapiens]
					ESTs, Highly similar to
1	1	1			CN01_HUMAN Protein C14orf1
			Q, R,		(HSPC288) (Protein AD-011)
2326	13055	AI179100	FFF		(x0006) [H.sapiens]
			1		ESTs, Highly similar to B Chain B,
				ļ	Three-Dimensional Structure Of
	İ				Human Electron Transfer
	1	ļ			Flavoprotein To 2.1 A Resolution
2331	17358	AI179147	PP, QQ		[H.sapiens]
					ESTs, Moderately similar to
					JC4760 SMT3 protein - human
2357	12516	AI179651	บบ		[H.sapiens]
			1		ESTs, Highly similar to T17270
l	1	1	1	}	hypothetical protein
		1	1		DKFZp434N241.1 - human
2363	14586	Al179865	LLL		(fragment) [H.sapiens]
		·			
1			1 .		ESTs, Highly similar to 1604368A
					gap junction protein Cx26 [Rattus
2369	23989	AI179953	PP		norvegicus] [R.norvegicus]
			111, 111,		
	1		General		ESTs, Moderately similar to
			Core Tox		hypothetical protein FLJ21634
2371	22569	AI179979	Markers		[Homo sapiens] [H.sapiens]

TABL	EI			A	10mey Docket 4/12/1-5033-0/1WC Document No. 1935323.1
Seq (3919 (II)	CONSERV AGG OT RESESTED	Modal .	Kinoxyin Centel Neme	Unigene Sequence Cluster Title
	1000,000	100.0000	ease:	Transcom codes activities	ESTs, Highly similar to S50853
			1		translation releasing factor eRF-1
2381	5481	Al180170	Z, AA		[validated] - human [H.sapiens]
2001	10401	7.1100170	2, 7		ESTs, Weakly similar to
		1	1	ĺ	Y310_HUMAN Hypothetical
2388	12556	AI180376	TT		protein KIAA0310 [H.sapiens]
2300	112000	171100370	N, HH,		ESTs, Highly similar to NBRT
		1	TT, XX,		apolipoprotein H precursor - rat
2390	7460	Al180413	YY		[R.norvegicus]
2390	17400	A1100413	D, BBB,		ESTs, Highly similar to
	İ	l	CCC,		
2422	24922	11220642			hypothetical protein MGC1936
2432	21822	Al228642	RRR		[Homo sapiens] [H.sapiens]
	[1	[ESTs, Highly similar to S27958
0.450	44507	41000007	{		transcription factor BTF2 62K
2456	11527	Al229307	ZZ		chain - human [H.sapiens]
		i	1		ESTs, Moderately similar to
		i			nucleolar cysteine-rich protein;
	1	1		,	zinc finger autoantigen 330
2457	2615	Al229318	K, Q		[Homo sapiens] [H.sapiens]
	1			,	ESTs, Highly similar to S30034
 		İ		,	translocating chain-associating
					membrane protein - human
2468	17245	AI229630	Τ		[H.sapiens]
			ļ ·		ESTs, Weakly similar to
	1	1			SERC_HUMAN Phosphoserine
		i .			aminotransferase (PSAT)
2484	15862	AI230228	ZZ, AAA		[H.sapiens]
	[1		ESTs, Weakly similar to T46458
	1			•	hypothetical protein
	1	1	i		DKFZp434M102.1 - human
2490	7084	Al230362	НН		(fragment) [H.sapiens]
					ESTs, Highly similar to S13293
		ĺ			KDEL receptor - human
2495	7416	AI230458	MM, TTT		[H.sapiens]
					ESTs, Weakly similar to T17271
		İ			hypothetical protein
	1				DKFZp434B0335.1 - human
2496	7881	AI230528	N		[H.sapiens]
					ESTs, Highly similar to HMBA-
			F, LLL,		inducible [Homo sapiens]
2510	8036	Al230884	SSS, UUU		[H.sapiens]
	1				EST, Weakly similar to T46347
					hypothetical protein
					DKFZp434K0614.1 - human
2514	13933	Al230991	i, j		(fragment) [H.sapiens]
	<u> </u>	<u> </u>			ESTs, Highly similar to KIAA1049
					protein [Homo sapiens]
2521	14303	AI231159	PP, QQ		[H.sapiens]
		1			(· · · = F · F · · F · F · F · F · F · F · F ·

TABL	E 1				iomey Docket 4/1921-5083-01/WO Document No. 1985323.1
\$9 ©.	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	Kentenk Accor Refseq ID	Model	Known Cede Kaine	Unigano Soquance Cluster Title
2530	13963	AI231388	11	LIDO:	ESTs, Highly similar to T17328 hypothetical protein DKFZp564K1964.1 - human [H.sapiens]
2536	13469	Al231479	w	UDP- glucose:ceramide glycosyltransferase	UDP-glucose:ceramide glycosyltransferase
2537	16073	Al231489	II		ESTs, Weakly similar to PCB3_MOUSE Poly(rC)-binding protein 3 (Alpha-CP3) [M.musculus]
2540	19271	Al231566	тт		ESTs, Highly similar to MAX_RAT MAX protein [R.norvegicus]
2553	24501	Al232006	General Alternate	translation elongation factor 1-delta subunit	
2562	13056	Al232155	FFF		ESTs, Highly similar to CN01_HUMAN Protein C14orf1 (HSPC288) (Protein AD-011) (x0006) [H.sapiens]
2584	3661	Al232506	м		ESTs, Weakly similar to T46908 hypothetical protein DKFZp761G2423.1 - human [H.sapiens]
2585	11269	Al232510	E		ESTs, Highly similar to T08712 hypothetical protein DKFZp566C0424.1 - human (fragment) [H.sapiens]
2605	17240	Al233054	N, QQ, XX, YY		ESTs, Weakly similar to UCRQ_HUMAN Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C (Ubiquinol-cytochrome C reductase complex 9.5 kDa protein) (Complex III subunit VII) [H.sapiens]
2627	18900	Al233570	X, Y, LLL, SSS, UUU		PSDs, Highly similar to PSDs_HUMAN 26S proteasome non-ATPase regulatory subunit 8 (26S proteasome regulatory subunit S14) (p31) [H.sapiens]

TABL	፪ ١ ়.			A	tomey Doctet 44921-5033-01WO Document No. 1985323.1
S 39	id ho Grec	Conson: Accor Refeed ID :	Model Coole	Known Cene Name	Unicia Sequence Cluster Title
					ESTs, Highly similar to
		1			SYR HUMAN ARGINYL-TRNA
	<u> </u>		FFF,		SYNTHETASE (ARGININE
	1		GGG,		TRNA LIGASE) (ARGRS)
İ			PPP,		[H.sapiens], ESTs, Moderately
	İ		General		similar to JC4365 argininetRNA
	1		Core Tox		ligase (EC 6.1.1.19) - human
2628	7888	AI233583	Markers		[H.sapiens]
			····		ESTs, Moderately similar to
ľ	1	1	General		ERHUAH coatomer complex
	l		Core Tox		alpha chain homolog - human
2633	7243	Al233717	Markers		[H.sapiens]
					ESTs, Moderately similar to
l	İ				PSD5_HUMAN 26S proteasome
					non-ATPase regulatory subunit 5
l					(26S proteasome subunit S5B)
			K, Q,		(26S protease subunit S5 basic)
2634	3816	AI233729	บบบ		[H.sapiens]
					ESTs, Highly similar to
			•		SNX6_HUMAN Sorting nexin 6
					(TRAF4-associated factor 2)
2665	17537	Al234497	VV		[H.sapiens]
					ESTs, Highly similar to .
					Y184_HUMAN HYPOTHETICAL
2690	18484	AI235349	Ζ .		PROTEIN KIAA0184 [H.sapiens]
					ESTs, Highly similar to
					mitochondrial ribosomal protein
Į.					L49; chromosome 11 open
			_		reading frame 4 [Homo sapiens]
2691	3645	Al235362	K		[H.sapiens]
İ]				ESTs, Moderately similar to
1					MAN1_HUMAN Inner nuclear
					membrane protein Man1
2695	11264	Al235493	НН	······································	[H.sapiens]
l	\				ESTs, Moderately similar to
0700					A56716 aromatic ester hydrolase
2702	11164	AI235739	A, B		(EC 3.1.1) - human [H.sapiens]
	ļ				ESTs, Moderately similar to
l	i .				T12473 hypothetical protein
0700	45000	41000500	General		DKFZp564G1762.1 - human
2736	15398	AI236566	Alternate		(fragment) [H.sapiens]
					ESTs, Highly similar to S41115
					probable flavoprotein-ubiquinone
2762	17000	A1227007			oxidoreductase (EC 1.6.5) -
2762	17922	AI237007	М		human [H.sapiens]
			0 0 00	LDC induced TMF	
2775	21652	A1227525		LPS-induced TNF-	I DS induced TNE sinhs factor
2775	21653	AI237535	EE, CCC	alpha factor	LPS-induced TNF-alpha factor

E 1			A	tomey Doctet 44921-5033-011WO
(D) (Yo.:	Accor			Unigene Sequence Cluster Title
14606	Al639342	ww		ESTs, Highly similar to YS64_HUMAN Hypothetical protein S164 [H.sapiens]
2434	Al639411	ww. fff		ESTs, Highly similar to T46344 hypothetical protein DKFZp434I1614.1 - human (fragment) [H.sapiens]
				ESTs, Highly similar to T46344 hypothetical protein DKFZp434I1614.1 - human
2435	Al639411	мм, ттт,		(fragment) [H.sapiens] ESTs, Moderately similar to 1914275A non-receptor Tyr
21864	H31144	General Alternate		kinase [Homo sapiens] [H.sapiens] ESTs, Moderately similar to
17913	H31707	BB, CC		T50621 hypothetical protein DKFZp762O076.1 - human (fragment) [H.sapiens]
4360	H31813	B, I, J, XX, YY, PPP, QQQ		ESTs, Moderately similar to T14781 hypothetical protein DKFZp586B1621.1 - human (fragment) [H.sapiens]
1336	L01267	PPP, QQQ		general transcription factor IIF, polypeptide 2 (30kD subunit)
4225	M31322	GG	sperm membrane protein (YWK-II)	sperm membrane protein (YWK-II)
1586	M57728	ввв, ссс		Rat general mitochondrial matrix processing protease (MPP) mRNA, 3' end
4940	NM_022526	U, BBB	mRNA. 12/2000 Length = 1440	гар7а
24648	NM_030985	F, LL, FFF	1a (Agtr1a), mRNA. 11/2002 Length = 1450	Angiotensin II receptor, type 1 (AT1A)
17734	NM 031970	Q, R	protein (Hsp27), mRNA. 11/2002	ESTs, Moderately similar to hypothetical protein MGC10974 [Homo sapiens] [H.sapiens], heat shock 27kD protein 1
			Heat shock 27 kDa protein (Hsp27), mRNA. 11/2002	ESTs, Moderately similar to hypothetical protein MGC10974 [Homo sapiens] [H.sapiens], heat shock 27kD protein 1
	2434 2435 2435 21864 17913 4360 1336 4225 1586 4940	Combants Acc or Ref Seq ID	CLGC Resear Model Research Model Researc	Clos Aee or RafSeq D Code Knewn Gene Name

TABL	E 1 :			A	tomey Docket 44921-5033-011W0 Document No. 1955323.1
509 ID ::		Consoni Accor: Reference	(Model : : : : : : : : : : : : : : : : : : :	emen ene name	Unigene Sequence Cluster Title
				Heat shock 27 kDa protein (Hsp27),	ESTs, Moderately similar to hypothetical protein MGC10974
3712	17736	NM_031970	Q, R, BBB, CCC	mRNA. 11/2002 Length = 787	[Homo sapiens] [H.sapiens], heat shock 27kD protein 1
				maternal G10 transcript (G10), mRNA. 11/2001	
3789	22919	NM_053556	RR	Length = 816 ATPase, vacuolar, 14	maternal G10 transcript
3846	20939	NM 053884	FFF	kD (Atp6s14), mRNA. 11/2001 Length = 667	
3040	20333	INIVI_U00004	I FF	Smhs1 protein	ATPase, vacuolar, 14 kD
3898	8820	NM_080399	S, LLL	(Smhs1), mRNA. 12/2001 Length = 1107	Smhs1 protein
3917	18027	NM 130407	K, GG, HH	UDP glycosyltransferase 1 family, polypeptide A7 (Ugt1a7), mRNA. 4/2002 Length = 2301	UDP glycosyltransferase 1 family, polypeptide A7
2025	47000			glutamate receptor, ionotropic, NMDA3B (Grin3b), mRNA. 5/2002 Length =	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal -
3935	17880	NM_133308	М	3178 GCIP-interacting protein p29 (P29), mRNA. 3/2002	human (fragments) [H.sapiens]
3940	19099	NM_133417	FF	Length = 1292 putative c-Myc- responsive (RcI), mRNA. 3/2002	GCIP-interacting protein p29
3943	21703	NM_133525	JJ, KK	Length = 564 cytosolic sorting	putative c-Myc-responsive
3964	7166	NM 134406	1 JI 1	protein PACS-1 (Pacs1), mRNA. 3/2002 Length = 4198	cytosolic sorting protein PACS-1
3304	, 100	1414100			cytosolic sorting protein PACS-1
3976	13563	NM_138530	HH, EEE,	MAWD binding protein (Mawbp), mRNA. 4/2002 Length = 1263	MAWD binding protein

TABL	E1			A	tomay Docket 44921-5088-01WC
Seq (D)		CONSERY ACC OT RefSeq ID	Model ; Code ;	Known Gene Kemie	Unigene Sequence Cluster Title
4012	22595	NM_139253	к	stem cell derived neuronal survival protein precursor (Sdnsf), mRNA. 5/2002 Length = 1771	stem cell derived neuronal survival protein precursor
4015	9775	NM_139334	z, ww	brain-enriched SH3- domain protein Besh3 (Besh3), mRNA. 11/2002 Length = 2362	brain-enriched SH3-domain protein Besh3
4015	9776	NM_139334	l, J	brain-enriched SH3- domain protein Besh3 (Besh3), mRNA. 11/2002 Length = 2362	brain-enriched SH3-domain protein Besh3
4015	9778	NM_139334	JJ, КК	brain-enriched SH3- domain protein Besh3 (Besh3), mRNA. 11/2002 Length = 2362 chloride ion pump-	brain-enriched SH3-domain protein Besh3
4022	23251	NM_145085	PP, QQ	associated 55 kDa protein (Clp55), mRNA. 11/2002 Length = 3742	Rattus norvegicus chloride ion pump-associated 55 kDa protein (Clp55) mRNA, complete cds
4033	6824	NM_147138	G, H, X, Y, GGG, HHH, LLL, SSS, UUU, General Core Tox Markers	SNAP25 interacting protein 30 (Sip30), mRNA. 11/2002 Length = 1496	Rattus norvegicus SNAP25 interacting protein 30 (Sip30) mRNA, complete cds
4050	6365	NM_153628	00	signal peptidase 21kDa subunit (Spc21), mRNA. 10/2002 Length = 679	Rattus norvegicus mRNA for signal peptidase 21kDa subunit, complete cds
4050	6366	NM_153628	CC, LL, NN, OO		Rattus norvegicus mRNA for signal peptidase 21kDa subunit, complete cds
4059	18457	S45812	XX, YY		ESTs, Highly similar to 1903159A monoamine oxidase A [Rattus norvegicus] [R.norvegicus]

TABL	E 1	. 4			iomay Docket 44921-5033-01W0 Document No. 1985323.1
S99 (D)	ID No.	Consoni Acc or Raiseg ID	Model Model	Known Cene Name	elitt reteine encepee encentue
4140	21654	U53184	Q, R, W	LPS-induced TNF- alpha factor	LPS-induced TNF-alpha factor
4177	23282	U90725	FF	lipoprotein-binding protein	lipoprotein-binding protein ESTs, Highly similar to R5RT18
4197	20810	X14181	EEE, MMM		ribosomal protein L18a, cytosolic [validated] - rat [R.norvegicus]
4203	7459	X15551	v		ESTs, Highly similar to NBRT apolipoprotein H precursor - rat [R.norvegicus]
4209	23987	X51615	B, PP, QQ, HHH		ESTs, Highly similar to 1604368A gap junction protein Cx26 [Rattus norvegicus] [R.norvegicus]
4293	8664	Z75029	Q, ZZ, AAA		ESTs, Moderately similar to T17342 hypothetical protein DKFZp586K1924.1 - human (fragment) [H.sapiens], R.norvegicus hsp70.2 mRNA for heat shock protein 70
65	13683	AA799788	General Alternate	HHs:cell division cycle 34	ESTs, Moderately similar to 154552 hypothetical serine proteinase - rat [R.norvegicus]
87	4832 13684	AA800190 AA818770	ZZ, AAA H	HHs:phosphorylase, glycogen; brain HHs:cell division cycle 34	ESTs, Highly similar to S37300 glycogen phosphorylase (EC 2.4.1.1), brain - rat [R.norvegicus] ESTs, Moderately similar to 154552 hypothetical serine proteinase - rat [R.norvegicus]
409	23336	AA859981	U, GG,	HHs:inositol(myo)- 1(or 4)- monophosphatase 2	ESTs, Weakly similar to MYOP_RAT Myo-inositol-1(or 4)- monophosphatase (IMPase) (IMP) (Inositol monophosphatase) (Lithium-sensitive myo-inositol monophosphatase A1) [R.norvegicus]
794	21821	, AA925664	LL	HHs:RAP1A, member of RAS oncogene family	ESTs, Highly similar to RAPA_HUMAN Ras-related protein RAP-1A (C21KG) (KREV- 1 protein) (GTP-binding protein SMG-P21A) (G-22K) [R.norvegicus]
1304	4833	Al009178	E	HHs:phosphorylase, glycogen; brain	ESTs, Highly similar to S37300 glycogen phosphorylase (EC 2.4.1.1), brain - rat [R.norvegicus]

TABL	E Ú		å.	A	iomey Docket 44921-5083-011WC Document No. 1935323.1
Soq ID:	id no Grec	Consonk Accor Resson ID	Model .	Known Gene Neme	
1665	17506	Al070068	I, J, L, M, Z	HHs:growth arrest and DNA-damage-inducible, beta	ESTs, Weakly similar to 2104282A Gadd45 gene [Rattus norvegicus] [R.norvegicus]
1897	23596	AI105435	w	HHs:glutaryl- Coenzyme A dehydrogenase	ESTs, Highly similar to GCDH_MOUSE Glutaryl-CoA dehydrogenase, mitochondrial precursor (GCD) [M.musculus]
2002	23152	AI169170	S	HHs:eukaryotic translation initiation factor 4A, isoform 2	ESTs, Highly similar to S00985 translation initiation factor eIF-4A II - mouse [M.musculus]
2062	15393	AI170663	FFF, General Alternate	HHs:sterol regulatory element binding transcription factor 2	ESTs, Weakly similar to A48085 transcription factor ADD1 - rat [R.norvegicus]
2973	13682	L38482	MM, FFF, TTT, General Alternate	HHs:cell division cycle 34	ESTs, Moderately similar to I54552 hypothetical serine proteinase - rat [R.norvegicus]
10	1600	AA686470	Q, R, EEE, MMM	DNA-damage inducible transcript 3	DNA-damage inducible transcript
37	1647	AA799575	G, H, II	Peptidylglycine alpha- amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
57	14250	AA799729	w	Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)- homolog phosphodiesterase E4)	ESTs, Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)
58	18061	AA799735	l, J	RuvB-like protein 1	RuvB-like protein 1
133	1650	AA817825	I I	Peptidylglycine alpha- amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
145	2696	AA817997	F, G, H, FFF	ribosomal protein L24 S -	ribosomal protein L24
203	576	AA819118	C, YY BB, CC,	adenosylmethionine synthetase	S - adenosylmethionine synthetase
204	6018	AA819140	PPP, QQQ	carbonic anhydrase 3	carbonic anhydrase 3
210	24654	AA819333	D, V	RAB3D, member RAS oncogene family	RAB3D, member RAS oncogene family
260	18673	AA849028		proteasome (prosome, macropain) subunit, alpha type 3	proteasome (prosome, macropain) subunit, alpha type 3

TABL			1. · 意志		tomey Docket 44921-5033-01Wo ************************************
Seq (D)	@L@C	LESSEN C. OI POSEN	Model	Known Cene Name	Unigena Sequence Cluster IIIIa
317	21713	AA851637	D	Lutheran blood group (Auberger b antigen included) glycoprotein	Lutheran blood group (Auberger b antigen included)
323	4048	AA851814	0, VV	(transmembrane) nmb	glycoprotein (transmembrane) nmb
416	17742	AA866302	нн, ww	4- hydroxyphenylpyruvi c acid dioxygenase	4-hydroxyphenylpyruvic acid dioxygenase
465	1644	AA891068	G, II	Peptidylglycine alpha- amidating monooxygenase procollagen, type I,	Peptidylglycine alpha-amidating monooxygenase
505	21674	AA891828	sss	alpha 2	procollagen, type I, alpha 2
509	3844	AA891857	U, FF, RRR, SSS, UUU B, PPP,	fractured callus expressed transcript 1 Aldolase B, fructose-	fractured callus expressed transcript 1
562	820	AA892395	QQQ	biphosphate	Aldolase B, fructose-biphosphate
624	1552	AA893219	O, P, X, Y, WW	Glycine methyltransferase	Glycine methyltransferase
694	17906	AA899762	NNN	Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (verbB) oncogene homolog (Erbb1)	Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (v-erbB) oncogene homolog (Erbb1)
738	20711	AA924267	U, FF, LL, XX, BBB, CCC, RRR, SSS	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
742	17116	AA924339	X, Y	Thymus cell surface antigen	Thymus cell surface antigen
818	3817	AA926328	w	Tyrosine 3- monooxygenase/trypt ophan 5- monooxygenase activation protein, zeta polypeptide	Tyrosine 3- monooxygenase/tryptophan 5- monooxygenase activation protein, zeta polypeptide
			Z, General Core Tox	endothelial differentiation sphingolipid G- protein-coupled	endothelial differentiation sphingolipid G-protein-coupled
850	19069	AA943737	Markers		receptor 1 G protein-coupled receptor kinase
857	867	AA943963	Р	· ·	6

TABL	图1 ,————————————————————————————————————		ξ		(Omay Docket 44921-5038-01000 Document No. 1935323.1
\$39 [D:	ELEC ELEC	Censenk Acc or Refseq ID			Unigene Sequence Cluster Title
880	15476	AA944426	ZZ, AAA	Calmodulin III	Calmodulin III
901	402	AA945143	C, E, DD, SS, WW, KKK, NNN	tryptophan-2,3- dioxygenase	tryptophan-2,3-dioxygenase
903	4185	AA945169	V, EE, HH, TT	Transthyretin (prealbumin, amyloidosis type I)	Transthyretin (prealbumin, amyloidosis type I)
903	4186	AA945169	нн, тт	Transthyretin (prealbumin, amyloidosis type I) solute carrier family	Transthyretin (prealbumin, amyloidosis type I)
911	211	AA945453	General Alternate	28 (sodium-coupled nucleoside transporter), member 2	solute carrier family 28 (sodium- coupled nucleoside transporter), member 2
914	22604	AA945578	U, FF, KK, XX, RRR	putative peroxisomal 2,4-dienoyl-CoA reductase	putative peroxisomal 2,4-dienoyl- CoA reductase
923	1707	AA945698	00	15-kDa selenoprotein Cytochrome P450,	15-kDa selenoprotein
1151	20712	AA997806	FFF	subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
1188 1202	3062 1382	AA998857 AB002406	H, T, GG, PPP, QQQ UU, VV	carboxypeptidase B2 (plasma) RuvB-like protein 1	carboxypeptidase B2 (plasma) RuvB-like protein 1
1203	926	AB003042	O, P, VV	complement component 5, receptor 1	complement component 5, receptor 1
1212	22567	AB017544	W, DD, EE	peroxisomal membrane anchor protein	peroxisomal membrane anchor protein
1216	2016	AF000578	PPP, QQQ	CDC5 (cell division cycle 5, S. pombe, homolog)-like	CDC5 (cell division cycle 5, S. pombe, homolog)-like
1221	1597	AF014503	W, MM, TTT	nuclear proten 1	nuclear proten 1
1234	22602	AF044574	U, FF, BBB, CCC, RRR, SSS	putative peroxisomal 2,4-dienoyl-CoA reductase	putative peroxisomal 2,4-dienoyl- CoA reductase
1234	22603		U, FF, LL, BBB, CCC, RRR, SSS	putative peroxisomal 2,4-dienoyl-CoA reductase	putative peroxisomal 2,4-dienoyl- CoA reductase

TABL		Direction of the		A	tomey Docket 44921-5033-01000 Document No. 1935323.1
S09 . ID -	ELEC	Consont Acc or RefSeq ID	Model i	Known Cene Name	Unigene Sequence Cluster Title
1238	145	AF064541	N	arginine vasopressin receptor 1B	arginine vasopressin receptor 1B
1230	143	AI 004341	14	HGF-regulated	argitime vasopressif receptor 15
				tyrosine kinase	HGF-regulated tyrosine kinase
1258	10108	AI007857	Q, R	substrate	substrate
			B, O, BB,		
			CC, GG,		
	2853	A1008888	NN, 00	Cystatin beta	Cystatin beta
1287	2854	AI008888	0	Cystatin beta HLA-B associated	Cystatin beta
1347	11460	AI010293	κ	transcript 3	HLA-B associated transcript 3
			General		
1000	47504	41040500	Core Tox	Growth hormone	
1362	17524	Al010568	Markers	receptor aminolevulinic acid	Growth hormone receptor
1384	21040	Al011734	K, L	synthase 1	aminolevulinic acid synthase 1
	:			Uteroglobin (Clara	Uteroglobin (Clara cell secretory
1397	17654	AI012117	LL, XX	cell secretory protein) receptor (calcitonin)	protein)
1				activity modifying	receptor (calcitonin) activity
1415	2791	AI012429	ZZ, AAA	protein 1	modifying protein 1
				Protein phosphatase	
İ			Q, R, General	2 (formerly 2A), catalytic subunit,	Protein phosphatase 2 (formerly
1424	3203	AI012595	Alternate	alpha isoform	2A), catalytic subunit, alpha isoform
-	0200			a.pria teoretti	
			A, B, M,		
			HH, SS,		
			UU, III, JJJ, KKK,		
			000, 1444,		
			General		
1420	1409	A1042002			Hydroxyacyl glutathione
1430	1409	AI012802	Markers	glutathione hydrolase	nydrolase
			E, DD,	Enolase 2, gamma,	
1497	1114	Al029917	KKK, NNN		Enolase 2, gamma, neuronal
			C, K, T,		
			W, DD, EE, KKK,		
			General	Sorbitol	
1507	1876	Al030175	Alternate	dehydrogenase	Sorbitol dehydrogenase
				Kirsten rat sarcoma	Kiroton rôt narooma viral
1586	6697	AI045340	MM, TTT	viral oncogene homologue 2 (active)	Kirsten råt sarcoma viral oncogene homologue 2 (active)
		100 10		cyclic AMP	
				phosphoprotein,	
1808	2057	AI102579	UUU	19kD	cyclic AMP phosphoprotein, 19kD

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TABL	E1:			# At	torney Docket 44921-5033-011WC : 44: Document No. 1985328.1
S09 ; ID	1D Ko. Grec	CONSENT ACCO RCISCO ID	Model Code	Known Cene Name	Unigano Sequence Cluster Title
1814	17234	AI102741	RR	Tissue inhibitor of metalloproteinase 3	Tissue inhibitor of metalloproteinase 3
				GDP-dissociation	
1842	18679	Al103496	AA	inhibitor 1 ADP-ribosylarginine	GDP-dissociation inhibitor 1
1850	3764	Al103651	С	hydrolase aldehyde	ADP-ribosylarginine hydrolase
1852	16884	Al103758	QQQ	dehydrogenase family 9, subfamily A1	aldehyde dehydrogenase family 9, subfamily A1
1853	1649	Al103782	Н	Peptidylglycine alpha- amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
1875	4235	Al104524	HHH, General Alternate	heterogeneous nuclear ribonucleoprotein A/B	heterogeneous nuclear ribonucleoprotein A/B
1890	16885	AI105188	PP, General Core Tox Markers	aldehyde dehydrogenase family 9, subfamily A1	aldehyde dehydrogenase family 9, subfamily A1
1908	4049	Al112012	o, vv	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb
1944	24803	Al137065	MM, VV,	Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase)	Alanine-glyoxylate aminotransferase (Serine- pyruvate aminotransferase)
1968	961	AI138143	11	glutathione S- transferase, theta 2	glutathione S-transferase, theta 2
2017	7253	AI169378	RR	Myelin basic protein	Myelin basic protein
		·	X, Y, FFF, GGG, General Core Tox Markers,		
2010	4004		General	Phosphoglycerate	.
2018 2019	4091 24341	AI169417 AI169421	Alternate GG	mutase 1 endosulfine alpha	Phosphoglycerate mutase 1 endosulfine alpha
2019	24341	A1169421	GG	proteasome	endosuitine aipna
				(prosome,	
	1		H, K, LLL.	macropain) subunit,	proteasome (prosome,
2021	3256	AI169479		alpha type 5	macropain) subunit, alpha type 5

TABL	eq :			A	iomay Docket 44921-5033-01WO Document No. 1985323.1
800) ID	id'not Grec	Conson: Ace or Roisog ID.	Model Gode	Known Gene Name!	Unigene Sequence Cluster Title
2088	14960	Al171319	G	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	ESTs, Highly similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1; integrase interactor 1 [Mus musculus] [M.musculus], guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
2160	21676	Al175101	sss, uuu		procollagen, type I, alpha 2
2193	6782	AI176170	FFF C, D, W,	FK506-binding protein 1 (12kD)	FK506-binding protein 1 (12kD)
2218	3431	AI176595	BB, CC, FF, KKK, NNN, OOO, General Core Tox Markers, General Alternate	Cathepsin L	Cathepsin L
2266	14989	AI177366	HHH	Integrin, beta 1	Integrin, beta 1
2269	14977	AI177386	JJ, KK	Protein tyrosine phosphatase, receptor type, D	Protein tyrosine phosphatase, receptor type, D
2272	26258	AI177501	υ	ribosomal protein S17	ribosomal protein S17
2291	659	Al178208	w	nuclear pore membrane glycoprotein 121 kD	nuclear pore membrane glycoprotein 121 kD
2309	6287	Al178652		brain-specific angiogenesis inhibitor 1-associated protein 2	brain-specific angiogenesis inhibitor 1-associated protein 2
2353	16081	AI179610		Heme oxygenase	Heme oxygenase
2411	1651	Al228068	F	Peptidylglycine alpha- amidating monooxygenase Phosphoglycerate	Peptidylglycine alpha-amidating monooxygenase
2437	4092	AI228723	The state of the s	mutase 1	Phosphoglycerate mutase 1
2452	16203		•	Synaptobrevin 1, Vesicle-associated membrane protein (synaptobrevin 2)	Synaptobrevin 1, Vesicle- associated membrane protein (synaptobrevin 2)

TABL	E1 :-	7		A	tomey Doctot 4/121-5033-01W0 Document No. 1985323.1
S09 . (D	ID Korr	Centent Accor Rowselld:	Model: Code :	emely eneo invenil	Unigene Sequence Cluster Title
2472	2088	Al229727	NN, 00	regulator of G-protein signaling 5 selenoprotein P,	regulator of G-protein signaling 5
2485	4280	AI230247 .	LL	plasma, 1 Cystatin C (cysteine	selenoprotein P, plasma, 1 Cystatin C (cysteine proteinase
2527	24326	Al231292	X, Y S, GGG,	proteinase inhibitor)	inhibitor)
2552	4093	AI232001	LLL	Phosphoglycerate mutase 1	Phosphoglycerate mutase 1
2578	19287	AI232379	LLL, UUU		Platelet-derived growth factor receptor alpha
2615	17907	Al233224	U	Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (verbB) oncogene homolog (Erbb1)	Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (v-erbB) oncogene homolog (Erbb1)
2629	16709	Al233602	PP, QQ	Adenosin kinase	Adenosin kinase
2642	1653	Al233806	F, G, II, UUU	Peptidylglycine alpha- amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
2659	21156	AI234248	N, PP, QQ, XX, YY	golgi SNAP receptor complex member 1	golgi SNAP receptor complex member 1
2660	1654	Al234258	X, Y, II	Peptidylglycine alpha- amidaling monooxygenase	Peptidylglycine alpha-amidating monooxygenase
2677	2789	Al234949	MM, TTT	preimplantation protein 3	preimplantation protein 3
2688	2746	Al235291	Z, AA	casein kinase 1, alpha 1	casein kinase 1, alpha 1
2743	2855	Al236707	EEE, MMM	Cystatin beta	Cystatin beta
2763	1488	Al237016	DDD	H2A histone family, member Y	H2A histone family, member Y
2836	19703	AJ001517	E, BB, CC, II	hemochromatosis	hemochromatosis
2840	18686	D00729	FF, LL, XX, YY	dodecenoyl- Coenzyme A delta isomerase (3,2 trans- enoyl-Coenyme A isomerase)	Rat mRNA for delta3, delta2- enoyl-CoA isomerase, dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl- Coenyme A isomerase)
2843	1306	D10262	GG	Choline kinase	Choline kinase
2040	24707		MM, PP, QQ, RR,	Alanine-glyoxylate aminotransferase (Serine-pyruvate	Alanine-glyoxylate aminotransferase (Serine-
2848	24797		TTT E, GG,	aminotransferase) cysteine-rich protein	pyruvate aminotransferase)
2852	2515		нн, GGG	2	cysteine-rich protein 2

TABL	3 1			XX.	iomey Docker 44921-5033-01W0
(10) (10)		LAGE OF SEASON	Model	Manya Gaza Nical	Unigene Sequence Cluster Title
2855	16610	D28557	D, PP, QQ, HHH, General Alternate	cold shock domain protein A	cold shock domain protein A
2857	2005	D29646	NN, OO, VV	CD38 antigen (ADP- ribosyl cyclase / cyclic ADP-ribose hydrolase)	CD38 antigen (ADP-ribosyl cyclase / cyclic ADP-ribose hydrolase)
2858	3743	D30666	ввв	fatty acid Coenzyme A ligase, long chain 3	fatty acid Coenzyme A ligase, long chain 3
2859	1396	D30735	RR	augmenter of liver regeneration	augmenter of liver regeneration
2866	1531	D43964	OO, PP, QQ, PPP, QQQ	bile acid-Coenzyme A dehydrogenase: amino acid n- acyltransferase	bile acid-Coenzyme A dehydrogenase: amino acid n- acyltransferase
2871	811	D63704	B, L, III, JJJ, OOO, QQQ, General Core Tox Markers OOO, PPP, QQQ,	dihydropyrimidinase	dihydropyrimidinase
2871	812	D63704	General Core Tox Markers	dihydropyrimidinase	dihydropyrimidinase
2872	1125	D82071	000	prostaglandin D2 synthase 2, hematopoietic	prostaglandin D2 synthase 2, hematopoietic
2880	1414	D89514		5-aminoimidazole-4- carboxamide ribonucleotide formyltransferase/IM P cyclohydrolase	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
2882	24799	E01050	SS, TTT	Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase)	Alanine-glyoxylate aminotransferase (Serine- pyruvate aminotransferase)
2884	1641	E03428	MMM, UUU	Peptidylglycine alpha- amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
2929	1421			N-acylaminoacyl- peptide hydrolase	N-acylaminoacyl-peptide hydrolase

TABL	≣1				tomey Doctat 44921-5083-011WO
599 10. :	id no. Grec	Geneank Acc or Refseq ID -	Model .	Known Cone Name	Unigene Sequence Cluster Title
				Steroid-5-alpha-	
				reductase, alpha	
			ŀ	polypeptide 1 (3-oxo-	Steroid-5-alpha-reductase, alpha
}				5 alpha-steroid delta	polypeptide 1 (3-oxo-5 alpha-
		105005		4-dehydrogenase	steroid delta 4-dehydrogenase
2930	20429	J05035	GGG, LLL		alpha 1)
1		ł		Steroid-5-alpha-	
ł		ł	E T CC	reductase, alpha	Storaid E olaba raduatasa alaba
1	([F, T, GG,		Steroid-5-alpha-reductase, alpha
1			GGG, General	5 alpha-steroid delta 4-dehydrogenase	polypeptide 1 (3-oxo-5 alpha- steroid delta 4-dehydrogenase
2020	20430	J05035	Alternate	alpha 1)	alpha 1)
2930	20430	303033	Alternate	Glutamylcysteine	aipila 1)
[1	1		gamma synthetase	Glutamylcysteine gamma
2931	1247	J05181	Q, R, S	light chain	synthetase light chain
2001	1247	000101	(4, 11, 5	ngik onom	Syntholico nghi chom
}			U, BBB,	Carnitine	
}			ccc.	palmitoyltransferase	
2932	1977	J05470	RRR, SSS		Carnitine palmitoyltransferase 2
2940	20865	L00117	F, M, Y	Elastase 1	Elastase 1
	ļ	}	C, E, LL,		
2941	5616	L00191	RRR, SSS	Fibronectin 1	Fibronectin 1
				Calcitonin receptor-	
2969	1632	L27487	GG	like receptor	Calcitonin receptor-like receptor
			G, H, JJ,	Glutathione	
2974	6405	L38615	KK, GGG	synthetase gene	Glutathione synthetase gene
	i			Glutathione	
2974	6406	L38615	GGG	synthetase gene	Glutathione synthetase gene
			O, P, X,		
2975	1427	L38644	Y, VV	Importin beta	Importin beta
			C, I, O,		
•			P, MM,		
			NNN,		
			TTT, General		40
			Core Tox		
2983	21097	M12112	Markers	Angiotensinogen	Angiotensinogen
2303	21001	14112112	I, J, U,	Cytochrome P450,	7 413101011311103011
1		}	FF, LL,	subfamily IVB,	Cytochrome P450, subfamily IVB,
2992	20714	M14972	XX, YY	polypeptide 1	polypeptide 1
			B, F, G,	1 Vb -b	E-WE-E-1
			NN, 00,		
•			GGG,		
			LLL,		
(General		
			Core Tox		
2995	2505	M16235	Markers	Lipase, hepatic	Lipase, hepatic
				procollagen, type I,	
3007	15571	M27207	M, II	alpha 1	procollagen, type I, alpha 1

TABL	E 1	7.77		A A	tomey Docket 44921-5038-011VO
	,	, .			Document No. 1935323.1
S09 :	ELEC	Luce or Respectively Consideration		Kinown Gene Keine	Unigane Sequence Cluster Title
				gamma-aminobutyric acid (GABA-A) receptor, subunit	gamma-aminobutyric acid (GABA-
3018	1241	M35162	D, Z, AA	delta	A) receptor, subunit delta
				Epidermal growth factor receptor, formerly avian erythroblastic	Epidermal growth factor receptor,
3022	16604	M37394	K, LLL, UUU	leukemia viral (v- erbB) oncogene homolog (Erbb1)	formerly avian erythroblastic leukemia viral (v-erbB) oncogene homolog (Erbb1)
3025	20713	M57718	U, EE, FF, LL, RRR	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
0007	70		K, GG, OO, General	histidine ammonia	
3027	70	M58308	Alternate	lyase Tropomyosin 1	histidine ammonia lyase
3031	457	м60666	w	(alpha)	Tropomyosin 1 (alpha)
3047	1694	M84716	F, III, JJJ, General Alternate	ribosomal protein S3a	ribosomal protein S3a
3048	291	M88347	IJ	Cystathionine beta synthase	Cystathionine beta synthase
		1000347	EEE, MMM, General	Sylidiase	Cystatrionine deta synthase
3055	1678	M96674	Alternate	glucagon receptor	glucagon receptor
			CCC, DDD, RRR,	acetyl-CoA acyltransferase, 3- oxo acyl-CoA thiolase A (Acaa), mRNA. 11/2002	Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A 1,
3058	23698	NM_012489	SSS, UUU U, FF,	Length = 1619 acetyl-CoA acyltransferase, 3- oxo acyl-CoA thiolase A (Acaa),	peroxisomal Acetyl-CoA acyltransferase, 3-
3058	23699	NM_012489	GG, HH, LL, DDD	mRNA. 11/2002 Length = 1619	oxo acyl-CoA thiolase A 1, peroxisomal
3060	7062	NM_012495		Aldolase A, fructose- bisphosphate (Aldoa), mRNA. 11/2000 Length = 1442	Aldolase A, fructose- bisphosphate

TABL	E 1			Ą	torney Doctot 44921-5033-911WO
809 ID	id kar erec	Consoni Accor Rossog ID	Model Codo:		Unigeno Sequence Cluster Title
3060	7063	NM_012495	QQ, UU, VV	Aldolase A, fructose- bisphosphate (Aldoa), mRNA. 11/2000 Length = 1442 Aldolase A, fructose-	Aldolase A, fructose- bisphosphate
3060	7064	NM_012495	II, VV, PPP, General Core Tox Markers	bisphosphate (Aldoa), mRNA. 11/2000 Length = 1442	Aldolase A, fructose- bisphosphate
3061	17785	NM_012501	M, V	apolipoprotein C-3 (Apoc3), mRNA. 11/2002 Length = 306 apolipoprotein C-3	Apolipoprotein C-III
3061	17787	NM_012501	S, DD, EE, HH, XX, YY	(Apoc3), mRNA. 11/2002 Length = 306 ATPase, Na+K+	Apolipoprotein C-III
3062	15675	NM_012504	H, DD, EE	transporting, alpha 1 (Atp1a1), mRNA. 11/2002 Length = 3636	ATPase, Na+K+ transporting, alpha 1 polypeptide
3062	15677	•	N, RR, WW	ATPase, Na+K+ transporting, alpha 1 (Atp1a1), mRNA. 11/2002 Length = 3636	ATPase, Na+K+ transporting, alpha 1 polypeptide
3064	7427	NM_012515	O, P, NN, OO, VV, EEE, MMM	Benzodiazepin receptor (peripheral) (Bzrp), mRNA. 11/2000 Length = 781	Benzodiazepin receptor (peripheral)
3066	20518	NM_012518	R	Calmodulin III (Calm3), mRNA. 11/2000 Length = 691	Calmodulin III
3067	15740	NM_012520	LL	Catalase (Cat), mRNA. 11/2002 Length = 2495 Catalase (Cat),	Catalase
3067	15741	NM_012520	EEE, MMM	mRNA. 11/2002 Length = 2495 cholinergic receptor,	Catalase
3069	24433	NM_012527	PP, QQ	muscarinic 3 (Chrm3), mRNA. 11/2002 Length = 3578	Cholinergic receptor, muscarinic

TABL	E-1	-1			tomey Docket 4X221-5033-01W0 Document No. 1935323.1
\$00 1D		Linguistans Accor Colorador	Model Code	Known Cene Name	Unigene Sequence Cluster Title
3071	11115	NM_012531	M	Catecholamine-O- methyltransferase (Comt), mRNA. 11/2000 Length = 1531	Catecholamine-O- methyltransferase
3071	11116	NM 012531	M	Catecholamine-O- methyltransferase (Comt), mRNA. 11/2000 Length = 1531	Catecholamine-O- methyltransferase
3073	488	NM_012540	A, C, L, GG, HH, DDD	cytochrome P450, 1a1 (Cyp1a1), mRNA. 10/2002 Length = 1575	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)
3073	489	NM_012540	C, L, GG, HH C, K, L,	cytochrome P450, 1a1 (Cyp1a1), mRNA, 10/2002 Length = 1575	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)
3073	20705	NM_012540	U, GG, HH, II, DDD, RRR	cytochrome P450, 1a1 (Cyp1a1), mRNA. 10/2002 Length = 1575	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)
3074	20703	NM_012541	C, K, L, M, U, Y, GG, HH, II, RRR, SSS	cytochrome P450, 1a2 (Cyp1a2), mRNA. 11/2002 Length = 1542	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)
3074	20704	NM_012541	C, K, L, T, GG, HH, DDD	cytochrome P450, 1a2 (Cyp1a2), mRNA. 11/2002 Length = 1542	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)
3075	23868		A, BB, CC, NNN	Early growth response 1 (Egr1), mRNA. 11/2002 Length = 3112 Early growth	Early growth response 1
3075	23869	NM_012551	A, BB, CC, NNN	response 1 (Egr1), mRNA. 11/2002 Length = 3112 Early growth	Early growth response 1
3075	23871	NM_012551		response 1 (Egr1), mRNA. 11/2002 Length = 3112 Early growth	Early growth response 1
3075	23872		A, OO,	response 1 (Egr1), mRNA. 11/2002 Length = 3112	Early growth response 1

TABL				A	iomey Docket 44921-5033-01WC Document No. 1985328.1
Seq ID:	idino"; erec	Conson! Acc or .i Rowco (D	Model Code	Known Cene Keme	Unigana Saquance Civeter Title
				Fatty acid binding protein 1, liver (Fabp1), mRNA. 11/2002 Length =	
3078	17676	NM_012556	N, HH	493	Fatty acid binding protein 1, liver
3082	4573	NM_012570	XX YY	Glutamate dehydrogenase (Glud1), mRNA. 11/2002 Length = 2874	Glutamate dehydrogenase
3002	4373	1410_012570	///, 11	Glutamate	Glotalitate dellydrogenase
3082	4574	NM_012570	GG, OO,	dehydrogenase (Glud1), mRNA. 11/2002 Length ≃ 2874	Glutamate dehydrogenase
				Histone H1-0 (H1f0),	
3084	16024	NM_012578	WW, ZZ, AAA	mRNA. 11/2000 Length = 1779	Histone H1-0
3004	10024	14W_012378	1	Histone H1-0 (H1f0),	Historie HT-0
3084	16025	NM_012578	WW, ZZ, AAA	mRNA. 11/2000 Length = 1779 Histone H1-0 (H1f0),	Histone H1-0
				mRNA. 11/2000	
3084	16026	NM_012578	ZZ, AAA	Length = 1779	Histone H1-0
3085	16080	NM_012580	E, OO, PP, EEE, MMM	Heme oxygenase (Hmox1), mRNA. 10/2002 Length = 870	Heme oxygenase
3087	20313	NM_012585	D, E	5-hydroxytryptamine (serotonin) receptor 1A (Htr1a), mRNA. 11/2002 Length = 1269	5-Hydroxytryptamine (serotonin) receptor 1A
3088	15097	 NM_012588	Z `	insulin-like growth factor binding protein 3 (Igfbp3), mRNA. 11/2002 Length = 2352	Insulin-like growth factor-binding protein (IGF-BP3)
3088	15098	NM_012588	GG, II	insulin-like growth factor binding protein 3 (Igfbp3), mRNA. 11/2002 Length = 2352	Insulin-like growth factor-binding protein (IGF-BP3)
3089	21162	NM_012591	w	Interferon regulatory factor 1 (Irf1), mRNA. 11/2002 Length = 2078	Interferon regulatory factor 1

TABL	E1		सम्बद्धाः भेजन्य	A STAN	10mg/Docket 4/921-5093-01WO Document No. 1935323.1
S09 (D, £,	ID Ko; ©L©C	CONSONIA ACCO ROSSONID :	Model Code ₇	Known Cene Neme	Walligane Sequence Cluster IIIIe
3090	4449	NM_012592	F, V, Z, AA, XX, YY, General Alternate	Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. 11/2002 Length = 2104	Isovaleryl Coenzyme A dehydrogenase
3090	4450	NM 012592	A, B, V, BB, CC, II, OOO, General Alternate	Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. 11/2002 Length = 2104	Isovaleryl Coenzyme A dehydrogenase
3090	4451	NM_012592	VV, General Alternate	Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. 11/2002 Length = 2104	Isovaleryl Coenzyme A dehydrogenase
3090	4452	NM_012592	VV, General Alternate	Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. 11/2002 Length = 2104	Isovaleryl Coenzyme A dehydrogenase
3094	2629	NM_012603	w	v-myc avian myelocytomatosis viral oncogene homolog (Myc), mRNA. 11/2002 Length = 2168	Avian myelocytomatosis viral (v- myc) oncogene homolog
3096	23522	NM_012615	A	Ornitine decarboxylase (Odc1), mRNA. 11/2000 Length = 2442	Ornitine decarboxylase
3096	23523	NM_012615	B, H, I, J	Ornitine decarboxylase (Odc1), mRNA. 11/2000 Length = 2442	Ornitine decarboxylase
3098	6055	NM_012619	RRR,	Phenylalanine hydroxylase (Pah), mRNA. 11/2002 Length = 1998 v-raf-1 murine	Phenylalanine hydroxylase
3100	20798	NM_012639	V, X, Y	leukemia viral oncogene homolog 1 (Raf1), mRNA. 11/2002 Length = 2524	Murine leukemia viral (v-raf-1) oncogene homolog 1 (3611-MSV)

TABL	ខ ា			7	torney Docket 44921-5033-01WC
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September 1		Consont :			State of the state
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(D).	र्गका १४०%	Resse ID	GGG :		Unigene Sequence Chister Tille
				v-raf-1 murine	
1			1	leukemia viral	
!	1			oncogene homolog 1 (Raf1), mRNA.	
				11/2002 Length =	Murine leukemia viral (v-raf-1)
3100	20799	NM 012639	h	2524	oncogene homolog 1 (3611-MSV)
0.00	20.00		i, J, L, U, W, EE,		consegure numbers (corr mev)
	Ì	Į.	NNN,		
	1	[000,	syndecan 4 (Sdc4),	
2402	0422	NINA 012610	General	mRNA. 11/2002	Dundaga (avadaga)
3103	9423	NM_012649	Alternate	Length = 2462	Ryudocan/syndecan 4
			C, L, W,	syndecan 4 (Sdc4),	
			DD, WW,	mRNA. 11/2002	
3103	9424	NM_012649	NNN	Length = 2462	Ryudocan/syndecan 4
	[Solute carrier family	
l]]		4, member 1, anion	
		1		exchange protein 1	
1				(kidney band 3)	
	1			(Slc4a1), mRNA.	Solute carrier family 4, member 1,
3104	16332	NM 012651	Z, AA	11/2000 Length = 2547	anion exchange protein 1 (kidney band 3)
3104	10332	14141_012031	۷, ۸۸	Secreted acidic	Dario 3)
				cystein-rich	
				glycoprotein	
			G, H, M,	(osteonectin)	
		-	EE, II,	(Sparc), mRNA.	
] .			11/2000 Length =	Secreted acidic cystein-rich
3105	16217	NM_012656	บบบ	2025	glycoprotein (osteonectin)
				Secreted acidic	
•		Ì		cystein-rich	
				glycoprotein	
				(osteonectin)	
				(Sparc), mRNA. 11/2000 Length =	Secreted acidic cystein-rich
3105	16221	NM_012656	м. оо	2025	glycoprotein (osteonectin)
13.55		012000	777, GCGC	tyrosine	grycoprotein (ostooneoun)
				aminotransferase	
i i				(Tat), mRNA.	
			C, D, I, J,	11/2002 Length =	
3109	24825	NM_012668	NNN	2362	Tyrosine aminotransferase

TABL	E 1:		五年 新文	A	tomay Docket 44921-5033-01000
Seq 10	id no: Grec	CONSTRUCTION OF THE CONTROL OF THE C	Modal Codo :	Known Cone Name	Unigeno Sequence Civeter Title
3110	24427	NM_012669	UU	Transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1): albumin proximal factor, also TCF1 (Tcf1), mRNA. 11/2000 Length = 3538	Transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1): albumin proximal factor, also TCF1
3111	17117	NM 012673	К	Thymus cell surface antigen (Thy1), mRNA. 11/2000 Length = 650	Thymus cell surface antigen
	20776		XX, YY	Tuberous sclerosis 2, (renal carcinoma) (Tsc2), mRNA. 11/2000 Length = 5573	Tuberous sclerosis 2, (renal carcinoma)
3115	24453	NM_012690	A	P-glycoprotein 3/ multidrug resistance 2 (Pgy3), mRNA. 11/2002 Length = 3912	ATP-binding cassette, sub-family B (MDR/TAP), member 4 (P- glycoprotein 3/ multidrug resistance 2
3118	139	NM_012694	ss, uu	Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA. 11/2002 Length = 3404	Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3
3120	1850	NM_012696	D, E, M, BB, CC, III, JJJ	T-kininogen (Kng), mRNA. 11/2002 Length = 1417	T-kininogen, see also D11Elh1 and D11Mit8
3120	1854	NM_012696	D, E, M, BB	T-kininogen (Kng), mRNA. 11/2002 Length = 1417	T-kininogen, see also D11Elh1 and D11Mit8
3123	4002	NM_012708	KKK	proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2) (Psmb9), mRNA. 11/2002 Length = 880	Low molecular mass polypeptide 2

TABL	E 1:	18 p.	Çiri e	XX, F	(omey Docker 44921-5039-01WO
	1-2		10	253	Document No. 1935323.1
S 99	ELEC :	Consant Accor Reference	Modaj Codo		elili televia, coneupes engigina
3123	4003	NM_012708	I, J, KKK	proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2) (Psmb9), mRNA. 11/2002 Length = 880	Low molecular mass polypeptide 2
3125	20888	NM_012716	CC, BBB, CCC	Solute carrier 16 (monocarboxylic acid transporter), member 1 (Slc16a1), mRNA. 11/2000 Length = 3320	Solute carrier 16 (monocarboxylic acid transporter), member 1
3125	20889	NM_012716	BB, CC, LL, TT	Solute carrier 16 (monocarboxylic acid transporter), member 1 (Slc16a1), mRNA. 11/2000 Length = 3320	Solute carrier 16 (monocarboxylic acid transporter), member 1
3126	22294	NM 012720	AA, SS	Myelin- associated/Oligodend rocytic Basic Protein- 81 (Mobp81), mRNA. 11/2002 Length = 3442	myelin-associated oligodendrocytic basic protein
			F, G, U,	kallikrein B, plasma 1 (Klk3), mRNA. 11/2002 Length = 2583	Plasma kallikrein
3130	1371	NM_012734	D, V, GG	Hexokinase 1 (Hk1), mRNA. 11/2002 Length = 3653 Hexokinase 2 (Hk2),	Hexokinase 1
3131	11839	NM_012735	Z, AA, NNN	mRNA. 11/2002 Length = 3635	Hexokinase 2 Apolipoprotein A-IV, ESTs,
3132	5318	NM_012737	PP, QQ	Apolipoprotein A-IV (Apoa4), mRNA. 5/2002 Length = 1423	Moderately similar to APA4_RAT APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) [R.norvegicus]
3132	18236	NM_012737	V	Apolipoprotein A-IV (Apoa4), mRNA. 5/2002 Length = 1423	ESTs, Moderately similar to APA4_RAT APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) [R.norvegicus]

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TABU	≣າ	1. d	i di di di di di di di di di di di di di	A STATE OF THE PARTY OF THE PAR	torney Docket 44921-5093-01WO Document No. 1935323.1
509 10 - 1		ingener Age or Referr			Unigene Sequence Cluster Tille
				basigin (Bsg), mRNA. 11/2002 Length =	Basigin (Ox47 antigen or CE-9) (EMMPRIN in human) (neurothelin, HT7 or 5A11 in
3139	11938	NM_012783	X, Y, EE	1443	avian)
3142	16947	NM 012793	N, T, HHH, PPP, QQQ, General Alternate	Guanidinoacetate methyltransferase (Gamt), mRNA. 11/2002 Length =	Guanidinoacetate methyltransferase
3142	10947	NIVI_012193	Aitemate	Guanidinoacetate	inetryitansierase
3142	16948	NM_012793	PPP, QQQ	methyltransferase (Gamt), mRNA. 11/2002 Length = 924	Guanidinoacetate methyltransferase
2440	000	ANA 040700	V, DD, EE, UU, III, JJJ, General	glutathione S- transferase, theta 2 (Gstt2), mRNA. 9/2002 Length =	
3143	960	NM_012796	Alternate	1258 Sialyltransferase 8a	glutathione S-transferase, theta 2 Sialyltransferase 8 A (alpha-N-
3148	835	NM_012813	SS	(Siat8a), mRNA. 10/2002 Length = 1223	acetylneuraminate: alpha-2,8- sialytransferase, GD3 synthase) GenBank no: U53883
2440	45022	NIM 040040	V V	alpha-methylacyl- CoA racemase (Amacr), mRNA. 11/2002 Length =	
3149	15032	NM_012816	X, Y	1504 Acyl Coenzyme A	alpha-methylacyl-CoA racemase
				dehydrogenase, long chain (Acadl), mRNA. 11/2000	Acyl Coenzyme A
3150	6780	NM_012819	U, RRR	Length = 1451	dehydrogenase, long chain
3150	6781	NM_012819	нн	Acyl Coenzyme A dehydrogenase, long chain (Acadl), mRNA. 11/2000 Length = 1451	Acyl Coenzyme A dehydrogenase, long chain
		012010		Apolipoprotein C1 (Apoc1), mRNA. 11/2000 Length =	donycrogonacc, long chem
3151	23670	NM_012824	s, v	435	Apolipoprotein C1
3152	20587	NM_012826	O, P, VV	alpha-2 - glycoprotein 1, zinc (Azgp1), mRNA. 11/2002 Length = 1250	Zn - alpha2 - glycoprotein

TABL	ਵੇਂ 1		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	A	Homey Docket 44921-5033-01000 Document No. 1935323.1
S09 D- :	id ko: Grec	Constant Acc or Rofsco ID	Model Code	emen eneo avoan	Unigene Sequence Gluster Tile
3153	373	NM_012833	NN, UU, KKK, NNN	ATP-binding cassette, sub-family C (CFTR/MRP), member 2 (Abcc2), mRNA. 11/2002 Length = 4918	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
3155	20885	NM_012842	11	epidermal growth factor (Egf), mRNA. 11/2002 Length = 4801	Epidermal growth factor
3156	17541	NM_012844	F, N, S, CC, II, NN, OO, PP, QQ, TT, DDD, EEE, LLL, MMM, SSS, UUU, General Alternate	Epoxide hydrolase 1 (microsomal xenobiotic hydrolase) (Ephx1), mRNA. 10/2002 Length = 1242	Epoxide hydrolase 1 (microsomal xenobiotic hydrolase)
3157	20819	NM_012847	W, General Alternate	Farnesyltransferase, subunit alpha (Fnta), mRNA. 11/2000 Length = 1680	Farnesyltransferase, subunit alpha
3161	17306	NM_012876	EE, MM, YY, TTT	Ribosomal protein S29 (Rps29), mRNA. 11/2002 Length = 318	Ribosomal protein S29
3162	15872	NM_012879	LLL, MMM, RRR,	2 A2 (gkucose transporter, type 2) (Slc2a2), mRNA. 11/2000 Length = 2573	Solute carrier family 2 A2 (gkucose transporter, type 2)
3163	494	NM_012880	General Alternate	Superoxide dismutase 3 (Sod3), mRNA. 12/2001 Length ≈ 1729	Superoxide dismutase 3
3165			R,	sulfotransferase, estrogen preferring (Ste), mRNA. 11/2002 Length = 1309	Estrogen sulfotransferase, selenoprotein P, plasma, 1

TABL	3 1				(10 They Docker 4/1221-5033-01\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
	erec	Acc or	Model	7.00	0 Document No. 1985323.1
.¥¥.	(D) KOL	Refseq (D)	GOOD	Thymopoietin (tamina associated polypeptide 2)	<u>Viiijajo Sequeñea Clustoi Villa</u>
3166	16871	NM_012887	T, EE, KKK, NNN	(Tmpo), mRNA. 11/2000 Length = 3508	Thymopoietin (lamina associated polypeptide 2)
				Thyroid stimulating hormone receptor (Tshr), mRNA. 11/2002 Length =	Thyroid stimulating hormone
3167	24857	NM_012888	RR, SS	5270 Adenosin kinase	receptor
3169	16708	NM_012895	UU, WW	(Adk), mRNA. 11/2002 Length = 1123	Adenosin kinase
			M S SS	alpha 2 HS- glycoprotein alpha 2 (fetuin) (Ahsg), mRNA, 11/2002	
3170	16274	NM_012898	TT	Length = 1490 alpha 2 HS-	alpha-2-HS-glycoprotein
3170	16275	NM_012898	HH, SS, NNN	glycoprotein alpha 2 (fetuin) (Ahsg), mRNA. 11/2002 Length = 1490	alpha-2-HS-glycoprotein
				aminolevulinate,delta- ,dehydratase (Alad), mRNA. 10/2001	aminolevulinate,delta-
3171	18564	NM_012899	Alternate	Length = 1116 Alpha-1 microglobulin/bikunin	,dehydratase
3172	7897	NM 012901	V, SS, NNN	(Ambp), mRNA. 1/2002 Length = 1162	Alpha-1 microglobulin/bikunin
9112	1001	- 12301		Alpha-1 microglobulin/bikunin (Ambp), mRNA. 1/2002 Length =	Alpha- i microglobulinbikuriin
3172	7898	NM_012901	NNN	1162 Alpha-1	Alpha-1 microglobulin/bikunin
3172	7899	NM_012901		microglobulin/bikunin (Ambp), mRNA. 1/2002 Length =	Alpha-1 microglobulin/bikunin

TABL	E1		11, 15, 18,	A	tomey Doctot 44221-5033-01W0 Document No. 1935323.1
\$29 : ID : :	ELEC	Kaisea ID :	Modal Codo	Known Gene Name	Unigano Sequence Cluster Title
3173	7197	NM_012904	0, P, W	Annexin 1 (p35) (Lipocortin 1) (Anx1), mRNA. 11/2002 Length = 1402 ATPase, Na+K+	Annexin 1 (p35) (Lipocortin 1)
3176	18119	NM_012913	vv	transporting, beta polypeptide 3 (Atp1b3), mRNA. 11/2000 Length = 1818	ATPase, Na+K+ transporting, beta polypeptide 3
3181	191	NM_012940	GG	Cytochrome P450 1b1 (Cyp1b1), mRNA. 11/2000 Length = 4964	Cytochrome P450 1b1
3182	20928	NM_012941	т	Cytochrom P450 Lanosterol 14 alphademethylase (Cyp51), mRNA. 11/2002 Length = 2260	Cytochrom P450 Lanosterol 14 alpha-demethylase
3182	20931	NM_012941	G, H, I, J, FF, General Alternate	Cytochrom P450 Lanosterol 14 alphademethylase (Cyp51), mRNA. 11/2002 Length = 2260	Cytochrom P450 Lanosterol 14 alpha-demethylase
3184	5033	NM_012966	L, PPP, QQQ	Heat shock 10 kD protein 1 (chaperonin 10) (Hspe1), mRNA. 11/2000 Length = 680	Heat shock 10 kD protein 1 (chaperonin 10)
3184	5034	NM_012966	RR	Heat shock 10 kD protein 1 (chaperonin 10) (Hspe1), mRNA. 11/2000 Length = 680	Heat shock 10 kD protein 1 (chaperonin 10)
3185	2554	NM_012967	w	Intercellular adhesion molecule 1 (Icam1), mRNA. 11/2000 Length = 2602	Intercellular adhesion molecule 1
3185	2555	NM_012967		Intercellular adhesion molecule 1 (Icam1), mRNA. 11/2000 Length = 2602	Intercellular adhesion molecule 1

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S09::	ID Kio:; @F@G'	Consoni Accor : Refseq ID :	Model / Codo :: }	Known Gene Neme	ellfi refevile sigeviles sacific
		_		Nuclear Factor IA (Nfia), mRNA. 11/2000 Length =	
3188	763	NM_012988	кк	3368	Nuclear Factor IA
				Nucleoplasmin-	
]			}	related protein	
İ	.			(Nuclear protein B23 (Npm1), mRNA.	
1			D, JJ,	11/2000 Length =	Nucleoplasmin-related protein
3189	17393	NM_012992	HHH	1232	(Nuclear protein B23
0.00				Nucleoplasmin-	Control Process
			•	related protein	
	1			(Nuclear protein B23	
		٠	FFF,	(Npm1), mRNA.	N
3189	17394	NM 012992	General Alternate	11/2000 Length = 1232	Nucleoplasmin-related protein (Nuclear protein B23
3103	17334	14101_012992	Alternate	Peptidylglycine alpha-	(Nuclear protein B23
				amidating	
ŀ				monooxygenase	
			İ	(Pam), mRNA.	
			II, LLL,	11/2002 Length =	Peptidylglycine alpha-amidating
3193	1640	NM_013000	บบบ	3770 Tyrosine 3-	monooxygenase
1				monooxygenase/trypt	
				ophan 5-	
				monooxygenase	
1		_		activation protein,	
		•		zeta polypeptide	Tyrosine 3-
				(Ywhaz), mRNA.	monooxygenase/tryptophan 5-
3195	3404	NM_013011	A, B, P, VV	11/2002 Length = 1687	monooxygenase activation protein, zeta polypeptide
3193	J-7-04	14W_013011	V V	Tyrosine 3-	protein, zeta porypeptide
				monooxygenase/trypt	
				ophan 5-	
				monooxygenase	
				activation protein,	Townsian O
				zeta polypeptide (Ywhaz), mRNA.	Tyrosine 3-
			O, P, R,	(Ywnaz), mRNA. 11/2002 Length =	monooxygenase/tryptophan 5- monooxygenase activation
3195	25279	NM 013011	Ο, Γ, Ι λ ,	1687	protein, zeta polypeptide
				Protein tyrosine	h
]				phosphatase, non-	
				receptor type	
				substrate 1 (SHP	
			E, BB,	substrate 1) (Ptpns1), mRNA.	Protein tyrosine phosphatase,
			PP, EEE,	11/2002 Length =	non-receptor type substrate 1
3197	11904	NM_013016	ш, ммм	3709	(SHP substrate 1)

TABL	E1 -	, -,			tomey Docket 44921-5033-011W0 *** : Document No. 1935828.1
Seq [D]	ELEC	Constant Age of Reference	Model : :	ened awond	Unigene Sequence Cluster Title
3198	1588	NM_013026	T, U, LLL, SSS A, HHH,	Syndecan (Synd1), mRNA. 11/2002 Length = 2410 Selenoprotein W	Syndecan 1
3199	17894	NM_013027	A, HHH, III, JJJ, General Alternate	muscle 1 (Sepw1), mRNA. 7/2001 Length = 664	Selenoprotein W muscle 1
3205	16683	NM_013052	w, ss, ннн	Tyrosine 3- monooxygenase/trypt ophan 5- monooxygenase activation protein, eta polypeptide (Ywhah), mRNA. 11/2002 Length = 1689	
3205	16684	NM_013052	W, JJ, GGG, HHH	Tyrosine 3- monooxygenase/trypt ophan 5- monooxygenase activation protein, eta polypeptide (Ywhah), mRNA. 11/2002 Length = 1689	
3207	12371	NM_013055	C	Zipper (leucine) protein kinase (Zpk), mRNA. 11/2002 Length = 3754	Mitogen activated protein kinase 12 (Zipper (leucine) protein kinase)
3210	21287	NM_013065	z	Protein phosphatase 1, catalytic subunit, beta isoform (Ppp1cb), mRNA. 11/2002 Length = 2706	Protein phosphatase 1, catalytic subunit, beta isoform
3214	13282	NM_013078		Ornithine carbamoyltransferas e (Otc), mRNA. 11/2000 Length = 1519	Ornithine carbamoyltransferase
3214			A, B, NN,	Ornithine carbamoyltransferas e (Otc), mRNA. 11/2000 Length =	Ornithine carbamoyltransferase
3220		NM_013102		FK506-binding protein 1 (12kD) (Fkbp1a), mRNA. 11/2000 Length =	FK506-binding protein 1 (12kD)

TABL	图1				tomey Docker 44921-5033-01000 .: Document No. 1935323.1
Sog : D ::		Consons Accor Rosson (D)			Únigang Sequence Civeter Tiúle
				FK506-binding protein 1 (12kD) (Fkbp1a), mRNA. 11/2000 Length =	
3220	15296	NM_013102	O, P, HH	554	FK506-binding protein 1 (12kD)
3222	19949	NM 013106		Guanine nucleotide binding, protein, alpha inhibiting polypeptide 3 (Gnai3), mRNA. 11/2000 Length =	Guanine nucleotide binding, protein, alpha inhibiting
3222	650	NM_013106 NM_013134	L, HHH	3072 3-hydroxy-3- methylglutaryl- Coenzyme A reductase (Hmgcr), mRNA. 11/2002 Length = 2664	polypeptide 3 3-hydroxy-3-methylglutaryl- Coenzyme A reductase
3226	651	NM_013134	a ·	3-hydroxy-3- methylglutaryl- Coenzyme A reductase (Hmgcr), mRNA. 11/2002 Length = 2664	3-hydroxy-3-methylglutaryl- Coenzyme A reductase
3226	652	NM_013134	Q, R	3-hydroxy-3- methylglutaryl- Coenzyme A reductase (Hmgcr), mRNA. 11/2002 Length = 2664	3-hydroxy-3-methylglutaryl- Coenzyme A reductase
3228	21681	NM_013154	D, GG, HH	CCAAT/enhancerbin ding, protein (C/EBP) delta (Cebpd), mRNA. 11/2000 Length = 1200	CCAAT/enhancerbinding, protein (C/EBP) delta
3229	3430	NM_013156	C, Q, W, MM, OOO, TTT	Cathepsin L (Ctsl), mRNA. 11/2002 Length = 1386	Cathepsin L
V223	J-50	141/1_013130		Carnitine palmitoyltransferase 1, muscle (Cpt1b), mRNA, 11/2002	Carnitine palmitoyltransferase 1
3234 3234	20854 20855	NM_013200 NM_013200		Length = 2826 Carnitine palmitoyltransferase 1, muscle (Cpt1b), mRNA. 11/2002 Length = 2826	beta, muscle isoform Carnitine palmitoyltransferase 1 beta, muscle isoform

TABU	≣1	7-2 78-2		AND AND AND AND AND AND AND AND AND AND	lomey Docket 44921-5033-01WO Document No. 1995323.1
Seq.: [D	(10 [176: 1-	ingened Legion Independent	Model Code	Kinown Cene Neme	والالا تفاصلاي ومتفياته ويتوارانا
3237	23362	NM_013216	JJ, GGG	Ras homolog enriched in brain (Rheb), mRNA. 11/2000 Length = 1088 Acyl-Coenzyme A	Ras homolog enriched in brain
3240	21078	NM_016986	T, U, X, TT, XX, YY, III, JJJ, RRR	dehydrogenase, C-4 to C-12 straight- chain (Acadm), mRNA. 11/2000 Length = 1866	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain
3241	15610	NM_016987	Z, AA	ATP citrate lyase (Acly), mRNA. 11/2002 Length = 4269 ATP citrate lyase	ATP citrate lyase
3241	15612	NM_016987	BB, CC, JJJ, OOO	(Acly), mRNA. 11/2002 Length = 4269	ATP citrate lyase
3241	15613	NM_016987	E, J, WW, OOO, General Core Tox Markers, General Alternate	ATP citrate lyase (Acly), mRNA. 11/2002 Length = 4269	ATP citrate lyase
3243	17972	NM 016989	Y	adenylate cyclase activating polypeptide 1 (Adcyap1), mRNA. 11/2002 Length = 2681	adenylate cyclase activating polypeptide 1
3244	24869	NM_016992	Z, AA	arginine vasopressin (Avp), mRNA. 11/2002 Length = 602	Arginine vasopressin (Diabetes insipidus)
3248	15621	NM_017005	MM, XX, YY, TTT	Fumarate hydratase (Fh), mRNA. 11/2000 Length = 1589	Fumarate hydratase
3249	1399	NM_017006	G, FF	Glucose-6-phosphate dehydrogenase (G6pd), mRNA. 11/2002 Length = 2324	Glucose-6-phosphate dehydrogenase

TABL	3 .0	719			tomey Doctat 44921-5068-011WO : Document No. 1995328.1
809 ID4		Consoni Accor Reisog ID	Model 4	Known Cene Name	Olili iclay (Checa Signal)
				Glucuronidase, beta (Gusb), mRNA. 11/2002 Length =	
3252	17815	NM_017015	NNN	2472	Glucuronidase, beta
3255	17807	NM_017025	C, U, FF, HH, YY	Lactate dehydrogenase A (Ldha), mRNA. 11/2002 Length = 1609	Lactate dehydrogenase A
3257	3202	NM_017039	B, Q, R, WW, General Alternate	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (Ppp2ca), mRNA. 11/2002 Length = 1804	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
3258	24596	NM_017040	Q, R, PP, QQ, SS, VV	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (Ppp2cb), mRNA. 11/2002 Length = 1843	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
3258	24597	NM 017040	В, ІІ	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (Ppp2cb), mRNA. 11/2002 Length = 1843	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
3259	21580	NM_017041	ZZ, AAA	protein phosphatase 3, catalytic subunit, alpha isoform (Ppp3ca), mRNA. 11/2002 Length = 2337	Calcineurin subunit A alpha
3260	24771	NM_017047	A, B, G, JJ, KK, CCC, EEE, FFF, GGG, HHH, MMM, General Core Tox Markers	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (Slc10a1), mRNA. 11/2002 Length = 1663	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1

TABU		. 4. 1. 10. 19.	建一点 。	ACC	torney, Docket 44924-5033-91000 Document No. 1935323.1
Seq.	@L@C	i ingeneral Accor Acco Acco	Model ;	Known Cene Name	Unigene Sequence Cluster Mile
				Superoxide dismutase 1, soluble (Sod1), mRNA. 12/2001 Length =	
3261	20876	NM_017050	N, UUU	650 Superoxide	Superoxide dismutase 1, soluble
3261	20877	NM 017050	м	dismutase 1, soluble (Sod1), mRNA. 12/2001 Length = 650	Superoxide dismutase 1, soluble
			LL, XX,	Lysosomal- associated membrane protein 2 (Lamp2), mRNA. 11/2000 Length =	Lysosomal-associated membrane
3265	6653	NM_017068	YY, LLL	Lysosomal- associated membrane protein 2 (Lamp2), mRNA. 11/2000 Length =	protein 2 Lysosomal-associated membrane
3265	6654	NM_017068	LL	1548 insulin receptor	protein 2
3266	24719	NM 017071	RR	(Insr), mRNA. 11/2002 Length = 5397	Insulin receptor
3267	20649	NM 017072	L. WW	Carboamyl- phosphate synthetase 1 (Cps1), mRNA. 11/2000 Length = 4503	Carboamyl-phosphate synthetase
			,	Acetyl-Co A acetyltransferase 1, mitochondrial (Acat1), mRNA. 11/2000 Length =	Acetyl-Co A acetyltransferase 1,
3270	18956	NM_017075	BBB	1715	mitochondrial
3270	18957	NM_017075	D, U, GG, XX, YY, BBB, CCC		Acetyl-Co A acetyltransferase 1, mitochondrial
3270	18958	NM_017075	U, FF, XX, BBB, CCC, RRR, SSS	Acetyl-Co A acetyltransferase 1, mitochondrial (Acat1), mRNA. 11/2000 Length = 1715	Acetyl-Co A acetyltransferase 1, mitochondrial

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Seq' ID (@1 @C	Constant Acc or Refeed ID	Modol	emili ened niveni	Unigene Sequence Cluster Tille
3273	1550	NM_017084	F, N, O, P, X, Y, EEE, GGG, MMM	Glycine methyltransferase (Gnmt), mRNA. 11/2000 Length = 988	Glycine methyltransferase
3273	1551	NM_017084	F, O, P, X, GGG, LLL, UUU	Glycine methyltransferase (Gnmt), mRNA. 11/2000 Length = 988	Glycine methyltransferase
3274	10886	NM 017094	B, H, S, LLL, PPP, QQQ, General Core Tox Markers, General Alternate	growth hormone receptor (Ghr), mRNA. 11/2002 Length = 2950	Growth hormone receptor
3274	10887	NM 017094	A, B, T, FF, NN, OO, General Alternate	growth hormone receptor (Ghr), mRNA. 11/2002 Length = 2950	Growth hormone receptor
3275	6013	NM_017096	DD, KKK, NNN, PPP, QQQ	C-reactive protein (Crp), mRNA. 10/2002 Length = 693	C-reactive protein
3276	2149	NM_017097	H, U, GGG, General Core Tox Markers, General Alternate	Cathepsin C (dipeptidyl peptidase I) (Ctsc), mRNA. 11/2000 Length = 1850	Cathepsin C (dipeptidyl peptidase
. 3276	2150	- NM_017097	LL, FFF, GGG, OOO, RRR, SSS, UUU, General Core Tox Markers, General Alternate	Cathepsin C (dipeptidyl peptidase I) (Ctsc), mRNA. 11/2000 Length = 1850	Cathepsin C (dipeptidyl peptidase

TABL	30			A PART OF THE PART	offrey Docket 44921-5033-01WO 25-2 Document No. 1985323.1
Seq :	ID Ko'; @f@@	Content Accor Roiseo D	Model :	Known Gene Kane	elilli rejevid concuped chegin
3277	15517		NN, OO	potassium inwardly- rectifying channel, subfamily J, member 8 (Kcnj8), mRNA. 11/2002 Length = 1580	Inwardly rectifying potassium channel gene, subfamily J-8 (ATP sensitive)
3279	15776	NM_017108	SS	potassium voltage- gated channel, subfamily H (eag- related), member 3 (Kcnh3), mRNA. 11/2002 Length = 3715	potassium voltage-gated channel, subfamily H (eag-related), member 3
				granulin (Grn), mRNA. 11/2002	
3280	20745	NM_017113	C, O, P	Length = 2113	granulin
3280	20746	NM 017113	O, P	granulin (Grn), mRNA. 11/2002 Length = 2113	granulin
3281	21538	NM_017116	P	calpain 2 (Capn2), mRNA. 11/2002 Length = 3252	calpain 2
3282	21663	NM_017126	E, BBB, CCC	ferredoxin 1 (Fdx1), mRNA. 11/2002 Length = 838	ferredoxin 1
3283	24693	NM_017134	C, General Alternate	arginase 1 (Arg1), mRNA. 11/2002 Length = 1386	arginase 1, liver
3284	16681	NM_017136	А, В	squalene epoxidase (Sqle), mRNA. 11/2002 Length = 2199	squalene epoxidase
3285	24885	NM_017138	F, G, H, General Alternate	laminin receptor 1 (67kD, ribosomal protein SA) (Lamr1), mRNA. 11/2002 Length = 1018	laminin receptor 1
3285	24886	NM_017138	F, G, H, VV	laminin receptor 1 (67kD, ribosomal protein SA) (Lamr1), mRNA. 11/2002 Length = 1018	laminin receptor 1
3286	24107	NM_017141	PP, QQ	DNA polymeráse beta (Polb), mRNA. 11/2002 Length = 3298	DNA polymerase beta

TABLI	31			AV.	torney Docket 44921-5033-01100 Document No. 1935323.1
		Centent .			
Seq .	@F@@	Acc or	Modal .		Unigane Sequence Cluster Tille
D is i	(D) No.;.	RefSeq ID			Unigene Sequence Chreter tille
			VV, FFF,	cofilin 1 (Cfl1),	
			General	mRNA. 11/2002	
3289	15365	NM_017147	Alternate	Length = 1039	cofilin 1, non-muscle
				ribosomal protein	
			CC, II,	S17 (Rps17), mRNA.	
2202	21643	NM 017152	EEE, MMM	11/2002 Length = 466	ribosomal protein S17
3292	21043	NIVI_017152	G, H, II,	400	ribosomai protein 317
			JJ, KK,		
			DDD,		
İ			FFF,	ribosomal protein S6	
	Ì		ннн,	(Rps6), mRNA.	
	ł		General	11/2002 Length =	
3295	17104	NM_017160	Alternate	801	ribosomal protein S6
				ribosomal protein S6	
			н, п,	(Rps6), mRNA.	
			General	11/2002 Length =	
3295	17105	NM_017160	Alternate	801	ribosomal protein S6
				ribosomal protein S6	,
				(Rps6), mRNA. 11/2002 Length =	
3295	17107	NM 017160	XX, YY	801	ribosomal protein S6
3233	17.107	14141_017100	/////////////////////////////////////	peroxiredoxin 2	inbosomai proteiri oo
	•			(Prdx2), mRNA.	i
				11/2002 Length =	
3298	14498	NM 017169	EE	877	peroxiredoxin 2
				T-cell death	
				associated gene	
l			\	(Tdag), mRNA.	
				11/2002 Length =	
3301	19031	NM_017180	Q, R	1353	T-cell death associated gene
			:	asialoglycoprotein	
				receptor 2 (Asgr2), mRNA. 11/2002	
3303	24670	NM 017189	1	Length = 1290	asialoglycoprotein receptor 2
3303	24070	14141_017109		Longui - 1230	asiaisgiyoopi otoiii toochtoi 2
				allograft inflammatory	
				factor 1 (Aif1),	allograft inflammatory factor 1,
				mRNA. 11/2002	balloon angioplasty responsive
3305	16269	NM_017196	V, X, Y	Length = 653	transcript
				S-	
				adenosylhomocystein e hydrolase (Ahcy),	
				mRNA. 11/2002	S-adenosylhomocysteine
3307	20779	NM_017201	I. J. HH	Length = 2029	hydrolase
555		0	., ., ., .		,

TABL	1 3			A A	tomey Docket 44921-5038-0100 : 'Document No. 1935323.1
Seq (D)	@r@c	Conson; Acc or . : RefSeq ID . :	Modol Codo	Kinowin Cente Name	Unigene Sequence Civeter Title
3308	14696	NM_017202	LL	cytochrome c oxidase, subunit 4a (Cox4a), mRNA. 11/2002 Length = 696	cytochrome c oxidase, subunit IVa
3314	17740	NM 017233	L, S, EE, TT, WW	4- hydroxyphenylpyruvi c acid dioxygenase (Hpd), mRNA. 11/2002 Length = 1361	4-hydroxyphenylpyruvic acid dioxygenase
3315	15598	NM_017236	V	phosphatidylethanola mine binding protein (Pbp), mRNA. 11/2002 Length = 1075	phosphatidylethanolamine binding
3315	15599	NM_017236	l. J. GG	phosphatidylethanola mine binding protein (Pbp), mRNA. 11/2002 Length = 1075	phosphatidylethanolamine binding
3318	18750	NM_017257	II, EEE, MMM	protease (prosome, macropain) 28 subunit, beta (Psme2), mRNA. 11/2002 Length = 806	protease (prosome, macropain) 28 subunit, beta
3319	15299	NM_017259	W, II, KKK, OOO, General Core Tox Markers	B-cell translocation gene 2 (Btg2), mRNA. 11/2002 Length = 2519	Early induced gene, B-cell translocation gene 2
3319	15300	NM_017259	W, 11	B-cell translocation gene 2 (Btg2), mRNA. 11/2002 Length = 2519	Early induced gene, B-cell translocation gene 2
3319	15301	NM_017259	A, B, W, II	B-cell translocation gene 2 (Btg2), mRNA. 11/2002 Length = 2519 protease (prosome,	Early induced gene, B-cell translocation gene 2
3320	15224	NM_017264	N, LL	macropain) 28 subunit, alpha (Psme1), mRNA. 11/2002 Length =	protease (prosome, macropain) 28 subunit, alpha

TABL	E 1				lomay Docket 44921-5033-01000 Document No. 1935323.1
Scq.	Erec	Contons Accor Resson (Dec	Model	Known Cene Neine	Unicado Sequênco Cluster Tille
3320	15225	NM_017264	N	protease (prosome, macropain) 28 subunit, alpha (Psme1), mRNA. 11/2002 Length = 921	protease (prosome, macropain) 28 subunit, alpha
3320	15227	NM_017264		protease (prosome, macropain) 28 subunit, alpha (Psme1), mRNA. 11/2002 Length = 921	protease (prosome, macropain) 28 subunit, alpha
3321	20600	NM 017268		3-hydroxy-3- methylglutaryl- Coenzyme A synthase 1 (Hmgcs1), mRNA. 11/2002 Length =	3-hydroxy-3-methylglutaryl- Coenzyme A synthase 1
3321	20601	NM 017268	G, H, J, JJ, KK, FFF, KKK, OOO, General Alternate	3-hydroxy-3- methylglutaryl- Coenzyme A	3-hydroxy-3-methylglutaryl- Coenzyme A synthase 1
3323	15141	NM 017278	A, D, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 1 (Psma1), mRNA. 11/2002 Length =	proteasome (prosome, macropain) subunit, alpha type 1
0020	10141	UNI 011210	D, General	proteasome (prosome, macropain) subunit, alpha type 2 (Psma2), mRNA. 11/2002 Length =	proteasome (prosome,
3324	5747	NM_017279	Alternate	852 proteasome (prosome, macropain) subunit, alpha type 2 (Psma2), mRNA.	macropain) subunit, alpha type 2
3324	5748	NM_017279	X, Y	11/2002 Length = 852	proteasomė (prosome, macropain) subunit, alpha type 2

TABL	E1			A CALL	10mey Docket 44921-5933-01WO Document No. 1955923.1
S00 ID	id ko	Indenda (al pestern	Code (Nodel	Kinowa Gone Neine	Unigana Saquance Ciuster IIIle
3324	5749	NM_017279	D, LL,	proteasome (prosome, macropain) subunit, alpha type 2 (Psma2), mRNA. 11/2002 Length = 852	proteasome (prosome, macropain) subunit, alpha type 2
3325	3987	NM_017280	GGG, HHH	proteasome (prosome, macropain) subunit, alpha type 3 (Psma3), mRNA. 11/2002 Length = 897	proteasome (prosome, macropain) subunit, alpha type 3
3326	1447	NM_017281	A, BBB, CCC, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 4 (Psma4), mRNA. 11/2002 Length = 1121	proteasome (prosome, macropain) subunit, alpha type 4
3327	3253	NM_017282	ZZ, AAA	proteasome (prosome, macropain) subunit, alpha type 5 (Psma5), mRNA. 11/2002 Length = 970	proteasome (prosome, macropain) subunit, alpha type 5
3327	3254	NM_017282	TT, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 5 (Psma5), mRNA. 11/2002 Length = 970	proteasome (prosome, macropain) subunit, alpha type 5
3329	8956	NM_017284	PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 2 (Psmb2), mRNA. 11/2002 Length = 792	proteasome (prosome, macropain) subunit, beta type, 2
3329	8957	NM_017284	PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 2 (Psmb2), mRNA. 11/2002 Length = 792	proteasome (prosome, macropain) subunit, beta type, 2

TABL	3 1				tomay Doctor 44921-5083-01W0
S00)	ID KJO*; Grēc*;	Conseni Acc or Resson (D)	Model ::		Unigaie Sequence Cluster Tide
3332	16839	NM_017291	AA	gamma-aminobutyric acid A receptor, rho 1 (Gabrr1), mRNA. 11/2002 Length = 4183	gamma-aminobutyric acid (GABA- A) receptor, subunit rho 1
3333	23825	NM_017299	KK, EEE, MMM	solute carrier family 19, member 1 (Slc19a1), mRNA. 11/2002 Length = 2402	solute carrier family 19 (sodium/hydrogen exchanger), member 1
3333	23826	NM_017299	D, Z, AA	solute carrier family 19, member 1 (Slc19a1), mRNA. 11/2002 Length = 2402	solute carrier family 19 (sodium/hydrogen exchanger), member 1
3334	14003	NM 017305		Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (Glclr), mRNA. 11/2002 Length = 1382	glutamate-cysteine ligase , modifier subunit
			Q, R, T,	Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (Glclr), mRNA. 11/2002	glutamate-cysteine ligase ,
3334	14004	NM_017305	KKK A, B, E, I, J, U, FF, LL,	Length = 1382 dodecenoyl- coenzyme A delta isomerase (Dci), mRNA. 11/2002	modifier subunit Rat mRNA for delta3, delta2- enoyl-CoA isomerase, dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-
3335	18687 20809	NM_017306 NM_017326	XX, YY	Length = 987 Calmodulin 2 (phosphorylase kinase, delta) (Calm2), mRNA. 5/2002 Length = 1112	Coenyme A isomerase) Calmodulin 2 (phosphorylase kinase, delta)
3352	455		н, vv	tropomyosin 1, alpha (Tpm1), mRNA. 11/2002 Length = 1004	Tropomyosin 1 (alpha)
3355	16227	NM_019137	ss, xx,	early growth response 4 (Egr4), mRNA. 11/2002 Length = 2145	Zinc-finger transcription factor NGFI-C (early response gene)

TABL	图 1		10 1 2 d	A	tomey Docker 44921-5033-01WO Document No. 1985823.1
Seq ;	ELEC ELEC	Refeed ID	Model Code	Enek ened award	<u> Viilgene Sequence Cluster Tille</u>
3356	14971	NM 019140	JJ, KK	protein tyrosine phosphatase, receptor type, D (Ptprd), mRNA. 11/2002 Length = 6469	Protein tyrosine phosphatase, receptor type, D
3356	14973	NM_019140	JJ, KK, General Alternate	protein tyrosine phosphatase, receptor type, D (Ptprd), mRNA. 11/2002 Length = 6469	Protein tyrosine phosphatase, receptor type, D
2256	14074	NIM 010140	T	protein tyrosine phosphatase, receptor type, D (Ptprd), mRNA. 11/2002 Length =	Protein tyrosine phosphatase,
3356	14974 5617	NM_019140 NM_019143	RR, SS, UU	6469 Fibronectin 1 (Fn1), mRNA. 11/2002 Length ≃ 8329	receptor type, D Fibronectin 1
3357	5619	NM 019143		Fibronectin 1 (Fn1), mRNA. 11/2002 Length = 8329	Fibronectin 1
3357	5621	NM_019143	T, PPP, QQQ	Fibronectin 1 (Fn1), mRNA. 11/2002 Length = 8329	Fibronectin 1
3357	5622	NM 019143	RRR,	Fibronectin 1 (Fn1), mRNA. 11/2002 Length = 8329	Fibronectin 1
3359	20373			cholinergic receptor, nicotinic, gamma polypeptide (Chrng), mRNA. 11/2002 Length = 1832	Cholinergic receptor, nicotinic, gamma polypeptide
3360	20863			calpain 1 (Capn1), mRNA. 11/2002 Length = 2917	calpain 1
3362	21090	NM_019158	KKK	aquaporin 8 (Aqp8), mRNA. 11/2002 Length = 1463	aquaporin 8

TABU	≣¶:;;;			A A	lonney Docket 44921-5033-01W0 Document No. 1985323.1
509 (D)	GLEC D Ko.	EM:EM3 Ace or A Refeat [D]	Model:	Known Gene Name	Unigene Sequence Cluster Tille
				presenilin 1 (Psen1), mRNA. 11/2002	
3363	20256	NM_019163	JJ, KK	Length = 1407	presenilin 1
0000				GATA-binding protein 6 (Gata6), mRNA. 3/2001 Length =	
3365	23481	NM_019185	Υ	1844	GATA-binding protein 6
2266	24040	NINA 040496	Q, R, General	ADP-ribosylation-like 4 (Arl4), mRNA. 11/2002 Length =	ADD ribogulation like 4
3366	24019	NM_019186	Alternate	MAD homolog 2	ADP-ribosylation-like 4
		·		(Drosophila) (Madh2), mRNA. 11/2002 Length =	
3367	15242	NM_019191	O, P, EE	2113	MAD homolog 2 (Drosophila)
2260	22062	NM_019195	ccc	integrin-associated protein (Cd47), mRNA. 11/2002 Length = 1053	integrin-associated protein
3368	22002	MM_019195	CCC	integrin-associated	Integrin-associated protein
				protein (Cd47), mRNA. 11/2002	
3368	22063	NM_019195	ввв, ссс	Length = 1053 C-terminal binding	integrin-associated protein
				protein 1 (Ctbp1), mRNA. 11/2002	
3369	18573	NM_019201	HHH	Length = 2430	C-terminal binding protein 1
2270	20435	NM_019202	UU	phospholipase A2, group 2C (Pla2g2c), mRNA. 11/2002 Length = 4372	phospholipase A2, group IIC
3370	20435	NW_019202	00	Serine/threonine kinase 10 (Stk10), mRNA. 11/2002	priospriorpase Az, group no
3371	19241	NM_019206	0	Length = 4301	Serine/threonine kinase 10
			-	amino-terminal enhancer of split (Aes), mRNA. 1/2002 Length =	
3373	2078	NM_019220	S, V	1356	amino-terminal enhancer of split
			General	amino-terminal enhancer of split (Aes), mRNA. 1/2002 Length =	
3373	2079	NM_019220	Alternate	1356	amino-terminal enhancer of split

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TABL		-		A PART OF A	tormey Docket 44921-5053-01000 : :: Document No. 1995323.1
Seq (. [D.	@L@C.	Consolid Cocor Reiseq id	Model Codo	Known Cene Neime:	ellit retzue egyennes Eduster Tille
				NADH dehydrogenase Fe-S protein 6 (Ndufs6), mRNA. 11/2002	NADH dehydrogenase Fe-S
3375	20938	NM_019223	V, EE	Length = 351 solute carrier family	protein 6
3376	16285	NM_019229	JJ, KK	12, member 4 (Slc12a4), mRNA. 11/2002 Length = 3726	solute carrier family 12, member 4
2270	16449		SS, KKK, OOO, General	farnesyl diphosphate farnesyl transferase 1 (Fdft1), mRNA. 11/2002 Length = 1662	farnesyl diphosphate farnesyl transferase 1
3378	16449	NM_019238	C, I, J, FF, OOO, General	farnesyl diphosphate farnesyl transferase	farnesyl diphosphate farnesyl
3378	16450	NM_019238	Alternate	1662	transferase 1
3380	21109	NM_019243	PP, QQ, BBB, CCC	prostaglandin F2 receptor negative regulator (Ptgfrn), mRNA. 11/2002 Length = 5825 splicing factor, arginine/serine-rich 5	prostaglandin F2 receptor negative regulator
3381	23419	NM_019257	I, J	(Sfrs5), mRNA. 11/2002 Length = 2781	splicing factor, arginine/serine- rich 5 (SRp40, HRS)
3382	15259	NM 019259	QQ, General Alternate	complement component 1, q subcomponent binding protein (C1qbp), mRNA. 11/2002 Length =	complement component 1, q subcomponent binding protein
3384	23625		BBB, CCC	solute carrier family 22, member 5 (Slc22a5), mRNA. 11/2002 Length = 3037	solute carrier family 22 (organic cation transporter), member 5
3385	1143	NM_019280	Z, AA	gap junction membrane channel protein alpha 5 (Gja5), mRNA. 11/2002 Length = 3115	gap junction membrane channel protein alpha 5 (connexin 40)

TABL	፭ ዓ	£ 3			iomey Docket 44921-5038-01WO Document No. 1985328.1
Seq . (D)	ELEC Blow	Keiseg (D Resertion)	Model	Known Cene Name	Unigene Sequence Cluster Title
3386	20734	NM_019283	QQQ, General Core Tox Markers	solute carrier family 3, member 2 (Slc3a2), mRNA. 11/2002 Length = 1940	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
3386	20735	NM_019283	G, H, L, R, II, UU, KKK, OOO, General Core Tox Markers	solute carrier family 3, member 2 (Slc3a2), mRNA. 11/2002 Length =	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
3389	6017	NM 019292	A, B, S, X, Y, GGG, HHH, General Core Tox Markers	carbonic anhydrase 3 (Ca3), mRNA. 11/2002 Length = 988	carbonic anhydrase 3
3401	23491	NM 019359		calponin 3, acidic (Cnn3), mRNA. 5/2002 Length =	calponin 3, acidic
3403	18820	NM_019367	D, V	palmitoyl-protein thioesterase 2 (Ppt2), mRNA. 11/2002 Length = 1660 Testis enhanced	palmitoyl-protein thioesterase 2
3408	24626	NM_019381	HHH, PPP, QQQ	gene transcript (Tegt), mRNA. 11/2002 Length = 940	Testis enhanced gene transcript
3414	18713	NM_020075	C, FFF	eukaryotic initiation factor 5 (eIF-5) (Eif5), mRNA. 11/2000 Length = 3504	eukaryotic initiation factor 5 (eIF-5)
3414	18715	NM_020075	R, UU, FFF	eukaryotic initiation factor 5 (eIF-5) (Eif5), mRNA. 11/2000 Length = 3504	eukaryotic initiation factor 5 (eIF- 5)
3415	20493	NM_020076	w	3-hydroxyanthranilate 3,4-dioxygenase (Haao), mRNA. 11/2002 Length = 1254	3-hydroxyanthranilate 3,4- dioxygenase

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TABL	3 15			A	omey Docket 44921-5033-01WO
S00/ ID:	erec:	Consent Accor Refseq ID	(ecce)		Unigene Sequence Cueter Tide
	21336		บบบ	frizzled homolog 1 (Drosophila) (Fzd1), mRNA. 11/2002 Length = 4540	Drosophila polarity gene (frizzled) homologue
2424	22046	NINA 021740	LIUU	prothymosin alpha (Ptma), mRNA. 11/2002 Length =	prothymosin alpha
3431	22916	NM_021740	HHH A, B,	1182	prodriginosin alpha
			General Core Tox Markers, General	nuclear receptor subfamily 1, group H, member 4 (Nr1h4), mRNA. 5/2002	nuclear receptor subfamily 1,
3433	19712	NM_021745	Alternate	Length = 2070	group H, member 4
3435	20090	NM 021757	E, TT, ZZ, JJJ	pleiotropic regulator 1 (Plrg1), mRNA. 11/2002 Length = 1545	pleiotropic regulator 1
	2000			progesterone receptor membrane component 1 (Pgrmc1), mRNA. 11/2002 Length =	progesterone receptor membrane
3437	17936	NM_021766	Υ	1885 Avian sarcoma virus	component 1
				17 (v-jun) oncogene homolog (Jun), mRNA. 4/2002	Avian sarcoma virus 17 (v-jun)
3438	22352	NM_021835	I, J, II	Length = 2573	oncogene homolog
3441	20114	NM_021842	BB, CC, PP, QQ	endosulfine alpha (Ensa), mRNA. 11/2002 Length = 366	endosulfine alpha
				syntaxin 7 (Stx7), mRNA. 11/2002	
3442	20187	NM_021869	М	Length = 786	syntaxin 7
				tissue inhibitor of metalloproteinase 2 (Timp2), mRNA. 11/2002 Length =	ESTs, tissue inhibitor of
3443	243	NM_021989	EE	1009	metalloproteinase 2
3452	20450	NM_022239	z, aa, ss	neuromedin (Nmu), mRNA. 11/2002 Length = 832	neuromedin U
3457	10509	NM_022268	B, I, J, V, GGG, OOO, General Core Tox Markers	liver glycogen phosphorylase (Pygl), mRNA. 11/2002 Length = 2715	liver glycogen phosphorylase

TABL	ਵੇਂ 1	1			omey Docket 44921-5093-01W0 Document No. 1935323.1
509 ID:	(10 Kg		Modol Codo	Known Cone Keine	Unigene Sequence Cluster Title
0.457	05044		I, FF, General	liver glycogen phosphorylase (Pygl), mRNA. 11/2002 Length =	
3457	25814	NM_022268	Alternate	2715 glutaredoxin 1 (thioltransferase) (Glrx1), mRNA. 5/2002 Length =	liver glycogen phosphorylase
3459_	4561	NM_022278	GG, HH	1255 lecithin-retinol acyltransferase (Lrat), mRNA.	glutaredoxin 1 (thioltransferase)
3460	10562	NM_022280	General Alternate	11/2002 Length = 5358 signal transducer and activator of transcription 5b (Stat5b), mRNA.	lecithin retinol acyltransferase
3462	1914	NM_022380	M, Z, AA	12/2000 Length = 2671 Proliferating cell	signal transducer and activator of transcription 5b
3463	11454	NM 022381	v	nuclear antigen (Pcna), mRNA. 11/2002 Length =	Proliferating cell nuclear antigen
3463	11455	NM_022381	VV, General Alternate	Proliferating cell nuclear antigen (Pcna), mRNA. 11/2002 Length =	Proliferating cell nuclear antigen
			CCC,	Aldehyde dehydrogenase 1, subfamily A1 (Aldh1a1), mRNA. 10/2001 Length =	Aldehyde dehydrogenase 1,
3472	20915	NM_022407	sss, uuu	methionine aminopeptidase 2 (Metap2), mRNA.	subfamily A1
3483	8983	NM_022539	D	5/2002 Length = 1944	methionine aminopeptidase 2

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809 (D.:	Gréc 🐇	Centenis Accor Refseq ID	Model . Code	Einel ened avond	Unigene Sequence Civeter Title
3483	8984	NM_022539	B, K, GGG, HHH, PPP, QQQ, General Alternate	methionine aminopeptidase 2 (Metap2), mRNA. 5/2002 Length = 1944	methionine aminopeptidase 2
3491	21076	NM_022584	QQ	thioredoxin reductase 2 (Txnrd2), mRNA. 11/2002 Length = 1999	thioredoxin reductase 2
3492	21062	NM 022585	DD, EE, MM, UU, TTT	ornithine decarboxylase antizyme inhibitor (Oazi), mRNA. 11/2002 Length = 4269	ornithine decarboxylase antizyme inhibitor
3492	21063	NM 022585	C, MM, UU, TTT	ornithine decarboxylase antizyme inhibitor (Oazi), mRNA. 11/2002 Length =	ornithine decarboxylase antizyme inhibitor
3503	17567	NM 022672	III, JJJ	ribosomal protein S14 (Rps14), mRNA. 11/2002 Length = 492	ribosomal protein S14
3509	17729	NM_022697	F, DDD, FFF	ribosomal protein L28 (Rpl28), mRNA. 11/2002 Length = 466	ribosomal protein L28
3512	24345	NM_022701	N, PP, QQ H, S, HH,	flotillin 1 (Flot1), mRNA. 11/2002 Length = 2157	flotillin 1
3513	24434	NM_022704	FFF, GGG, General Core Tox Markers	mannose-binding protein C (liver) (Mbl2), mRNA. 2/2002 Length = 1037	mannose-binding protein C (liver)
3519	24838	NM_022924	PPP, QQQ	coagulation factor 2 (F2), mRNA. 11/2002 Length = 2045	coagulation factor II

Section Marcon	TABL	3 1	.,.	B. S. A. S.	A	torney Docket 44921-5093-01WO Document No. 1985923.1
	S99 :	@L@C	Consoni Accor	Model		
polyphosphate phosphatase-like	(D) : ::	no Kio.	kersed in	C000 154: -:		nuidana zadrianaa enraan 1111a
phosphatase-like 1 (Impl1), mRNA.						
(Inpp11), mRNA. 11/2002 Length = ARB7, member RAS oncogene family (Rab7), mRNA. 11/2002 Length = Family RAB7, member RAS oncogene family (Rab7), mRNA. 11/2002 Length = Family RAB7, member RAS oncogene family (Rab7), mRNA. 11/2002 Length = Family RAB7, member RAS oncogene family RAB7, member RAS oncogene						
11/2002 Length = SH2-containing inositol phosphatase 2	1					
19669	1					CLI2 containing inspital
RAB7, member RAS oncogene family RAB7, member RAS oncogene family RAB7, mRNA. 11/2002 Length = RAB7, member RAS oncogene family RAB7, member RAS	2522	10660	NINA 022044	77	1 -	_
Same	3523	19009	14141_022944	22		priospriatase 2
(Rab7), mRNA 11/2002 Length = RAB7, member RAS oncogene RaB7, member RAS oncogene Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5)	1					
11/2002 Length = RAB7, member RAS oncogene Rab7, member rab8, for member Rab7, member rab8, for member Rab7, member rab8, for member Rab7, member rab8, for member Rab7, member rab8, for member Rab7, member rab8, for member Rab7, member rab8, for member Rab7, member rab8, for member Rab7, member rab8, for member Rab7, member rab8, for member Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5) Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5) Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5) DNA-damage-inducible transcript 1						
3532 4228	1					RAB7, member RAS oncogene
CCAAT/enhancer binding protein (C/EBP), beta (Cebpb), mRNA. 11/2002 Length = 1408 Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5)	3532	4228	NM 023950	lv	_	
(C/EBP), beta (Cebpb), mRNA. 1, J, MM, 1/2002 Length = 1408 3534 21238 NM_024125 TTT C/CAAT/enhancer binding protein (C/EBP), beta (Cebpb), mRNA. 1/2002 Length = 1/2002 Leng					CCAAT/enhancer	
21238						
1, J, MM, 11/2002 Length = also NF-IL6, nuclear factor-IL6, previously designated TCF5					•	
3534 21238						
CCAAT/enhancer binding protein (C/EBP), beta (Cebpb), mRNA. (Cebpb), mRNA. (11/2002 Length = 1408 11/2002 Length = 1408	0504	04000	1114 004405			
State	3534	21238	NW_024125	111		previously designated TCF5)
MM, TTT, General MM, TTT, General 11/2002 Length = 1408 Gadd45a), mRNA.	1				1	
MM, TTT, General Alternate	1	1				
3534 21239 NM_024125 Alternate 11/2002 Length = 1408 also NF-IL6, nuclear factor-IL6, previously designated TCF5) 3535 351	1			мм, ттт,		Liver activating protein (LAP,
Signature Sign						
DNA-damage- inducible 45 alpha (Gadd45a), mRNA. 11/2002 Length = 711 3535 351 NM_024127 C 711 growth arrest and DNA-damage- inducible 45 alpha (Gadd45a), mRNA. 11/2002 Length = 711 DNA-damage- inducible 45 alpha (Gadd45a), mRNA. 11/2002 Length = 711 DNA-damage- inducible 45 alpha (Gadd45a), mRNA. C, HH, 11/2002 Length = 711 DNA-damage- inducible 45 alpha (Gadd45a), mRNA. C, FF, II, 11/2002 Length = 711 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 D-dopachrome tautomerase D-dopachrome tautomerase (Ddt), mRNA. 11/2002	3534	21239	NM_024125	Alternate	1408	previously designated TCF5)
inducible 45 alpha (Gadd45a), mRNA. 11/2002 Length = 711					1 -	
Gadd45a), mRNA.					_	<u>.</u>
11/2002 Length = DNA-damage-inducible transcript 1	1			Ì	1	
3535 351 NM_024127 C 711 1 1 growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA. 11/2002 Length = DNA-damage-inducible transcript 1 growth arrest and DNA-damage-inducible transcript 1 growth arrest and DNA-damage-inducible transcript 1 growth arrest and DNA-damage-inducible transcript 1 growth arrest and DNA-damage-inducible transcript 1 growth arrest and DNA-damage-inducible transcript 1 DNA-damage-inducible transcript 1 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 3536 17226 NM_024131 Q, R, Y Length = 628 D-dopachrome tautomerase D-dopachrome tautomerase (Ddt), mRNA. 11/2002	1				1 .	DNA-damage-inducible transcript
growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA. 11/2002 Length = DNA-damage-inducible transcript 1 growth arrest and DNA-damage-inducible transcript 1 growth arrest and DNA-damage-inducible transcript 1 growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA. 11/2002 Length = DNA-damage-inducible transcript 1 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 D-dopachrome tautomerase (Ddt), mRNA. 11/2002	3535	351	NM 024127	C	_	· 1
DNA-damage- inducible 45 alpha (Gadd45a), mRNA. C, HH, 11/2002 Length = 711 growth arrest and DNA-damage- inducible 45 alpha (Gadd45a), mRNA. DNA-damage- inducible 45 alpha (Gadd45a), mRNA. C, FF, II, 11/2002 Length = DNA-damage-inducible transcript 1 3535 354 NM_024127 PP, NNN 711 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 D-dopachrome tautomerase D-dopachrome tautomerase (Ddt), mRNA. 11/2002 D-dopachrome tautomerase D-dopachrome tautomerase (Ddt), mRNA. 11/2002	0000	-	021121	<u> </u>		
Second Color Col						
C, HH, 11/2002 Length = DNA-damage-inducible transcript 1					inducible 45 alpha	
3535 353 NM_024127 PP, QQ 711 1 growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA. 3535 354 NM_024127 PP, NNN 711 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 3536 17226 NM_024131 Q, R, Y Length = 628 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 D-dopachrome tautomerase (Ddt), mRNA. 11/2002						
growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA. C, FF, II, 11/2002 Length = DNA-damage-inducible transcript 1 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 Length = 628 D-dopachrome tautomerase D-dopachrome tautomerase D-dopachrome tautomerase D-dopachrome tautomerase D-dopachrome tautomerase D-dopachrome tautomerase D-dopachrome tautomerase					11/2002 Length =	DNA-damage-inducible transcript
DNA-damage- inducible 45 alpha (Gadd45a), mRNA. C, FF, II, 11/2002 Length = DNA-damage-inducible transcript DNA-damage-inducible transcript DNA-damage-inducible transcript D-dopachrome tautomerase (Ddt), mRNA. 11/2002 Length = 628 D-dopachrome tautomerase D-dopachrome tautomerase (Ddt), mRNA. 11/2002	3535	353	NM_024127	PP, QQ	<u> </u>	1
inducible 45 alpha (Gadd45a), mRNA. C, FF, II, 11/2002 Length = DNA-damage-inducible transcript 1 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 D-dopachrome tautomerase (Ddt), mRNA. 11/2002					1~	
3535 354 NM_024127 PP, NNN 711 1 1 1 1 1 1 1 1						
C, FF, II, 11/2002 Length = DNA-damage-inducible transcript 1 1 1 1 1 1 1 1 1						
3535 354 NM_024127 PP, NNN 711 1 D-dopachrome tautomerase (Ddt), mRNA. 11/2002 Length = 628 D-dopachrome tautomerase (Ddt), mRNA. 11/2002		· ·		C. FF. II.	• • • • • • • • • • • • • • • • • • • •	DNA-damage-inducible transcript
D-dopachrome tautomerase (Ddt), mRNA. 11/2002 Length = 628 D-dopachrome tautomerase D-dopachrome tautomerase D-dopachrome tautomerase (Ddt), mRNA. 11/2002	3535	354	NM_024127		•	
MRNA. 11/2002 D-dopachrome tautomerase D-dopachrome tautomerase D-dopachrome tautomerase D-dopachrome tautomerase (Ddt), mRNA. 11/2002 MRNA. 11/2002 D-dopachrome tautomerase D-dopachrome tautome						
3536						
D-dopachrome tautomerase (Ddt), mRNA. 11/2002	0500	17000	NINA 004404	0 0 1		D december to the contract of
tautomerase (Ddt), mRNA. 11/2002	3536	17226	NM_024131	Q, R, Y		D-dopachrome tautomerase
mRNA. 11/2002	1	· ·			•	
			ļ			
	3536	17227	NM 024131	F, N		D-dopachrome tautomerase

TABL	፪ ብ				iomay Docket 4/4221-5033-011WO
Scq ID	E COLOR	CONSERVA AGG OT ROSSOG ID::	Model (*) Godo	Kinown Cenje Name.	Unicono Sequence Cluster Title
			FFF.	apurinic/apyrimidinic endonuclease 1 (Apex), mRNA. 5/2002 Length =	apurinic/apyrimidinic
3537	20801	NM_024148	QQQ	1213 complement factor I	endonuclease 1
3543	22079	NM_024157	ввв, ссс	(Cfi), mRNA. 2/2001 Length = 2021	complement factor I
3547	10980	NM_024349	Z, AA	adenylate kinase 1 (Ak1), mRNA. 10/2002 Length = 585	Adenylate kinase 1
				Heat shock cognate protein 70 (Hsc70), mRNA. 11/2002	
3548	17764	NM_024351	Z, AA, FF	Length = 2073 Heat shock cognate protein 70 (Hsc70), mRNA. 11/2002	heat shock 70kD protein 8
3548	17765	NM_024351	GG	Length = 2073 GTP cyclohydrolase 1 (Gch), mRNA.	heat shock 70kD protein 8
3549	15350	NM_024356	L	11/2002 Length = 1016	GTP cyclohydrolase 1
	·			heterogeneous nuclear ribonucleoproteins methyltransferase- like 2 (S. cerevisiae) (Hrmt1l2), mRNA. 11/2002 Length =	heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S.
3550	20772	NM_024363	Α	1201	cerevisiae)
				5-hydroxytryptamine (serotonin) receptor 6 (Htr6), mRNA. 11/2002 Length =	5-hydroxytryptamine (serotonin)
3551	767	NM_024365	UU	1929	receptor 6
3554	20380	NM_024381	HHH, General Core Tox Markers, General Alternate	glycerol kinase (Gyk), mRNA. 11/2002 Length = 2989	Glycerol kinase
3557	19992	NM_024398	WW, LLL, RRR,	mitochondrial aconitase (nuclear aco2 gene) (Aco2), mRNA. 1/2002 Length = 2744	mitochondrial aconitase (nuclear aco2 gene)

TABL	3 1				tomay Docket 44921-5033-011WO Document No. 1935323.1
S09 (D)	(10) Kjor - (6) (6)	Gensenz Assor Refer ID	Codo	Known.Gene Name	Unigene Sequence Cluster Tittle
			Z, AA,	mitochondrial aconitase (nuclear aco2 gene) (Aco2), mRNA, 1/2002	mitochondrial aconitase (nuclear
3557	19993	NM_024398	GGG	Length = 2744	aco2 gene)
				mitochondrial aconitase (nuclear aco2 gene) (Aco2), mRNA. 1/2002	mitochondrial aconitase (nuclear
3557	19994	NM_024398	ww	Length = 2744 adrenergic receptor,	aco2 gene)
3560	1835	NM 024483	НН	alpha 1d (Adra1d), mRNA. 11/2002 Length = 2939	adrenergic receptor, alpha 1d
				aminolevulinic acid synthase 1 (Alas1), mRNA. 11/2002	
3561	21038	NM_024484	TT	Length = 2052 aminolevulinic acid	aminolevulinic acid synthase 1
			K, QQ,	synthase 1 (Alas1), mRNA. 11/2002	
3561	21039	NM_024484	П	Length = 2052 Serine-pyruvate	aminolevulinic acid synthase 1
3563	24798	NM_030656		aminotransferase (Spat), mRNA. 11/2002 Length = 1595	Alanine-glyoxylate aminotransferase (Serine- pyruvate aminotransferase)
3563	24800	NM 030656	MM, RR, SS, TTT	Serine-pyruvate aminotransferase (Spat), mRNA. 11/2002 Length = 1595	Alanine-glyoxylate aminotransferase (Serine- pyruvate aminotransferase)
3563	24801	 NM_030656		Serine-pyruvate aminotransferase (Spat), mRNA. 11/2002 Length = 1595	Alanine-glyoxylate aminotransferase (Serine- pyruvate aminotransferase)
				Adenylate kinase 2 (Ak2), mRNA. 11/2002 Length =	
3574	17050	NM_030986	UU	889 Tumor protein p53 (Li	Adenylate kinase 2
3576	17377	NM_030989	CC, NN, OO	Fraumeni syndrome) (Tp53), mRNA. 4/2001 Length = 1786	Tumor protein p53 (Li-Fraumeni syndrome)
3579	1792	NM_030996	к, ккк	opioid receptor, sigma 1 (Oprs1), mRNA. 11/2002 Length = 1590	opioid receptor, sigma 1

TABL	3 0			AV	tomey Docket 4/1221-5033-011WO Document No. 1935328.1
SÓQ [D,	id ko Gree	. Insince i to sea Oi pearsi	Model 👬	Come Memos avoid	Unigene Sequence Cluster. Title
3581	15683	NM_031011	мм, ттт	S- Adenosylmethionine decarboxylase 1A (Amd1a), mRNA. 11/2002 Length = 3102	S-Adenosylmethionine decarboxylase 1
2502	15700	NIA/ 031013		liver multidrug resistance- associated protein 6 (Abcc6), mRNA. 4/2001 Length =	liver multidrug resistance- associated protein 6
3582		NM_031013	A, B, G, H, RR, EEE, MMM, UUU, General	ribosomal protein · L10a (Rpl10a), mRNA. 11/2002	
3594 3602	20462	NM_031065 NM_031102	G, H, EEE, MMM	Length = 710 ribosomal protein L18 (Rpl18), mRNA. 11/2002 Length = 607	ribosomal protein L10a
3609	24615	NM_031112	JJ, KK, FFF	ribosomal protein S24 (Rps24), mRNA. 11/2002 Length = 466	ribosomal protein S24
3622	12313	NM_031241	JJ, KK, HHH	cytochrome P450, 8b1, sterol 12 alpha- hydrolase (Cyp8b1), mRNA. 11/2002 Length = 1965	cytochrome P450, 8b1, sterol 12 alpha-hydrolase
3623	1857	NM_031315	FF, LL	cytosolic acyl-CoA thioesterase 1 (Cte1), mRNA. 11/2002 Length = 1591	acyl-CoA thioesterase 1, cytosolic
3624	15662	NM_031318	P, ZZ, AAA	t-complex testis expressed 1 (Tctex1), mRNA. 11/2002 Length = 698	t-complex testis expressed 1

TABL	ड्री. :			A	tomey Docket 44921-5093-01000
S09 ;	GLGG:	Consoni Accor Reiseg ID	Model Codo	Known Cene Keine	Unitene Sequence Cluster Title
3626	4234	NM_031330	A, B, I, L, Y, MM, HHH, KKK, OOO, TTT, General Alternate	heterogeneous nuclear ribonucleoprotein A/B (Hnrpab), mRNA. 11/2002 Length = 3061	heterogeneous nuclear ribonucleoprotein A/B
3633	24645	NM_031502	GGG, OOO, General Core Tox Markers	Amylase 1 (Amy1), mRNA. 11/2002 Length = 1574	Amylase 1
3637	9369	NM_031527	E	Protein phosphatase type 1 alpha, catalytic subunit (Ppp1ca), mRNA. 5/2001 Length = 1392	Protein phosphatase type 1 alpha, catalytic subunit
3637	9370	NM_031527	RR, SS	Protein phosphatase type 1 alpha, catalytic subunit (Ppp1ca), mRNA. 5/2001 Length = 1392	Protein phosphatase type 1 alpha, catalytic subunit
3642	16048	NM_031541	NN, OO	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 (Cd36I1), mRNA. 10/2002 Length = 2497	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 (scavanger receptor class B type 1)
3644	18389	NM_031545	PP, UU, III	natriuretic peptide precursor type B (Nppb), mRNA. 11/2002 Length = 628	Brain natriuretic factor
3645	28	NM_031546	H, I, J, FF, FFF, OOO, SSS, UUU, General Core Tox Markers, General Alternate	Regucalcin (Rgn), mRNA. 11/2002 Length = 1605	Regucalcin

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Seq [D: -	CLCC D. No. :	Conson; Accor Refseqio	Model Codo		Unigene Sequence Cluster Title
3646	15411	NM_031559	J	carnitine palmitoyltransferase 1 (Cpt1a), mRNA. 11/2002 Length = 4377	Carnitine palmitoyltransferase 1 alpha, liver isoform
3647	18315	NM_031561		cd36 antigen (Cd36), mRNA. 11/2002 Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
3647	18316	NM_031561	A, B, II, BBB, CCC, RRR	cd36 antigen (Cd36), mRNA. 11/2002 Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
3647	18318	NM_031561	BBB, HHH, RRR	cd36 antigen (Cd36), mRNA. 11/2002 Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
3647	18319	NM_031561	ввв, ссс	cd36 antigen (Cd36), mRNA. 11/2002 Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
3648	16163	NM_031563	мм, ттт	nuclease sensitive element binding protein 1 (Nsep1), mRNA. 11/2002 Length = 1489	nuclease sensitive element binding protein 1
3648	16164	NM_031563	RR, VV	nuclease sensitive element binding protein 1 (Nsep1), mRNA. 11/2002 Length = 1489	nuclease sensitive element binding protein 1
3648	16165	NM_031563	D	nuclease sensitive element binding protein 1 (Nsep1), mRNA. 11/2002 Length = 1489	nuclease sensitive element binding protein 1
3652	24219	NM_031579	B, I, J, DD, EE, NN, OO, SS, III, JJJ	protein tyrosine phosphatase 4a1 (Ptp4a1), mRNA. 11/2002 Length = 2638	protein tyrosine phosphatase 4a1

TABLE	30:		and the state of	A CAN	omey Docket 44921-5038-01W0 Document No. 1935323.1
	id no: Grec	CONSINI ACCOT: ROSSOND:	Model Code	Cone Name	Unigeno Seguenço Ciuster IIIle
3653	5496	NM_031589	U, W, TT, WW, EEE, LLL, MMM, RRR, SSS, UUU, General Alternate	glucose-6- phosphatase, transport protein 1 (G6pt1), mRNA. 11/2002 Length = 1930	glucose-6-phosphatase, transport protein 1
3653	5497	NM_031589	TT, WW,		glucose-6-phosphatase, transport protein 1
3656	19340	NM 031603	НН	tyrosine 3- monooxygenase/trypt ophan 5- monooxygenase activation protein, epsilon polypeptide (Ywhae), mRNA. 11/2002 Length =	tyrosine 3- monooxygenase/tryptophan 5- monooxygenase activatioprotein, epsilon polypeptide
3657	24234	NM 031614	G, H, Q,	thioredoxin reductase 1 (Txnrd1), mRNA. 11/2002 Length = 3360	
3657	24235	NM_031614	Q, HH, ZZ, AAA, HHH	thioredoxin reductase 1 (Txnrd1), mRNA. 11/2002 Length = 3360	thioredoxin reductase 1
3660	20940	NM_031629	G, H, X, Y, SSS	proteasome (prosome, macropain) subunit, beta type 4 (Psmb4), mRNA. 11/2002 Length = 831	proteasome (prosome, macropain) subunit, beta type, 4
3660	20942	NM_031629	บบบ	proteasome (prosome, macropain) subunit, beta type 4 (Psmb4), mRNA. 11/2002 Length = 831	proteasome (prosome, macropain) subunit, beta type, 4

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TABL	31	3.0		AS AS	torney Docket 4/4221-5033-01/1/0 Document No. 1935/23.1
	id no.	Consent Acc or RefSeq ID	Model : : :	Kajva Gene Name	Unigana Sequence Civeter Title
				chloride channel, nucleotide-sensitive, 1A (Clns1a), mRNA. 11/2002 Length =	chloride channel, nucleotide-
3676	19048	NM_031719	RR, SS	1399	sensitive, 1A
3678	23884	NM 031731	U	aldehyde dehydrogenase family 3, subfamily A2 (Aldh3a2), mRNA. 11/2002 Length = 2977	alcohol dehydrogenase family 3, subfamily A2
3679	24810	NM 031732	A, G, II, GGG, PPP, QQQ, General Alternate	sulfotransferase family 1A, phenol- preferring, member 2 (Sult1a2), mRNA. 11/2002 Length = 1363	sulfotransferase family 1A, phenol- preferring, member 2
3679	24811	NM 031732	A, B, G, S, VV, GGG, PPP, QQQ, General Core Tox Markers, General Alternate	sulfotransferase family 1A, phenol- preferring, member 2 (Sult1a2), mRNA. 11/2002 Length = 1363	sulfotransferase family 1A, phenol- preferring, member 2
				gamma-glutamyl carboxylase (Ggcx), mRNA. 11/2002	
3684	11611	NM_031756	C, FF	Length = 2754 rab acceptor 1	gamma-glutamyl carboxylase
3686	14953	NM_031774	UU, XX, YY	(prenylated) (Rabac1), mRNA.	rab acceptor 1 (prenylated)
3691	15864	NM_031797	ww, 000	kangai 1 (Kai1), mRNA. 11/2002 Length ≃ 1740	ESTs, Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))
3693	17941	NM_031812	T, XX, YY, PPP, QQQ	CD164 antigen (Cd164), mRNA. 11/2002 Length = 2836	endolyn
3694	17194	NM_031814	ZZ, AAA	G protein-coupled receptor kinase-interactor 1 (Git1), mRNA. 11/2002 Length = 3236	G protein-coupled receptor kinase associated ADP ribosylation factor GTPase-activating protein (GIT1)

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60g (D)		Consonk Acc or Refseq ID.	Model Code	Kyjowin Gene Name	ellii tetevid eenevoez eneginu
3697	15840	NM_031817	ww	osteomodulin (osteoadherin) (Omd), mRNA. 5/2001 Length = 1536	osteomodulin (osteoadherin)
3699	10167	NM 031830	PP, QQ	flotillin 2 (Flot2), mRNA. 11/2002 Length = 2629	flotillin 2
3700	22321	NM_031832	O, BB, PP, VV, EEE, MMM, General Alternate	lectin, galactose binding, soluble 3 (Lgals3), mRNA. 5/2002 Length = 948	lectin, galactose binding, soluble 3
	·		A, B, BB, CC, HH, OO, EEE, GGG, III, JJJ, MMM, General Core Tox	Ketohexokinase (Khk), mRNA. 11/2002 Length =	
3710	16726 19191	NM_031855 NM_031969	Markers O, P	1342 Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. 11/2002 Length = 3513	Ketohexokinase Calmodulin 1 (phosphorylase kinase, delta)
	25802	NM 031969	EEE,	Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. 11/2002 Length = 3513	Calmodulin 1 (phosphorylase kinase, delta)
3716	17601	NM_031976	K, U, X, Y, LLL, SSS	protein kinase, AMP- activated, beta 1 non- catalytic subunit (Prkab1), mRNA. 11/2002 Length = 1978 26S proteasome,	5'-AMP-activated protein kinase, beta subunit
3717	15469	NM_031978	Q, R	subunit p112 (PSMD1), mRNA. 5/2001 Length =	26S proteasome, subunit p112

TABL	E 1	19.			tomey Docket 44921-5093-91WO Document No. 1995328.1
Seq (0)	id ka: Grec:	Consini Accor Roboq (D	Model Gode	Emen ened avoor	Unicene Sequence Cluster Tille
3722	20554	NM_031987	U, LL, BBB, CCC, RRR, SSS		carnitine O-octanoyltransferase
3722	20555	NM_031987	U, FF, BBB, CCC, RRR	carnitine O- octanoyltransferase (Crot), mRNA. 11/2002 Length = 2681	carnitine O-octanoyltransferase
3723	18640	NM 032057	C, I, J, TT, 000	Inositol (myo)-1(or 4)- monophosphatase 1 (Impa1), mRNA. 11/2002 Length = 2075	Inositol (myo)-1(or 4)- monophosphatase 1
3726	21809	NM_032067	ZZ, AAA	RalA binding protein 1 (Ralbp1), mRNA. 5/2001 Length = 3622	RalA binding protein 1
3726	21810	NM_032067	ZZ, AAA	RalA binding protein 1 (Ralbp1), mRNA. 5/2001 Length = 3622	RalA binding protein 1
3730	17474	NM_032614	F	thioredoxin-like 2 (Txnl2), mRNA. 11/2002 Length = 1089	thioredoxin-like 2
3730	17475	NM_032614	F .	thioredoxin-like 2 (Txnl2), mRNA. 11/2002 Length = 1089	thioredoxin-like 2
3736	12363	NM 033351	Z	Fc receptor, IgG, alpha chain transporter (Fcgrt), mRNA. 11/2002 Length = 1552	Fc fragment immunoglobulin G receptor
3736	12365	NM 033351		Fc receptor, IgG, alpha chain transporter (Fcgrt), mRNA. 11/2002 Length = 1552	Fc fragment immunoglobulin G receptor
3737	23895		A, B, ·	PRKC, apoptosis, WT1, regulator (Pawr), mRNA. 11/2002 Length = 2122	Prostate apoptosis response protein 4

TABL	31 24				10th ay Docket 44921-5033-01W0 Document No. 1985823.1
Soq . [D.~;	id kie Gree	Conson; Acc or dis Refect ID	Model	Known Gene Name	Unigeno Sequence Cluster Title
3739	25431	NM 052807		Insulin-like growth factor 1 receptor (Igf1r), mRNA. 10/2001 Length = 4696	Insulin-like growth factor 1
3739	25431	NM_052807	D, SS	cytosolic cysteine dioxygenase 1	receptor
3740	15028	NM_052809	A, B, T, LLL	(Cdo1), mRNA. 5/2002 Length = 1458	cytosolic cysteine dioxygenase 1
3740	25024	NM_052809	A, YY	cytosolic cysteine dioxygenase 1 (Cdo1), mRNA. 5/2002 Length = 1458	gytosolia gyataina diavyganaga 1
			A, D, V, BB, III,	cyclin H (Ccnh), mRNA. 11/2002	cytosolic cysteine dioxygenase 1
3741	12577	NM_052981	JJJ, KK, GGG,	Length = 1116 Phosphoglycerate mutase 1 (Pgam1), mRNA. 10/2002	cyclin H
3743	4090	NM_053290	HHH	Length = 1754 Phosphoglycerate mutase 1 (Pgam1),	Phosphoglycerate mutase 1
3743	25499	NM_053290	G, H, X, Y	mRNA. 10/2002 Length = 1754 Glutathione S-	Phosphoglycerate mutase 1
3744	1524	NM 053293	V, General Alternate	transferase 1 (theta) (Gstt1), mRNA. 11/2001 Length = 914	Glutathione S-transferase 1 (theta)
0747	47470			dynein, cytoplasmic, light chain 1 (Pin), mRNA. 11/2002	
3747	17473	NM_053319	GGG	Length = 505	dynein, cytoplasmic, light chain 1
3749	21977		G, BB, CC, GGG, III, JJJ, KKK, LLL, NNN, OOO, PPP, QQQ, SSS, General Core Tox Markers	insulin-like growth factor binding protein, acid labile subunit (Igfals), mRNA. 11/2002 Length = 1812	insulin-like growth factor binding protein, acid labile subunit

TABL	3 9 .:		the state of	A	tomey/Doctet 44921-5099-01000 Document No. 1935323.1
809 ID	©L©©. 10 No.	(CON-EM); AGG OT . RE/SEQ ID ;	Model Code	emen eneo awean	Oliff edevlə səncupez eneginU
3749	21978	NM_053329	BB, PPP, QQQ, General Core Tox Markers	insulin-like growth factor binding protein, acid labile subunit (Igfals), mRNA. 11/2002 Length = 1812	insulin-like growth factor binding protein, acid labile subunit
3749	25480	NM_053329	G, S, CC, GGG, III, JJJ, KKK, OOO, PPP, QQQ, General Core Tox Markers	insulin-like growth factor binding protein, acid labile subunit (Igfals), mRNA. 11/2002 Length =	insulin-like growth factor binding protein, acid labile subunit
00	20100	14M_000023	Warkers	Msx-interacting-zinc finger (Miz1), mRNA.	protein, acid labile subunit
3751	14934	NM_053337	т, оо	11/2002 Length = 1858	Msx-interacting-zinc finger
3754	6155	NM 053356	G, M, II	procollagen, type I, alpha 2 (Col1a2), mRNA. 11/2002 Length = 4474	procollagen, type I, alpha 2
3754	6156	NM 053356	M	procollagen, type I, alpha 2 (Col1a2), mRNA. 11/2002 Length = 4474	procollagen, type I, alpha 2
3754	6157	NM_053356	S	procollagen, type I, alpha 2 (Col1a2), mRNA. 11/2002 Length = 4474	procollagen, type I, alpha 2
3756	3842	NM_053371	ввв, ссс	fractured callus expressed transcript 1 (Fxc1), mRNA. 5/2002 Length = 780	fractured callus expressed transcript 1
3760	17252	NM_053402		wingless-type MMTV integration site family, member 4 (Wnt4), mRNA. 11/2001 Length = 1213	wingless-type MMTV integration site family, member 4
3762	19322	NM_053409		melanoma antigen, family D, 1 (Maged1), mRNA. 11/2002 Length = 2824	melanoma antigen, family D, 1

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300 (D: 1	GL. GC. GC.	Kesseni Ace or ** 	Code (Known Cone Name	Unigen Sequence Cluster Title
3770	22586	NM_053469	L, M	hepcidin antimicrobial peptide (Hamp), mRNA. 11/2002 Length = 367	hepcidin antimicrobial peptide
3771	21866	NM_053472	V, RR, UU	cytochrome c oxidase, subunit 4b (Cox4b), mRNA. 11/2002 Length = 704	cytochrome c oxidase, subunit
3791	9267	NM_053567	00, PP, TT	formiminotransferase cyclodeaminase (Ftcd), mRNA. 11/2002 Length = 1942	formiminotransferase cyclodeaminase
3793	19252	NM_053576	G, H, L, N, HH	peroxiredoxin 5 (Prdx5), mRNA. 10/2002 Length = 1414	peroxiredoxin 5
3793	19253	NM_053576	G, H	peroxiredoxin 5 (Prdx5), mRNA. 10/2002 Length = 1414 peroxiredoxin 5	peroxiredoxin 5
3793	19254	NM_053576	G, H, L	(Prdx5), mRNA. 10/2002 Length = 1414	peroxiredoxin 5
3794	21153	NM_053584	Т	golgi SNAP receptor complex member 1 (Gosr1), mRNA. 11/2002 Length = 2412	golgi SNAP receptor complex member 1
				ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6 (Atp5j), mRNA. 11/2001 Length =	ATP synthase, H+ transporting, mitochondrial F0 complex,
3802	20725	NM_053602	Q, R	573 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6 (Atp5j), mRNA. 11/2001 Length =	ATP synthase, H+ transporting, mitochondrial F0 complex,
3802	20726	NM_053602	LL	573	subunit F6

TABL	E 1			A	tomey Docket 44921-5033-01000 Document No. 1995323.1
S09 [D,	ELEC.	Ressed ID Geographic Resservant	Coop Model	Known Gene Name	Unigene Sequence Clyster Title
				fatty acid Coenzyme A ligase, long chain 5 (Facl5), mRNA.	
3803	15925	NM_053607	В	10/2002 Length = 2454	long-chain fatty acid coenzyme A ligase 5
			I, J, General	fatty acid Coenzyme A ligase, long chain 5 (Facl5), mRNA. 10/2002 Length =	long-chain fatty acid coenzyme A
3803	15926	NM_053607	Alternate	2454 casein kinase 1,	ligase 5
3804	20243	NM_053615	w	alpha 1 (Csnk1a1), mRNA. 11/2001 Length = 978	casein kinase 1, alpha 1
3809	15090	NM 053638	В, ННН	isocitrate dehydrogenase 3 (NAD+) alpha (Idh3a), mRNA. 11/2002 Length = 2449	isocitrate dehydrogenase 3 (NAD+) alpha
3809	23305	NM 053638	KK, WW,	isocitrate dehydrogenase 3 (NAD+) alpha (Idh3a), mRNA. 11/2002 Length = 2449	isocitrate dehydrogenase 3 (NAD+) alpha
3817	13368	NM 053742	T, PP, QQ	phosphotidylinositol transfer protein, beta (Pitpnb), mRNA. 11/2002 Length = 2680	phosphotidylinositol transfer
3817	13369	NM 053742	C, UU, HHH, General Alternate	phosphotidylinositol transfer protein, beta (Pitpnb), mRNA. 11/2002 Length = 2680	phosphotidylinositol transfer
3818	15376	NM_053747	Q, R, T	ubiquilin 1 (Ubqln1), mRNA. 11/2002 Length = 2131	ubiquifin 1
3822	24621	NM_053764	Z, AA	regulator of G-protein signaling 14 (Rgs14), mRNA. 11/2001 Length = 2854	

TABL	E 1	170.7		A	tomey Doctet 44921-5938-011W0 Document No. 1985323.1
Seq :	39.19 (1)	Consons Acc or Acc Reference	Model &	emski sneð hvonk	Unigana Saquanca Cluster Titla
3823	7927	NM 053765	I, U, X, Y, DDD, LLL	UDP-N- acetylglucosamine-2- epimerase/N- acetylmannosamine kinase (Uae1), mRNA. 11/2002 Length = 2508	UDP-N-acetylglucosamine-2- epimerase/N-acetylmannosamine kinase
3825	15995	NM_053769	LJOR	protein tyrosine phosphatase, non- receptor type 16 (Ptpn16), mRNA. 11/2002 Length =	protein tyrosine phosphatase, non- receptor type 16
3825	15996	NM_053769		protein tyrosine phosphatase, non- receptor type 16 (Ptpn16), mRNA. 11/2002 Length = 1908	protein tyrosine phosphatase, non-receptor type 16
3825	15997	NM_053769	I, J, R	protein tyrosine phosphatase, non- receptor type 16 (Ptpn16), mRNA. 11/2002 Length = 1908	protein tyrosine phosphatase, non- receptor type 16
3844	11405	NM_053866	Q, R, PPP, QQQ	phospholipase A2, activating protein (Plaa), mRNA. 11/2001 Length = 2451 polymerase (RNA) II	phospholipase A2, activating protein
3854	15857	NM_053948	ZZ, AAA	(DNA) directed)polypeptide G (Polr2g), mRNA. 11/2001 Length = 864	polymerase (RNA) II (DNA directed)polypeptide G
3875	22849	NM_057099	G, Н	proteasome (prosome, macropain) subunit, beta type 6 (Psmb6), mRNA. 11/2002 Length = 760	proteasome (prosome, macropain) subunit, beta type 6
3875	25253	NM_057099 ·	В, G, H, РРР, QQQ	proteasome (prosome, macropain) subunit, beta type 6 (Psmb6), mRNA. 11/2002 Length = 760	proteasome (prosome, macropain) subunit, beta type 6

TABL					(Omey Docket 44921-5033-01WO E: Document No. 1935323.1
S00 :	id ko Grec	Refee or Refee or	Model Code 😭	Engliere awoni	Unigene Sequence Cluster Tille
3878	9527	NM_057104	E, Y, CC, HH, General Alternate	ectonucleotide pyrophosphatase/pho sphodiesterase 2 (Enpp2), mRNA. 11/2002 Length = 3216	ectonucleotide pyrophosphatase/phosphodiester ase 2
3878	9528	NM_057104	HH, General Alternate	ectonucleotide pyrophosphatase/pho sphodiesterase 2 (Enpp2), mRNA. 11/2002 Length = 3216	ectonucleotide pyrophosphatase/phosphodiester ase 2
3879	5492	NM_057105	G, K, GG, HH, WW, DDD	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 1/2002 Length = 1593	ESTs, UDP glycosyltransferase 1 family, polypeptide A6
3879	5493	NM 057105	G, K, GG, HH, TT, WW, DDD	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 1/2002 Length = 1593	ESTs, UDP glycosyltransferase 1 family, polypeptide A6
3879	15124	NM_057105	J, K, L, N, S, U, FF, GG, HH, TT,	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 1/2002 Length =	UDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransferase 1 family, polypeptide A7, UDP-glucuronosyltransferase 1 family, member 1
3879	15125	NM_057105	GG, PP, QQ, TT,	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 1/2002 Length = 1593	UDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransferase 1 family, polypeptide A7
3879	15126	NM_057105	M, N, U, X, Y, GG,	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 1/2002 Length = 1593	UDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransferase 1 family, polypeptide A7, UDP-glucuronosyltransferase 1 family, member 1

TABL	E1 :		1		(Ofney Docket 44921-5009-01000
Seq. (D)	(D) (VO.)	Conson; Acc or Resseq ID	Model Code		Uilgane Sequence Cluster Title
3879	15127	NM_057105	I, J, K, L, M, S, U, X, GG, HH, TT, LLL, SSS, UUU	glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA.	UDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransferase 1 family, polypeptide A7, UDP-glucuronosyltransferase 1 family, member 1
3886	19833	NM_057139	GG	transporter protein; system N1 Na+ and H+-coupled glutamine transporter (Hnrpu), mRNA. 11/2001 Length = 3563	transporter protein; system N1 Na+ and H+-coupled glutamine transporter
3889	6613	NM_057186	Α, υ	L-3-hydroxyacyl- Coenzyme A dehydrogenase, short chain (Hadhsc), mRNA. 11/2002 Length = 1660	hydroxylacyl-Coenzyme A dehydrogenase, short chain
3891	15408	NM_057197	M, U, FF, XX, YY, BBB, CCC	2,4-dienoyl CoA reductase 1, mitochondrial (Decr1), mRNA. 11/2002 Length = 1109	2,4-dienoyl CoA reductase 1,
3891	15409	NM 057197		2,4-dienoyl CoA reductase 1, mitochondrial (Decr1), mRNA. 11/2002 Length = 1109	2,4-dienoyl CoA reductase 1,
3897	21562	NM_078623		enoyl Coenzyme A hydratase, short chain 1 (Echs1), mRNA. 11/2002 Length = 1454	Enoyl-CoA hydratase, short chain 1, mitochondrial
3901	17956	NM_080583	JJ, KK, HHH	adaptor-related protein complex 2, beta 1 subunit (Ap2b1), mRNA. 11/2002 Length = 5413	adaptor-related protein complex 2, beta 1 subunit

TABL	፪1	2		A	tomey Docket 44921-5063-011WO Document No. 1935328.1
Seq - [p: -6	id ko erec	Consent Accor Rowsog (D	Model Godo		elill retaris enging
3902	16108	NM_080585	Z, AA	N-ethylmaleimide sensitive fusion protein attachment protein alpha (Napa), mRNA. 1/2002 Length = 1505	N-ethylmaleimide sensitive fusion protein attachment protein alpha
3902	16109	NM 080585	RR, SS	N-ethylmaleimide sensitive fusion protein attachment protein alpha (Napa), mRNA. 1/2002 Length = 1505	N-ethylmaleimide sensitive fusion protein attachment protein alpha
				proteasome (prosome, macropain) subunit, beta type, 8 (low molecular mass polypeptide 7) (Psmb8), mRNA. 10/2002 Length =	Proteasome (prosome, macropain) subunit, beta type, 8 (low molecular mass polypeptide
3906	25252	NM_080767	O, P, HH	1018 coatomer protein	7)
3907	19831	NM_080781	U	complex, subunit beta 1 (Copb1), mRNA. 1/2002 Length = 3073 sterol-C4-methyl	coatomer protein complex, subunit beta 1
3909	21842	NM_080886	l, J, II, XX, FFF	oxidase-like (Sc4mol), mRNA. 3/2002 Length = 1712	sterol-C4-methyl oxidase-like
3920	21391	NM_130416	X, Y	annexin A7 (Anxa7), mRNA. 1/2002 Length = 2912	annexin A7
3924	14959	NM_130734	A, B, JJ, KK, FFF, GGG, HHH, General Alternate	guanine nucleotide binding protein, beta polypeptide 2-like 1 (Gnb2l1), mRNA. 11/2002 Length = 1089	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
3927	9268	NM_130756	U, LL, BBB, CCC, LLL, RRR, SSS, UUU	4,8-dimethylnonanoyl- CoA thioesterase (Pte1), mRNA. 10/2002 Length = 1145	peroxisomal acyl-CoA thioesterase 1

TABL	፪ ብ፡	· · · · · · · · · · · · · · · · · · ·	164 Marie	A PART CARREST AND AND	tomey Doctor 44921-5088-01WO
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S99 ID:	eree :	ලක තැ Acc ග Refseq (D	Model Code	Known Cone Kame	Unigene Sequence Cluster Title
3933	20879	NM_133295	D, V, NN, OO, FFF	carboxylesterase 3 (Ces3), mRNA. 11/2002 Length = 1935	carboxylesterase 3
3933	20880	NM_133295	LL	carboxylesterase 3 (Ces3), mRNA. 11/2002 Length = 1935	carboxylesterase 3
	10456		O B \\\	glycoprotein (transmembrane) nmb (Gpnmb), mRNA. 2/2002	glycoprotein (transmembrane)
3934	19456	NM_133298	O, P, VV	Length = 2320 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (Atp5g2), mRNA. 11/2002 Length =	ATP synthase, H+ transporting, mitochondrial F0 complex,
3948	15524	NM_133556	v	593	subunit c (subunit 9), isoform 2
3968	21098	NM_134432	C, L, DD, NNN	angiotensinogen (Agt), mRNA. 11/2002 Length = 1434 monoglyceride lipase (Mgll), mRNA.	Angiotensinogen
3972	12215	NM_138502	K, BBB	11/2002 Length = 912	monoglyceride lipase
			L, LL,	Sterol carrier protein 2, liver (Scp2), mRNA. 11/2002	,
3973	16180 14822	NM_138508 NM_138708	Q, R, JJ, KK, MM, FFF, TTT	Length = 2599 Rab geranylgeranyl transferase componenet, subunit beta (Rabggtb), mRNA. 4/2002 Length = 996	Sterol carrier protein 2, liver Rab geranylgeranyl transferase componenet, subunit beta
				apolipoprotein E (Apoe), mRNA. 11/2002 Length =	
4002	17203	NM_138828 NM_139099	S RRR	936 ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit (Atp5e), mRNA. 5/2002 Length = 404	Apolipoprotein E, ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit

TABL	E1	. 10	· · · · · · · · · · · · · · · · · · ·		tomey Docket 44921-5033-01W0 Document No. 1935323.1
509 (D	id ko: :	Conson: Acc or Refseq ID	Model Code ;	enien enema	Unigene Sequence Ciuster Tille
4003	17549	NM_139100	G, H,	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3 (Slc25a3), mRNA. 11/2002 Length = 1263 aldehyde reductase	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3
4026	9096	NM 145771	RRR	(aldose reductase) like 6 (Aldrl6), mRNA 11/2002 Length = 1006	hypothetical protein LOC56728
		140711	IWW	ribosomal protein	hypothetical protein LOC30/28
4053	11850	R46985	G	L10a	ribosomal protein L10a
4055	18356	R47042	D	decorin	decorin
4056	16223	R47122 R47128	Z, AA PP, QQ	Fibronectin 1 Secreted acidic cystein-rich glycoprotein (osteonectin)	Fibronectin 1 Secreted acidic cystein-rich glycoprotein (osteonectin)
4069	1471	S68809	RR		ESTs, Highly similar to S10A_RAT S-100 protein, alpha chain [R.norvegicus]
4087	40	U02096	II, MM, XX, YY, FFF, TTT	fatty acid binding protein 7, brain Solute carrier family	fatty acid binding protein 7, brain
4089	313	U03120	JJ, KK	5, member alpha 1 (Na+/glucose cotransporter)	Solute carrier family 5, member alpha 1 (Na+/glucose cotransporter)
4097	1928	U10357		pyruvate dehydrogenase kinase 2 subunit p45 (PDK2)	pyruvate dehydrogenase kinase 2 subunit p45 (PDK2)
4101	1424	U14746	w	von Hippel-Lindau syndrome	von Hippel-Lindau syndrome
4113	1340	U25651	ss	phosphofructokinase, muscle	phosphofructokinase, muscle
4115	317	U29339		avian erythroblastosis oncogene B 3	avian erythroblastosis oncogene B 3
4125	368	U38379	XX, YY	Gamma-glutarnyl hydrolase	Gamma-glutamyl hydrolase
4130		U42719	ввв, ссс	Complement component 4	Complement component 4
4131	19543			cysteine-rich protein 2	cysteine-rich protein 2

TABLI	3	E		A	tomey Docket 44921-5038-0100 : Document No. 1935323.1
Seq (ID	@r@€	Consini Accor Rosco (D	Model Code	emen erre vivorin	Unigene Sequence Civeler Tille
4138	1960	U52102	FF	Collapsin response mediator protein 1	Collapsin response mediator protein 1
1100			<u></u>	MAD (mothers against decapentaplegic, Drosophila) homolog	MAD (mothers against decapentaplegic, Drosophila)
4155	871	U66479	BB, CC	3	homolog 3
4158	794	U68168	B, G, M, GG, HH, NN, OO, FFF, GGG, III, JJJ, General Core Tox Markers	kynureninase (L- kynurenine hydrolase)	kynureninase (L-kynurenine hydrolase)
			A, B, III, JJJ, KKK, OOO, PPP, QQQ, General Core Tox	fatty acid amide	
4162	851	U72497	Markers W, BB,	hydrolase A kinase (PRKA)	fatty acid amide hydrolase
			CC, ZZ,	anchor protein	A kinase (PRKA) anchor protein
4166	2153	U75404	AAA	(gravin) 12	(gravin) 12
4171	1520	U77777	V	interleukin 18	interleukin 18
4178	1401	U93692	ZZ, AAA	preimplantation protein 2	preimplantation protein 2
4181	412	V01216	D, E, BB, CC, III, JJJ	Orosomucoid 1	Orosomucoid 1
4183	818	X02291	HH, SS	Aldolase B, fructose- biphosphate	Aldolase B, fructose-biphosphate
4188	614	X04070	General Alternate	gap junction membrane channel protein beta 1	gap junction membrane channel protein beta 1
4192	20715	X07259		Cytochrome P450, subfamily IVB, polypeptide 1 Arginosuccinate	Cytochrome P450, subfamily IVB, polypeptide 1
4194	20597	X12459	BBB	synthetase 1 Fibroblast growth factor 1 (heparin	Arginosuccinate synthetase 1 Fibroblast growth factor 1
4199	644	X14232	X, Y	binding)	(heparin binding)

TABL	31	TO THE	a aş vara Yeşkir		tomey.Docket 44921-5033-01W0 ****** Document No. 1935323.1
Seq.	id ko: Gréc:	Ressens Ressens Pleases	Model	Known Cene Name	Unicene Sequence Cluster Title
4201	21152	X14848	F, S, FF, HH, SS, WW	golgi SNAP receptor complex member 1	golgi SNAP receptor complex member 1
4205	575	X15734	F, L, T, RR, SS, WW, SSS, UUU	S - adenosylmethionine synthetase	S - adenosylmethionine synthetase
4206	15626	X17665	F, H, BB, CC, EEE, MMM	ribosomal protein S16	ESTs, Highly similar to R3RT16 ribosomal protein S16, cytosolic [validated] - rat [R.norvegicus]
4207	1893	X51529	NN, EEE, MMM	phospholipase A2, group IIA (platelets, synovial fluid)	phospholipase A2, group IIA (platelets, synovial fluid)
4215 4218	20427	X53378 X53944	FFF, HHH, General Alternate RR	ribosomal protein S13 dopamine receptor 3	ribosomal protein S13 dopamine receptor 3
4219	670	X54096	XX, YY, CCC, PPP, QQQ	Lecithin-cholesterol acyltransferase	Lecithin-cholesterol acyltransferase
4221	21122	X56228	R, DDD, PPP, QQQ	Thiosulfate sulphurtransferase (rhodanese)	Thiosulfate sulphurtransferase (rhodanese)
4221	21123	X56228	Q, R, SS, DDD, PPP, QQQ, General Alternate	Thiosulfate sulphurtransferase (rhodanese)	Thiosulfate sulphurtransferase (rhodanese)
4228	10109 ·	X58465	G, H, II, VV, DDD, EEE, FFF, GGG, III, JJJ, MMM, General Core Tox Markers	Ribosomal protein S5	Ribosomal protein S5

TABL					termay Dockat 44921-5033-011770 Document No. 1986323.1
809 10	രുപര്ദ	Consoni Acc or Rowseq ID	Model Codo	Sing Vience (accord	Ünigene Sequence Civeter Title
			X, Y, JJ, KK, FFF,		
			GGG, HHH, III,		
			JJJ,		
			General Core Tox		
4228	25702	X58465	Markers	Ribosomal protein S5	Ribosomal protein S5
4229	1719	X59267	Z, AA, SS		drebrin 1
4045	545	V02054		Transporter 2, ABC (ATP binding	Transporter 2, ABC (ATP binding
4245	515	X63854	UU O, P,	cassette)	cassette)
			FFF, General	peroxisomal membrane protein 2,	peroxisomal membrane protein 2,
4253	405	X70223	Alternate W, DD,	22 kDa	22 kDa
			EE, SS, WW, XX,		
			YY, General		
			Core Tox	Sorbitol	
4260	1877	X74593	Markers	dehydrogenase Cholecystokinin B	Sorbitol dehydrogenase
4266	447	X79208	RR	receptor	Cholecystokinin B receptor
4269	570	X82445	ввв, ссс	nuclear distribution gene C homolog (Aspergillus)	nuclear distribution gene C homolog (Aspergillus)
4273	764	X84210	F, HH, JJ, KK	Nuclear Factor IA	Nuclear Factor IA
				alcohol	
4277	420	X90710	U, RRR, SSS	dehydrogenase 4 (class II), pi polypeptide	alcohol dehydrogenase 4 (class II), pi polypeptide
				hypoxia inducible	
4284	1146	Y09507	ww	factor 1, alpha subunit	hypoxia inducible factor 1, alpha subunit
4288	442	Z22867	Z, AA	phosphodiesterase 3B, cGMP-inhibited	phosphodiesterase 3B, cGMP-inhibited
					ESTs, Highly similar to T30827
					nascent polypeptide-associated complex alpha chain, non-muscle
8	6050	AA686190	N, V		splice form - mouse [M.musculus]
			KK, GGG,	•	
			HHH, General	NADH ubiquinone oxidoreductase	NADH ubiquinone oxidoreductase
22	15654	AA799501	Alternate	subunit B13	subunit B13

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TABL	E 1			AL AL	1000 000 0000 0000 0000 0000 00000 00000 0000
	1	10dom) • Iomie	·		Document No. 1996323.1
000	en ee	CONSTRAINT	Model		
(10) Seq	(B) No. (Accor Roßeg (D:	(COGO	Known Cone Name	eneups Sanguard Cluster Title
	1		T, MM,		ESTs, Highly similar to
	İ	1	PPP,		ITMB_MOUSE Integral
İ		į	QQQ,		membrane protein 2B (E25B
25	16942	AA799520	TTT,		protein) [M.musculus]
	1.00.12	7 00020	1		ESTs, Highly similar to RIKEN
					cDNA 1700043E15 [Mus
27	21120	AA799526	s		musculus] [M.musculus]
			1		ESTs, Moderately similar to
					RIKEN cDNA 9130413122 [Mus
33	16959	AA799550	ННН		musculus] [M.musculus]
-	1		1	<u> </u>	ESTs, Weakly similar to A55071
					hydrogen peroxide-inducible
					protein hic-5 - mouse
46	20093	AA799637	ใบบบ		[M.musculus]
					ESTs, Moderately similar to
	İ				I53063 testicular tumor
		į			overexpressed protein - mouse
47	18227	AA799641	Z, AA		[M.musculus]
					ESTs, Moderately similar to
			i		predicted gene
					ICRFP703B1614Q5.6;
					ICRFP703N2430Q5.6; C11orf17
66	18880	AA799801	D		[Mus musculus] [M.musculus]
	ţ				ESTs, Highly similar to DDRT
			R, MM,		helix-destabilizing protein - rat
74	15011	AA799893	TTT		[R.norvegicus]
			ł		ESTs, ESTs, Moderately similar
		1			to predicted gene ICRFP703B1614Q5.6;
		1			ICRFP703B1014Q5.6; ICRFP703N2430Q5.6; C11orf17
70	18883	AA799992	7 00		[Mus musculus] [M.musculus]
78	10003	AA799992	Z, AA Q, R,		[Mus musculus] [M.musculus]
79	2098	AA799995	QQQ	ribosomal protein I 14	ribosomal protein L14
	12000	744733333	- Cara	Tibosomai protoni E14	ESTs, Highly similar to JC7136
			II, ZZ,		peptidylprolyl isomerase (EC
86	21064	AA800175	AAA		5.2.1.8) - mouse [M.musculus]
-	1-11-1				ESTs, Weakly similar to B39066
l	}				proline-rich protein 15 - rat
90	15659	AA800199	Р		[R.norvegicus]
	1				ESTs, Moderately similar to low
l					density lipoprotein B [Mus
94	18442	AA800258	ZZ, AAA		musculus] [M.musculus]
				HMm:tumor necrosis	ESTs, Highly similar to tumor
1				factor (ligand)	necrosis factor (ligand)
				superfamily, member	
117	9092	AA800814	Z, AA ·	13	musculus] [M.musculus]
					ESTs, Moderately similar to
			1		0806162L protein URF5 [Mus
118	22025	AA800849	S, TT		musculus] [M.musculus]

TABL	31 %		No. 144 An Alberta	A CONTRACTOR OF THE CONTRACTOR	isiney Docket 44921-5038-01W0
\$99 [D. ; ; ;	ID No.	Conson; Accor Rowseq ID	Modol Codo	Known Cene Neme	Unigaçã Sequênca Circia Tille
			· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·	ESTs, Highly similar to S11661
122	21416	AA800962	O, X, Y		talin - mouse [M.musculus]
				Testis-specific	
124	23115	AA801165	11	histone 2a	Testis-specific histone 2a
					ESTs, Weakly similar to plexin
					B3; plexin 6 [Mus musculus]
126	11166	AA801346	บบ		[M.musculus]
					ESTs, Weakly similar to
		1			PSD7_MOUSE 26S proteasome
		Ì			non-ATPase regulatory subunit 7
ļ				. *	(26S proteasome regulatory
					subunit S12) (Proteasome subunit
					p40) (Mov34 protein)
148	2845	AA818026	บบบ		[M.musculus]
					ESTs, Highly similar to RIKEN
	ļ				cDNA 0610009M10; RIKEN
					cDNA 0610009M10 gene [Mus
180	4245	AA818692	GG, RR		musculus] [M.musculus]
			O, P, V,		Rattus norvegicus mRNA for
189	4491	AA818798	VV .		cathepsin Y, partial cds
191	7690	AA818875	ННН	uroguanylin	uroguanylin
					ESTs, Moderately similar to
					MBNL_MOUSE Muscleblind-like
					protein (Triplet-expansion RNA-
197	22175	AA818999	ww		binding protein) [M.musculus]
1					ESTs, Moderately similar to
					S31799 apolipoprotein C2
206	6329	AA819259	XX, YY		precursor - mouse [M.musculus]
					ESTs, Highly similar to
240	47004	1 4040000			hypothetical protein MGC7474
212	17824	AA819362	LL		[Mus musculus] [M.musculus] ESTs, Highly similar to R3RT27
1		ļ			ribosomal protein S27, cytosolic
240	17097	AA819501	F, II		[validated] - rat [R.norvegicus]
218	17037	AA019301	YY, PPP,		Rattus norvegicus complement
236	230	AA819870	QQQ		C8 beta (C8b) mRNA, partial cds
230	230	77013010	ada	stearoyl-Coenzyme A	stearoyl-Coenzyme A desaturase
237	320	AA819905	U	desaturase 1	1
201	020	74013300	<u> </u>	MAP-kinase	<u> </u>
				activating death	MAP-kinase activating death
258	21171	AA848979	D	domain	domain
		1.3.5.55.5		Protein-L-	
				isoaspartate (D-	
ł				aspartate) O-	Protein-L-isoaspartate (D-
274	17179	AA849797	GGG	methyltransferase	aspartate) O-methyltransferase
	 			cyclase-associated	cyclase-associated protein
277	23981	AA850040	0, P	protein homologue	homologue
					ESTs, Moderately similar to
					0806162L protein URF5 [Mus
279	22027	AA850060	v, 000		musculus] [M.musculus]

TABL		1			tomey Docket 44921-5033-0100 Document No. 1985323.1
	id ko	Regod (D) Vee of Regions	Mogol 👙 🟃		Uniganè Saquanca Clustar Tilla
070	22022	4.4.05.0000	000		ESTs, Moderately similar to 0806162L protein URF5 [Mus
279	22028	AA850060	ccc		musculus] [M.musculus] ESTs, Highly similar to Tnf
		<u> </u>	JJ, KK,	\	receptor associated factor 4 [Mus
285	16329	AA850542	FFF	•	musculus] [M.musculus]
-	1,0020				ESTs, Highly similar to T09123
					hybrid receptor SorLA precursor -
287	14507	AA850618	RRR		mouse (fragment) [M.musculus]
<u> </u>					ESTs, Highly similar to ring-box
		•			1; ring-box protein 1 [Mus
289	22797	AA850733	LL	HMm:ring-box 1	musculus] [M.musculus]
					ESTs, Highly similar to
1					peptidylprolyl isomerase D
	1				(cyclophilin D) [Mus musculus]
292	22721	AA850781	V		[M.musculus]
l	İ			unknown Glu-Pro	
	10400	* * * * * * * * * * * * * * * * * * * *	E, S, T,	dipeptide repeat	unknown Glu-Pro dipeptide
294	16132	AA850885	HH, NNN	protein	repeat protein
			W 000		ESTs, Highly similar to
299	3924	AA851017	W, DDD, LLL		molybdenum cofactor synthesis 2 [Mus musculus] [M.musculus]
299	3924	AA051017	LLL		ESTs, Highly similar to
1			Q, R,		molybdenum cofactor synthesis 2
299	3925	AA851017	WW, LLL		[Mus musculus] [M.musculus]
200	10020	7 0 00 10 17	17777, 222	ribosomal protein	[mas massaras] [m.massaras]
302	2103	AA851135	YY	S27	ribosomal protein S27
			O, P, VV,		Rattus norvegicus mRNA for
303	4490	AA851184	ннн		cathepsin Y, partial cds
					ESTs, Highly similar to
i					SNX5_MOUSE Sorting nexin 5
312	883	AA851347	O, P		[M.musculus]
					ESTs, Weakly similar to I49523
1					tumor necrosis factor alpha-
l					induced protein 2 - mouse
315	21489	AA851443	GG		[M.musculus]
					ESTs, Weakly similar to
204	44000	A A D 5 4 7 0 4			CBP_MOUSE CREB-binding
321	14292	AA851791	R		protein [M.musculus]
			1		ESTs, Highly similar to UB6B MOUSE Ubiquitin-
					conjugating enzyme E2-23 kDa
					(Ubiquitin-protein ligase)
1]		(Ubiquitin carrier protein)
337	15284	AA858551	вв, сс		[M.musculus]
 		7 3 1000001	155, 55		ESTs, Highly similar to S20444
				HMm:leukotriene A4	leukotriene-A4 hydrolase (EC
338	13523	AA858552	NN, 00	hydrolase	3.3.2.6) - rat [R.norvegicus]
<u> </u>					- · - · - · · · · · · · · · · · · · · ·

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TABL	31	a de la companya de la companya de la companya de la companya de la companya de la companya de la companya de La companya de la companya de la companya de la companya de la companya de la companya de la companya de la co			tomey Docket 44921-5093-01W0
Seq: ID:::	ELGE SOLO	Refeet ID	Modeli Code	Emel Meme.	Unigene Sequence Cluster Mile
			LL, EEE,		
340	18001	AA858573	MMM, UUU	spp-24 precursor	spp-24 precursor
			A, B, I, J,		COT- Alichte de la landa
	l		SS,		ESTs, Highly similar to
İ			General Core Tox	'	EXT1_MOUSE Exostosin-1 (Multiple exostoses protein 1
350	17334	AA858704	Markers		homolog) [M.musculus]
330	117334	AA636704	IVIAIREIS		ESTs, Weakly similar to RIKEN
					cDNA 1500031O19 [Mus
351	6380	AA858758	FF, LL		musculus] [M.musculus]
00.	0000	7 4 1000 7 00	,		ESTs, Highly similar to
					proteasome (prosome,
		ļ	A, B, G,		macropain) 26S subunit, non-
			H, S,		ATPase, 13; 26S proteasome
			PPP,		subunit p40.5 [Mus musculus]
356	6403	AA858879	QQQ		[M.musculus]
					ESTs, Weakly similar to JC2524
	1		Q, R,		phosphoprotein phosphatase (EC
			General		3.1.3.16) 1A-beta - rat
366	6440	AA859130	Alternate		[R.norvegicus]
					R.norvegicus mRNA for
					tropomyosin isoform 6, Rattus
1					norvegicus nonmuscle
					tropomyosin 5 (Tpm5) isoforms
274	44404	A A 0 5 0 2 0 5			NM 5 and NM 6 mRNA, partial cds
371	14124	AA859305	VV, HHH		ESTs, Highly similar to
					UBPA MOUSE UBIQUITIN
					CARBOXYL-TERMINAL
į					HYDROLASE 10 (UBIQUITIN
					THIOLESTERASE 10)
					(UBIQUITIN-SPECIFIC
					PROCESSING PROTEASE 10)
			PPP,		(DEUBIQUITINATING ENZYME
372	15149	AA859327	QQQ		10) [M.musculus]
					ESTs, Highly similar to
	1				BAG3_MOUSE BAG-family
					molecular chaperone regulator-3
1					(BCL-2 binding athanogene-3)
					(BAG-3) (Bcl-2-binding protein
375	15172	AA859362	XX, YY		Bis) [M.musculus]
	I				EST, Moderately similar to
200	17140	A A 9 5 0 0 4 0	l		0806162J protein URF4 [Mus
386	17142	AA859612	J, LL		musculus] [M.musculus]

TABL	31				tomey Docket 44921-5093-01WO The Document No. 1935823.1
500 10	elec.	Kefseg ID .	Code	Ejüdiləne anvonil	Valgano Soquence Cluster Tille
389	11635	AA859645	A, B, F, G, S, FFF, GGG, III, JJJ, OOO, General Core Tox Markers	attractin	attractin
393	14138	AA859700	E, General Alternate	HMm:protoporphyrin	ESTs, Highly similar to PPOX_MOUSE PROTOPORPHYRINOGEN OXIDASE (PPO) [M.musculus]
			E, III, JJJ, NNN, General	HMm:protoporphyrin	ESTs, Highly similar to PPOX_MOUSE PROTOPORPHYRINOGEN
393	14139	AA859700	Alternate	ogen oxidase	OXIDASE (PPO) [M.musculus] ESTs, Highly similar to SAP3_MOUSE Ganglioside GM2 activator precursor (GM2-AP) (Cerebroside sulfate activator protein) (Shingolipid activator
396 410	22374 4222	AA859804 AA860024	P KK		protein 3) (SAP-3) [M.musculus] ESTs, Highly similar to EF1G_MOUSE Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) [M.musculus]
411	13974	AA860030	O, P, VV		Rattus norvegicus mRNA for class I beta-tubulin, complete cds
415	15884	AA866276	O, P, PP		ESTs, Weakly similar to A60543 protein kinase (EC 2.7.1.37), cAMP-dependent, catalytic chain - rat (fragment) [R.norvegicus]
424	16013	AA866482	Q, R, PPP, QQQ		ESTs, Highly similar to FGD1_MOUSE Putative Rho/Rac guanine nucleotide exchange factor (Rho/Rac GEF) (Faciogenital dysplasia protein homolog) [M.musculus]
426	22781	AA874926	V, RR, SS		ESTs, Weakly similar to dual- specificity phosphatase [Mus musculus] [M.musculus]
428	16167	AA874941	С		ESTs, Moderately similar to ADFP_MOUSE ADIPOPHILIN (ADIPOSE DIFFERENTIATION-RELATED PROTEIN) (ADRP) [M.musculus]

11.50	E 1				tomay Docket 44921-5083-0100 Document No. 1935823.1
509 (D	erec erec	Consens Aceor Reisen ID	Model Code	Known Cene Name	
430	17303	AA874990	บบ		ESTs, Weakly similar to RIKEN cDNA 6330407G11 [Mus musculus] [M.musculus]
447	15887	AA875225	PP, QQ	GTP-binding protein (G-alpha-i2)	GTP-binding protein (G-alpha-i2)
447	15888	AA875225	O, P, X, NN, OO, VV, ZZ, AAA	GTP-binding protein (G-alpha-i2)	GTP-binding protein (G-alpha-i2)
455	24470	AA875523	GG	(S dipita 12)	ESTs, Highly similar to MLES_RAT Myosin light chain alkali, smooth-muscle isoform (MLC3SM) [R.norvegicus]
461	2846	AA875639	v		ESTs, Weakly similar to FAS_RAT FATTY ACID SYNTHASE [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14] [R.norvegicus]
464	5384	AA891041	W, BB, CC, DD, EE, PP, QQ, III, NNN	iun B proto-oncogene	jun B proto-oncogene
476	21951	AA891535	MM, ZZ, AAA, TTT	, ,	ESTs, Highly similar to hippocampus abundant gene transcript 1 [Mus musculus] [M.musculus]
480	17225	AA891553	General Core Tox Markers		ESTs, Moderately similar to IF37_MOUSE Eukaryotic translation initiation factor 3 subunit 7 (eIF-3 zeta) (eIF3 p66) [M.musculus]
483	22858	AA891591	D	programmed cell death 8 (apoptosis- inducing factor)	programmed cell death 8 (apoptosis-inducing factor)
485	22860	AA891681	N, MM, TTT		ESTs, Highly similar to UNRI_MOUSE UNR-interacting protein (Serine-threonine kinase receptor-associated protein) [M.musculus]
487	9091	AA891690	vv	factor (ligand) superfamily, member 13	ESTs, Highly similar to tumor necrosis factor (ligand) superfamily, member 13 [Mus musculus] [M.musculus]
502	6967	AA891810	S		ESTs, Moderately similar to g1- related zinc finger protein [Mus musculus] [M.musculus]

TABL				- A	Homey Doctet 44921-5083-01W0
Seq -	Gree!	kessed (D :	Model Code :	Known Cene Name	Unigene Sequence Cluster Title
502	6968	AA891810	м		ESTs, Moderately similar to 'g1- related zinc finger protein [Mus musculus] [M.musculus]
504	7050	AA891824	SS		Rattus norvegicus clone ZG52 mRNA sequence
510	16023	AA891872	000		ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) [M.musculus]
519	17333	AA891940	EEE, MMM		ESTs, Highly similar to RHOC_MOUSE TRANSFORMING PROTEIN RHOC [M.musculus]
527	16836	AA892005	BBB, CCC		ESTs, Weakly similar to PGC1_RAT Membrane associated progesterone receptor component 1 (Acidic 25 kDa protein) (25-DX) [R.norvegicus]
534	19469	AA892112	V, NN, EEE, MMM		ESTs, Weakly similar to PROD_MOUSE PROLINE OXIDASE, MITOCHONDRIAL PRECURSOR (PROLINE DEHYDROGENASE) [M.musculus]
543	3427	AA892246	С, НН	· ·	ESTs, Weakly similar to serine/threonine kinase 25 (yeast); Ste20-like kinase; serine/threonine kinase 25 (Ste20, yeast homolog); Yeast Sps1/Ste20-related kinase 1 [Mus musculus] [M.musculus]
550	7226	AA892297	D	histone deacetylase 2	histone deacetylase 2
554	18209	AA892318	ww		ESTs, Highly similar to JC7219 nuclear protein SR-25 - mouse [M.musculus]
564	23194	AA892417	I, J, W	ephrin A1	ephrin A1
572	15154	AA892532	I, J, K, FF, 000		R.norvegicus (Wistar) CaBP1 mRNA
573	17468	AA892545	E, I, J, KKK, NNN, OOO		ESTs, Moderately similar to organic cationic transporter-like 2 [Mus musculus] [M.musculus]

TABL	E 1	1 1		A A A A A A A A A A A A A A A A A A A	tomay Docket 44921-5033-01WO Document No. 1935323.1
S09, [D,:	ID No.	Consoni Ace or Rosso (D	Model . Code .	Known Cene Name	Unicene Sequence Cluster, Title
					ESTs, Highly similar to S15892
				HMm:pyruvate	pyruvate dehydrogenase
			, · · ·	déhydrogenase	(lipoamide) (EC 1.2.4.1) beta
594	11997	AA892828	TTT	(lipoamide) beta	chain - rat [R.norvegicus] ESTs, Highly similar to S15892
	1			HMm:pyruvate	pyruvate dehydrogenase
	1	}		dehydrogenase	(lipoamide) (EC 1.2.4.1) beta
594	11998	AA892828	MM, TTT	(lipoamide) beta	chain - rat [R.norvegicus]
004	11330	74032020	100000	(iipodifiido) bota	ESTs, Moderately similar to
					BTF3_MOUSE Transcription
			ĺ		factor BTF3 (RNA polymerase B
					transcription factor 3)
597	17581	AA892835	DDD		[M.musculus]
608	24280	AA892919	v	nucleolar	nucleolar phosphoprotein p130
000	24200	AA092919	<u> </u>	phosphoprotein prou	ESTs, Moderately similar to high
]	1				mobility group protein 20 B;
	ļ		x, ccc,		BRCA2-associated factor 35 [Mus
612	3381	AA892993	SSS, UUU		musculus] [M.musculus]
-	10001	7 0 00 2000	000, 000		ESTs, Weakly similar to
ļ					THDE_RAT Thyrotropin-releasing
	İ				hormone degrading ectoenzyme
ļ	1				(TRH-degrading ectoenzyme)
1					(TRH-DE) (TRH-specific
				•	aminopeptidase)
					(Thyroliberinase) (Pyroglutamyl-
					peptidase II) (PAP-II)
617	3865	AA893065	ZZ, AAA		[R.norvegicus]
				MAP/microtubule	
000	2000	A A O O O O A Z		affinity-regulating	MAP/microtubule affinity-
630	3880	AA893247	LL	kinase 3	regulating kinase 3
		}			ESTs, Moderately similar to ADFP MOUSE ADIPOPHILIN
ł				1	(ADIPOSE DIFFERENTIATION-
					RELATED PROTEIN) (ADRP)
631	16168	AA893280	С		[M.musculus]
			A, B, F,		
			н, х, ү,	ornithine	
633	4242	AA893325	LLL	aminotransferase	ornithine aminotransferase
					ESTs, Moderately similar to
					C54354 calnexin precursor - rat
634	11935	AA893328	LL		[R.norvegicus]

TABL	E 1:			经工程的	lomey Docket 44921-5133-011WO Document No. 1925323.1
\$39 (ID :	GLGG GLGG	Consoni Accor Rakan ID	Model:	Knovin Cone Name	Unigene Sequence Cluster Title
			A, G, BB,	provide Auditor (Class Code de	
	İ		CC, TT,		
			FFF.		
j	Î		GGG,		
•		4	ннн,		
	1	j	General		ESTs, Highly similar to A40066
			Core Tox		corticosteroid-binding globulin
639	13088	AA893495	Markers	i	precursor - rat [R.norvegicus]
					ESTs, Highly similar to neuronal
	ļ		I, J, Z,		protein 15.6 [Mus musculus]
650	16912	AA893690	AA, LL		[M.musculus]
					ESTs, Moderately similar to
ł		1			maternal inhibition of
					differentiation; maternal
					inhibitation of differentiation;
1	İ				stage specific embryonic cDNA-8
651	19171	AA893699	С		[Mus musculus] [M.musculus]
					ESTs, Highly similar to A31568
					electron transfer flavoprotein
i					alpha chain precursor - rat
667	16434	AA894174	ввв, ссс		[R.norvegicus]
					ESTs, Highly similar to A31568
	1				electron transfer flavoprotein
					alpha chain precursor - rat
667	16435	AA894174	J, M, U		[R.norvegicus]
					ESTs, Highly similar to
					MLES_RAT Myosin light chain
					alkali, smooth-muscle isoform
669	24473	AA894200	Z, AA		(MLC3SM) [R.norvegicus]
					ESTs, Highly similar to
l					MLES_RAT Myosin light chain
					alkali, smooth-muscle isoform
669	24474	AA894200	GG		(MLC3SM) [R.norvegicus]
ł					ESTs, Weakly similar to dual-
					specificity phosphatase [Mus
670	22783	AA894207	SS		musculus] [M.musculus]
1					ESTs, Weakly similar to JC4863
	20004	4 4 000 155	_ , , , , , ,		homeobox protein zhx-1 - mouse
686	22981	AA899455	Z, AA, SS		[M.musculus]
1					ESTs, Weakly similar to A45988
					dentin matrix acidic
715	2044	A A O O C C C C	JJ, KK,		phosphoprotein AG1 - rat
715	3944	AA900688	MM, TTT		[R.norvegicus]
1			000,		
			General Core Toy		
	[Core Tox		ESTa Highly similar to DAN
			Markers, General		ESTs, Highly similar to RAN binding protein 16 [Mus
720	16465	AA901042	Alternate		musculus] [M.musculus]
120	10400	1044 1044	I LIGHT HALE		muscums [ivi.muscuius]

TABL				ALC: A	tomey Docket 44921-5083-011W0 Document No. 1985328.1
Seq D:		Conson; Accor Rower ID,	Model Code	Kitowii Cene Kame	Unigene Sequence Cluster Tille
723	4857	AA901237	RR		ESTs, Weakly similar to CYCK_MOUSE Cyclin K [M.musculus]
732	22578	AA924105	X, Y		ESTs, Weakly similar to SY03_RAT Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha) [R.norvegicus]
744	4944	AA924405	KK, HHH, General Core Tox Markers		ESTs, Weakly similar to NFH_MOUSE Neurofilament triplet H protein (200 kDa neurofilament protein) (Neurofilament heavy polypeptide) (NF-H) [M.musculus]
768	23173	AA925057	o, vv		ESTs, Highly similar to GYRTI cysteine-rich intestinal protein - rat [R.norvegicus]
778	23159	AA925318	General Alternate	I-kappa-B-beta	I-kappa-B-beta
815	11691	AA926193	м, х, ү	sulfotransferase family, cytosolic, 1C, member 2	sulfotransferase family, cytosolic, 1C, member 2
817	1897	AA926292	нн	trans-golgi network protein 1	trans-golgi network protein 1
826	22677	AA942718	C, F, W, HH, II	B cell lymphoma 2 like	B cell lymphoma 2 like ESTs, Moderately similar to
829	12247	AA942812	General Alternate	·	putative homeodomain transcription factor [Mus musculus] [M.musculus]
838	24262	AA943116	X, Ý, UUU	HMm:thymidylate kinase	ESTs, Highly similar to KTHY_MOUSE Thymidylate kinase (dTMP kinase) [M.musculus]
841	15319	AA943307	D	tyrosine protein kinase pp60-c-src	tyrosine protein kinase pp60-c-src
859	24369	AA944011	н		ESTs, Highly similar to NUB2_MOUSE Nucleotide binding protein 2 (NBP 2) [M.musculus]
865	2762	AA944165	General Core Tox Markers		ESTs, Highly similar to C10_MOUSE Putative C10 protein (B-cell receptor- associated protein 37) [M.musculus]

TABL		# 7.24 10.84 10.84 10.84 10.84			torney Doctor 44921-5033-011WO Document No. 1985323.1
Seq ; [D	(ID Ko.* Grec	Lassed Case or Resear (D	Model Code	Knovn Cene Name	Unigeno Seguence Cluster Title
			·		ESTs, Moderately similar to PIM1_RAT Proto-oncogene serine/threonine-protein kinase
866	22017	AA944209	III, JJJ		pim-1 [R.norvegicus] ESTs, Weakly similar to
870	22392	AA944269	RRR		ML64_MOUSE MLN 64 protein (ES 64 protein) [M.musculus]
870	22392	PA944209	INK		ESTs, Moderately similar to Pxmp4; PMP24 protein; 24 kDa
885	22452	AA944542	L, T, KKK		intrinsic membrane protein [Mus musculus] [M.musculus] ESTs, Highly similar to
904	16635	AA945171	D		APC4_RAT APOLIPOPROTEIN C-IV PRECURSOR (APO-CIV) (APOLIPOPROTEIN E-LINKED) (ECL) [R.norvegicus]
	22029	AA945284			ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]
908	22029	AA943204	K, N		ESTs, Highly similar to IMA3_MOUSE Importin alpha-3 subunit (Karyopherin alpha-3 subunit) (Importin alpha Q2)
909	7683	AA945320	E, Y, MM,		[M.musculus] R.norvegicus alpha-1- macroglobulin mRNA, complete
912	1798	AA945569	NNN, TTT		ESTs, Weakly similar to JC5105 stromal cell-derived factor 2 -
916 917	12314	AA945596	G, GG, HH, VV		mouse [M.musculus] ESTs, Moderately similar to LCT2_MOUSE Leukocyte cell- derived chemotaxin 2 precursor (Chondromodulin II) (ChM-II) [M.musculus]
<i>311</i>			,		ESTs, Highly similar to R5RT12 acidic ribosomal protein P1, cytosolic [validated] - rat
921	24521	AA945636	DDD	synaptosomal-	[R.norvegicus]
924	13751	AA945699	нн	associated protein, 23 kD	synaptosomal-associated protein, 23 kD
					ESTs, Highly similar to COXG_MOUSE Cytochrome c oxidase polypeptide VIb (AED)
944	20832	AA946040	F		[M.musculus] ESTs, Moderately similar to methyl-CpG binding domain
951	19044	AA946379	BBB		protein 2 [Mus musculus] [M.musculus]

TABL					tomey Docket 44921-5093-01WO Document No. 1935923.1
	<u>ଜ୍ୟୁଡ</u> େ	Constant Acc or Refer ID	Model Gode	Known Gene Namea	Unigane Sequence Cluster Thic
			E, V, W, BB, CC, VV, EEE, III, JJJ,		
961	1809	AA946503	MMM	lipocalin 2	lipocalin 2
100.					EST, EST, Moderately similar to
					FBRL_MOUSE Fibrillarin
					(Nucleolar protein 1)
1			1		[M.musculus], ESTs, Highly
				_	similar to S38342 fibrillarin -
998	17540	AA955914	А, В		mouse [M.musculus]
}	ŀ				ESTs, Weakly similar to
	1				FLAP RAT 5-lipoxygenase
			G, H,		activating protein (FLAP) (MK-886
1004	22576	AA955983	NNN		binding protein) [R.norvegicus]
					ESTs, Weakly similar to I58376
	}				hypothetical protein unp - mouse
1021	23463	AA956794	Q, R		[M.musculus]
					ESTs, Highly similar to RIKEN
	Ī		i		cDNA 2310011M22 [Mus
1025	22251	AA957037	EE		musculus] [M.musculus]
					ESTs, Highly similar to S15892
				HMm:pyruvate	pyruvate dehydrogenase
				dehydrogenase	(lipoamide) (EC 1.2.4.1) beta
1028	12000	AA957319	MM, TTT	(lipoamide) beta	chain - rat [R.norvegicus]
					Rattus norvegicus hypothetical
1]		RNA binding protein RDA288
1036	22358	AA957624	T, V		mRNA, complete cds
					ESTs, Weakly similar to
		<u> </u>			FBL5_RAT Fibulin-5 precursor
1			1		(FIBL-5) (Developmental arteries
					and neural crest EGF-like protein)
			:		(Dance) (Embryonic vascular
					EGF repeat-containing protein)
1039	24135	AA957736	S		(EVEC) [R.norvegicus]
			İ		ESTs, Highly similar to R3RT28
1					ribosomal protein S28, cytosolic
1047	20827	AA963185	Т		[validated] - rat [R.norvegicus]
			ĺ		Rattus norvegicus NonO/p54nrb
1060	8430	AA964033	ННН		homolog mRNA, partial cds
ŀ					ESTs, Highly similar to
			1		LSM4_MOUSE U6 snRNA-
	0505		l		associated Sm-like protein LSm4
1062	2588	AA964080	บบบ	ļ	[M.musculus]
					ESTs, Weakly similar to
1000			General		CALM_HUMAN Calmodulin
1090	24233	AA964756	Alternate		[R.norvegicus]

TABL	ਵ ੀ		2.4.1.1 2.4.1.1	A	torney Docket 44921-5033-011WO Document No. 1935323.1
Seq : ID : ::	@L@G =	Consoni Accor Ressen ID	Model ::	Known Cone Name	Unigene Sequence Cluster Title
1002	2402	A A O C 4 B C C	W 00		ESTs, Moderately similar to A49947 interferon gamma receptor beta subunit - mouse [M.musculus]
1093	2492	AA964866	W, QQ		ESTs, Moderately similar to RIKEN cDNA 1700030G05 [Mus
1097	2542	AA965035	нн		musculus] [M.musculus] ESTs, Highly similar to
1112	2828	AA996529	บบบ		CLN3_MOUSE CLN3 PROTEIN (BATTENIN) [M.musculus]
1121	2939	AA996885	BB, CC, UU, DDD		ESTs, Moderately similar to SY19_MOUSE Small inducible cytokine A19 precursor (CCL19) (Epstein-Barr virus induced molecule 1 ligand chemokine) (EBI1-ligand chemokine) (ELC) [M.musculus]
					EST, Moderately similar to RED_MOUSE Red protein (RER protein) [M.musculus], ESTs, Highly similar to RED_MOUSE Red protein (RER protein)
1125	8786	AA996993	K		[M.musculus] ESTs, Weakly similar to dual-
1127	3112	AA997122	NN, 00	adrenomedullin receptor	specificity phosphatase [Mus musculus] [M.musculus], adrenomedullin receptor
1133	3496	AA997304	F		ESTs, Highly similar to ribosomal protein, mitochondrial, S22 [Mus musculus]
1135	16883	AA997345	A, B, General Core Tox Markers		ESTs, Highly similar to RIKEN cDNA 1190017B19 [Mus musculus] [M.musculus]
					ESTs, Highly similar to PSA7_RAT Proteasome subunit alpha type 7 (Proteasome subunit
1137	3172	AA997406	AA	stromal cell derived	RC6-1) [R.norvegicus]
1154	3458 14149	AA997861 AA998172	GG	factor 4 platelet-activating factor acetylhydrolase alpha 2 subunit (PAF-AH alpha 2)	platelet-activating factor acetylhydrolase alpha 2 subunit (PAF-AH alpha 2)
	24094	AA998435	xx		ESTs, Highly similar to RIKEN cDNA 2210412K09 [Mus musculus] [M.musculus]

TABL	31	\$.		A	tomey/Doctact 44921-5093-011W0
Seq ; [D :	ELEC SON OI	CONSONIA ACC OT RCESON ID	Codo Modal		Uhigane Sequence Cluster Title
1198	1557	AB000216	General Alternate	Cca3 protein	Cca3 protein
1199	1291	AB000491	Н, S	for proteasomal ATPase (SUG1)	for proteasomal ATPase (SUG1)
1200	1201	AB000929	D	zona pellucida 2 glycoprotein	zona pellucida 2 glycoprotein
1206	16304	AB008424	PP, QQ, EEE, FFF, MMM		Rat cytochrome P-450 IID3 mRNA, complete cds
1208	13973	AB011679	O, P		Rattus norvegicus mRNA for class I beta-tubulin, complete cds
1217	1058	AF003835	в, XX, YY	isopentenyl- diphosphate delta isomerase	isopentenyl-diphosphate delta isomerase
1230	4292	AF034896	Z, AA		Rattus norvegicus olfactory receptor-like protein (SCR D-8) mRNA, complete cds
1232	8426	AF036335	JJ, KK, HHH		Rattus norvegicus NonO/p54nrb homolog mRNA, partial cds Rattus norvegicus NonO/p54nrb
1232	8427	AF036335	в, ннн	nucleoside	homolog mRNA, partial cds
1235	17597	AF051943	O, P	nucleoside diphosphate kinase type 6	nucleoside diphosphate kinase type 6
1236	16762	AF059530	บบ	protein arginine N- methyltransferase 3(hnRNP methyltransferase S. cerevisiae)-like 3	protein arginine N- methyltransferase 3(hnRNP methyltransferase S. cerevisiae)- like 3
1237	18675	AF061947	A, B, DD, EE	cain	cain
1246	20236	AF091570	Z, AA, RR	olfactory receptor 41	olfactory receptor 41 ESTs, ESTs, Highly similar to
1255	15848	Al007820	J, K, FF		HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
1259	4032	Al007875	Z, AA	x-ray repair cross- complementing group 1 protein	x-ray repair cross-complementing group 1 protein
1267	15849	Al008074	XX, YY		ESTs, ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus] ESTs, Moderately similar to
1271	22018	A1008309	III, JJJ, KKK		PIM1_RAT Proto-oncogene serine/threonine-protein kinase pim-1 [R.norvegicus]

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S09 : (D::_{_}	۱۵ گاہ۔ :: ©لو©	Geneeni Aggor Reiseg ID	Model Model	Kajewa Cene Neme	ellit ieteile emeupee emeginu
				ribosomal protein	
1277	22126	AI008511	RR	S27	ribosomal protein S27
1285	16701	A1008838	U, FF, TT, UU, DDD, SSS, UUU, General Core Tox Markers		ESTs, Highly similar to RIKEN cDNA 1300002A08 [Mus musculus] [M.musculus]
				low density	
			General	lipoprotein receptor- related protein	low density lipoprotein receptor- related protein associated protein
1292	410	A1008974	Alternate	associated protein 1	11
1202	410	7.1000374	, atomato	cell division cycle	
1293	1830	A1009002	т	25B	cell division cycle 25B
1306	9150	Al009198	A, B, Q, R		ESTs, Highly similar to UNRI_MOUSE UNR-interacting protein (Serine-threonine kinase receptor-associated protein) [M.musculus]
1300	3130	71003130	I, J, BB,		[W.Masoalas]
1309	24249	AI009273	cc	fatty acid synthase	fatty acid synthase
1313	3665	Al009376	A, B, HHH U, X, Y,		ESTs, Moderately similar to A34168 nucleolar phosphoprotein B23.2 - rat [R.norvegicus] . ESTs, Weakly similar to ABC2_MOUSE ATP-BINDING CASSETTE TRANSPORTER 2
1314	12071	AI009456	LLL, UUU		[M.musculus]
1319	19092	Al009501	KKK		ESTs, Highly similar to SUI1_MOUSE Protein translation factor SUI1 homolog [M.musculus]
				transmembrane 4	
1320	3828	AI009601	V	superfamily member 4	transmembrane 4 superfamily member 4
1330	8431	AI009761	L		Rattus norvegicus NonO/p54nrb homolog mRNA, partial cds
					ESTs, Highly similar to R3RT16 ribosomal protein S16, cytosolic
1333	15627	AI009810	ccc	MAP/microtubule	[validated] - rat [R.norvegicus]
1343	3882	Al010191	D, U	affinity-regulating kinase 3	MAP/microtubule affinity- regulating kinase 3
1344	15644	AI010256	C, L, W, WW		H3 histone, family 3B
1356	15624	AI010449	к	follistatin-related protein precursor	follistatin-related protein precursor

TABL					iomey Docket 44921-5033-01000
Seq:	ELEC	Rowson id Rowson id Rowson id	(Cocc)	Kinown Cena Name	Unigene Sequence Cluster Title
1363	21659	AI010584	LL		Rattus norvegicus interferon- inducible protein variant 10 mRNA, complete cds
1369	13296	AI011020	YY		ESTs, Moderately similar to MTM1_MOUSE Myotubularin [M.musculus]
1371	22030	Al011177	N, BB, CC		ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]
1381	3995	AI011678	GGG, General Core Tox Markers	Ryudocan/syndecan 2	Ryudocan/syndecan 2 ESTs, Highly similar to
1385	14267	Al011738	U, FF		P044_RAT 0-44 protein [R.norvegicus] ESTs, Weakly similar to RIKEN
1388	15033	AI011754	SSS, UUU		cDNA 0610008N23 [Mus musculus] [M.musculus]
1392	2516	AI011843	w		ESTs, Moderately similar to SELX_MOUSE Selenoprotein X 1 (Selenoprotein R) [M.musculus]
1393	4286	Al011920	V		ESTs, Moderately similar to WDR1_MOUSE WD-repeat protein 1 (Actin interacting protein 1) [M.musculus]
1401	13093	Al012177	Т		ESTs, Highly similar to S14538 transition protein - mouse [M.musculus]
1402	6547	Al012181	E, JJ, KK		ESTs, Highly similar to 2206297A folylpoly-gamma-Glu synthetase [Mus musculus] [M.musculus]
1417	15443	Al012480	D		ESTs, Highly similar to EXT2_MOUSE Exostosin-2 (Multiple exostoses protein 2 homolog) [M.musculus]
1418	12766		sss		ESTs, Highly similar to diacylglycerol O-acyltransferase 2; diacylglycerol acyltransferase 2 [Mus musculus]
1426	2242			· .	flavin-containing monooxygenase 3
1427	17132		KKK		ESTs, Moderately similar to RIKEN cDNA 1110055L24 [Mus musculus] [M.musculus]

TABL	₫ 1	2000 - 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No.		A	torney Docket 44921-5033-91000 Document No. 1985323.1
		Consonk Accor Reseald	Model Code	Knovn Cene Name	Unigene Sequence Civeter Title
				cell division cycle	
1433	1828	AI012942	D	25B	cell division cycle 25B
1447	22709	AI013404	В	RAP1B, member of RAS oncogene family	RAP1B, member of RAS oncogene family
1456	16584	Al013464	W	Arrestin, beta 2	Arrestin, beta 2
1430	10304	A1013703	G,	Arrestin, Deta 2	Arestin, beta 2
1459	21950	Al013861	General Alternate	3-hydroxyisobutyrate dehydrogenase	3-hydroxyisobutyrate dehydrogenase
			-		ESTs, Highly similar to MKR1_MOUSE Makorin 1
1462	7316	AI013883	Υ .		[M.musculus]
1496	16840	Al029733	Q, R		ESTs, Highly similar to RIKEN cDNA 2010100012 [Mus musculus] [M.musculus]
					ESTs, Moderately similar to ADFP_MOUSE ADIPOPHILIN (ADIPOSE DIFFERENTIATION- RELATED PROTEIN) (ADRP)
1523	16169	AI030932	С		[M.musculus]
		·	F, S,		ESTs, Moderately similar to CLPP_MOUSE Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial precursor (Endopeptidase Clp)
1524	3167	AI031012	RRR		[M.musculus]
1529	7913	AI043655 AI043849	O, P, YY DD, EE, WW	spp-24 precursor	spp-24 precursor ESTs, Weakly similar to ELL_MOUSE RNA POLYMERASE II ELONGATION FACTOR ELL (ELEVEN- NINETEEN LYSINE-RICH LEUKEMIA PROTEIN) [M.musculus]
				putative cell surface	
1550	976	Al044259	Z, AA	antigen	putative cell surface antigen ESTs, Highly similar to proteasome (prosome, macropain) 26S subunit, non- ATPase, 12 [Mus musculus]
1552	5451	A1044322	DD, EE		[M.musculus] ESTs, Weakly similar to
1561	. 3428	Al044653	С		serine/threonine kinase 25 (yeast); Ste20-like kinase; serine/threonine kinase 25 (Ste20, yeast homolog); Yeast Sps1/Ste20-related kinase 1 [Mus musculus] [M.musculus]

TABL	E 1				iomey Docket 44921-5088-01WG Document No. 1985828.t
Seq :	elec	Kee or	Model		
D.	ID K.	RefSeq ID	. ebco	Known Cene Name.	建铁铁铁 化二氯基甲基甲基甲酰乙酰甲酰 医神经病 医二甲基磺酸二甲
					ESTs, Moderately similar to
1564	5634	AI044883	FFF		RIKEN cDNA 2810430M08 [Mus musculus] [M.musculus]
1004	10001	7.10 7.4000	 		ESTs, Highly similar to S04328
					protein-tyrosine kinase (EC
	1				2.7.1.112) flk - rat (fragment)
1565	6941	AI044892	DDD, LLL		[R.norvegicus]
		1	1	LIMm: dibudralia comi	ESTs, Weakly similar to A Chain A, Mammalian Thioredoxin
1578	5697	AI045119	ww	HMm:dihydrolipoami de dehydrogenase	Reductase [R.norvegicus]
1310	3037	1/1045115	10000	de deriyurogenase	Treductase [Tr.Horvegicus]
	}	1			ESTs, Moderately similar to
	}	j			ORC5_MOUSE Origin recognition
1582	5712	Al045154	XX, YY		complex subunit 5 [M.musculus]
					ESTs, Weakly similar to
1501	5722	Al045191	PPP,		FSPO_RAT F-spondin precursor
1584	5723	A1045191	QQQ	 	[R.norvegicus] ESTs, Weakly similar to
	Í	[FIBG RAT Fibrinogen gamma
1628	5573	AI059063	D	1	chain precursor [R.norvegicus]
	 				ESTs, Weakly similar to
	1			İ	CNE6_MOUSE Copine VI
					(Neuronal-copine) (N-copine)
1631	10169	AI059204	KKK	ļ 	[M.musculus]
				ļ	ESTs, Highly similar to YY1 associated factor 2 [Mus
1637	6906	AI059403	DDD		musculus] [M.musculus]
1007	10000	7000 100	1000	vacuolar protein	inoccidoj (m.moccicoj
		1	1	sorting homolog r-	vacuolar protein sorting homolog r
1649	900_	AI059963	T	vps33b	vps33b
			T		ESTs, Highly similar to histone
4000	10040	1070400		}	acetyltransferase [Mus musculus]
1669	12243	AI070133	RR	 	[M.musculus]
	1				ESTs, Highly similar to
	1	1			SYV2_MOUSE ValyI-tRNA
		1		HMm:valyl-tRNA	synthetase 2 (ValinetRNA ligase
1684	2838	Al070511	G, H	synthetase 2	2) (VALRS 2) [M.musculus]
				cell division cycle	
1694	1831	Al071137	<u> </u> T	25B	cell division cycle 25B
1700	9604	AI071230	JJ, KK		ESTs, Weakly similar to 148842
1700	3004	1230	133, KK		testin - mouse [M.musculus] ESTs, Weakly similar to
	1		1		NPA1_MOUSE Neuronal PAS
	Į				domain protein 1 (Neuronal
1718	9795	Al071989	D, E		PAS1) [M.musculus]
					ESTs, Weakly similar to S42077
4704	0050	A1070 400			finger protein 30 - mouse
1731	8856	AI072402	FF		[M.musculus]

				-103-	
TABL	20 (1)			A	tomey/Poets:(44921-5098-011W0 Document No. 1935323.1
Seq ID	id no::	Constant Acc of Refseq ID.::	Model Code	Known Gene Name	Unigaje Sequence Cluster Title
1747	9399	Al072812	General Core Tox Markers	·	ESTs, Highly similar to glioma- amplified sequence-41 [Mus musculus] [M.musculus]
1769	15192	Al101099	т		ESTs, Highly similar to SMRT2 metallothionein II - rat [R.norvegicus]
1782	3537	Al101690	MM, PPP,	dishevelled 1	dishevelled 1 ESTs, Moderately similar to NIF1_MOUSE Nuclear LIM interactor-interacting factor 1 (NLI-
1791	15080	AI102045	QQQ, TTT		interacting factor 1) (NIF-like protein) [M.musculus] Rattus norvegicus clone ZG52
1792	7051	Al102055	ZZ, AAA		mRNA sequence ESTs, Moderately similar to
1801	15218	Al102495	PPP, QQQ		PNPH_MOUSE Purine nucleoside phosphorylase (Inosine phosphorylase) (PNP) [M.musculus]
1802	11953	Al102505	LL	cytochrome c oxidase, subunit VIIIa	cytochrome c oxidase, subunit VIIIa
1802	11954	Al102505	F, LL, RRR, UUU	cytochrome c oxidase, subunit VIIIa	
1807	22487	Al102578	A		ESTs, Highly similar to I49523 tumor necrosis factor alpha- induced protein 2 - mouse [M.musculus]
1828	17400	Al103097	ккк	HMm:ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	ESTs, Highly similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2; hypothetical protein, clone:2-31 [Mus musculus]
1833	13305	Al103332	E		ESTs, Highly similar to CA1B_MOUSE Collagen alpha 1(XI) chain precursor [M.musculus]
1843	23874	Al103556	L, General Core Tox Markers, General Alternate	HMm:CDC28 protein kinase 1	ESTs, Highly similar to CDC28 protein kinase 1; cyclindependent kinase regulatory subunit 1 [Mus musculus] [M.musculus]

TABL	E 1/-			W. Company	Comey Docket 44921-5033-011WO
Seq_ [D	ELEC	Centank Acc or Refseq (D.	Good Good Model	Known Cene Neme	Augara Sconauca Gregor Lina
					ESTs, Highly similar to
					SAP3_MOUSE Ganglioside GM2 activator precursor (GM2-AP)
					(Cerebroside sulfate activator
					protein) (Shingolipid activator
1845	2297	AI103602	GGG		protein 3) (SAP-3) [M.musculus]
					ESTs, Moderately similar to
					RIKEN cDNA 2810411G23 [Mus
1847	13317	AI103637	VV		musculus] [M.musculus]
			\		ESTs, Highly similar to
					COXG_MOUSE Cytochrome c
1857	20833	AI104035	SS		oxidase polypeptide VIb (AED) [M.musculus]
1007	20033	A1104035	55	Protein-L-	[M.Husculus]
				isoaspartate (D-	
				aspartate) O-	Protein-L-isoaspartate (D-
1873	21832	AI104521	LL	methyltransferase	aspartate) O-methyltransferase
			BB, CC,	B-cell CLL/lymphoma	
1879	3504	AI104659	PP, QQ	10	B-cell CLL/lymphoma 10
	1		U, FF, LL,		ESTs, Highly similar to lung
			XX, BBB,		alpha/beta hydrolase 1;
			RRR,	·	alpha/beta hydrolase-1 [Mus
1886	18742	AI105131	ຣຣຣ, ບບບ		musculus] [M.musculus]
					ESTs, Highly similar to
					H33_HUMAN Histone H3.3
1005	0.4044		_		(H3.A) (H3.B) (H3.3Q)
1905	24211	AI111853	E	protein tyrosine	[M.musculus]
				phosphatase type	protein tyrosine phosphatase type
1917	9575	AI112250	SS	IVA, member 2	IVA, member 2
				ubiquitin fusion	
1918	2501	AI112343	Q, R	degradation 1-like	ubiquitin fusion degradation 1-like
					ESTs, Highly similar to
					SAP3_MOUSE Ganglioside GM2
					activator precursor (GM2-AP)
	}				(Cerebroside sulfate activator
1005	2206	A1112070	CCC		protein) (Shingolipid activator
1925	2296	AI112979	GGG		protein 3) (SAP-3) [M.musculus] ESTs, Highly similar to
					MKR1 MOUSE Makorin 1
1929	7317	AI136123	Т		[M.musculus]
					ESTs, Weakly similar to plexin
			PPP,		B3; plexin 6 [Mus musculus]
1930	11165	Al136372	QQQ		[M.musculus]
					ESTs, Highly similar to
					H33_HUMAN Histone H3.3
4000	104040	01400747	PPP,		(H3.A) (H3.B) (H3.3Q)
1936	24212	AI136747	QQQ		[M.musculus]

TABL	39	in interest to the second of		A.C.	omey Docket 44921-5033-0100 Document No. 1935323.1
Seq ;	id no: Gree	Conseni Acc or Reference	Model Code	建 基	Unigene Sequence Cluster Tible
1942	13090	Al136977	JJ, KK, KKK		ESTs, Highly similar to S14538 transition protein - mouse [M.musculus]
1942	13091	AI136977	T, W, JJ, KK		ESTs, Highly similar to S14538 transition protein - mouse [M.musculus] ESTs, Weakly similar to
1943	10754	AI137038	FF		TO1B_MOUSE Torsin B precursor [M.musculus] ESTs, Highly similar to Ras and
1947	21520	AI137332	Т	·	a-factor-converting enzyme 1 homolog (S. cerevisiae) [Mus musculus] [M.musculus]
1950	9166	AI137406	BB, CC		ESTs, Moderately similar to A55945 endothelial cell protein C receptor precursor - mouse [M.musculus]
1954	18943	AI137495	F, II		ESTs, Highly similar to H2A1_RAT Histone H2A.1 [R.norvegicus]
1960	11321	AI137752	S		ESTs, Weakly similar to RL7_RAT 60S RIBOSOMAL PROTEIN L7 [R.norvegicus] ESTs, Weakly similar to S43429
1966	13157	AI138020	М		diamine N-acetyltransferase (EC 2.3.1.57) - mouse [M.musculus] ESTs, Moderately similar to
1988	11363	Al145997	S, LL		2206377B MHR23B gene [Mus musculus] [M.musculus]
1991	11693	Al168953	X, III, JJJ, General Core Tox Markers	sulfotransferase family, cytosolic, 1C, member 2	sulfotransferase family, cytosolic, 1C, member 2
		Al169171	GGG		ESTs, Highly similar to ERH_HUMAN Enhancer of rudimentary homolog [M.musculus]
2003	14962				ESTs, Highly similar to H33_HUMAN Histone H3.3 (H3.A) (H3.B) (H3.3Q)
2009	24213	AI169289	U, BBB,		[M.musculus] ESTs, Weakly similar to B30605 acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, short-chain-
2013	23427	AI169321	CCC		specific - rat [R.norvegicus] ESTs, Highly similar to RU1C_MOUSE U1 small nuclear
2016	15286	Al169361	UUU		ribonucleoprotein C (U1-C) [M.musculus]

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\$ 9 0	രിക്കു	AGE OF	Model:		
(D)	ID No.	Rosog ID	Code	Known Cone Name	Unicene Sequence Cluster Title
					Rattus norvegicus interferon-
			BB, EEE,	,	inducible protein variant 10
2030	21660	AI169751	MMM		mRNA, complete cds
			B, PPP,	solute carrier family	
			General	(organic anion	
			Core Tox	transporter) member	solute carrier family (organic
2031	20503	AI169779	Markers	10	anion transporter) member 10
					ESTs, Moderately similar to
ŀ	1				lymphocyte antigen 96 [Mus
2034	3909	AI169903	O, P		musculus] [M.musculus]
				Page terms	
	1	1	1	discs, large	diana lawa (Danasahila) kamalas
	0704	11170000			discs, large (Drosophila) homolog
2037	8794	AI170002	СС	2 (chapsyn-110)	2 (chapsyn-110) ESTs, Weakly similar to
	ł		ļ		serine/threonine kinase 25
	ŀ				(yeast); Ste20-like kinase;
	l		ļ		serine/threonine kinase 25
		1			(Ste20, yeast homolog); Yeast
					Sps1/Ste20-related kinase 1 [Mus
2042	3429	AI170124	с, нн		musculus] [M.musculus]
2042	3423	71170124	PPP,	complement	mascalas [im.mascalas]
2045	3579	AI170314	aaa	component factor h	complement component factor h
	1				ESTs, Highly similar to
	}		ĺ		A3B1 MOUSE Adapter-related
			•		protein complex 3 beta 1 subunit
l	ł				(Beta-adaptin 3A) (AP-3 complex
					beta-3A subunit) (Beta-3A-
2046	2248	AI170332	BB, CC		adaptin) [M.musculus]
			-		ESTs, Highly similar to T14265
2056	3013	AI170532	D		golgin-245 - mouse [M.musculus]
					ESTs, Moderately similar to
	1		ļ		ADFP_MOUSE ADIPOPHILIN
	1	1	ł		(ADIPOSE DIFFERENTIATION-
					RELATED PROTEIN) (ADRP)
2078	16170	AI170894	W		[M.musculus]
2004	22240	A1474076			ESTs, Weakly similar to S11661
2084	22340	AI171276	HH, KKK		talin - mouse [M.musculus]
1	ł		•		ESTs, Weakly similar to HCD2_RAT 3-hydroxyacyl-CoA
	1		l		dehydrogenase type II (Type II
		İ			HADH) (Endoplasmic reticulum-
		1	1		associated amyloid beta-peptide
2094	17529	Al171460	lww		binding protein) [R.norvegicus]
2034	111343	7.117.1400	1 * * * *	I	parioning protein / [1 /2101 vegleda]

TABU					iomey Doctet 44921-5033-011WO Document No. 1935823.1
S00 ID	10 Kg	Conseni Ace or h Rasso ID	Model Code	Kacva Genellame	energia Seguenée Cluster illile
			KK, FFF, HHH, General Core Tox Markers,		ESTs, Weakly similar to PAB1_MOUSE Polyadenylate- binding protein 1 (Poly(A)-binding
2096	15684	AI171535	General Alternate		protein 1) (PABP 1) (PABP1) [M.musculus] ESTs, Highly similar to
2098	16102	AI171586	G, Н	·	ZPR1_MOUSE Zinc-finger protein ZPR1 (Zinc finger protein 259) [M.musculus] ESTs, Weakly similar to I67424
2105	6582	AI171726	z, 000		hERR-2 homolog - rat (fragment) [R.norvegicus]
2118	20783	Al171966	O, P, V, NN, OO		R.norvegicus mRNA for RT1.Mb
2122	2218	Al172011	RR		ESTs, Moderately similar to S12207 hypothetical protein (B2 element) - mouse [M.musculus]
2124	7642	Al172045 Al172086	C, MM, TTT .	HMm:histone deacetylase 5	ESTs, Highly similar to HDA5_MOUSE Histone deacetylase 5 (HD5) (Histone deacetylase mHDA1) [M.musculus] ESTs, Highly similar to SH3 domain binding glutamic acid-rich protein-like 3 [Mus musculus] [M.musculus]
2132	1957	AI172143	ккк	phytanoyl-CoA hydroxylase (Refsum disease)	phytanoyl-CoA hydroxylase (Refsum disease)
2137	2140	Al172272	XX, General Alternate		ESTs, Weakly similar to A53004 transcription elongation factor S-II - rat [R.norvegicus]
2138	4193	Al172274	PPP		ESTs, Weakly similar to A Chain A, 2-Enoyl-Coa Hydratase, Data Collected At 100 K, Ph 6.5 [R.norvegicus]
2147	11623	Al172471	N, XX, YY, PPP, QQQ	·	ESTs, Highly similar to small EDRK-rich factor 2; 4F5rel (4F5 related); modifier of spinal muscular atrophy candidate 1-like [Mus musculus] [M.musculus] ESTs, Moderately similar to
2154	15557	Al175019	R		RIKEN cDNA 2410001H17 [Mus musculus] [M.musculus] ESTs, Highly similar to RIKEN
2162	22105	Al175221	RR		cDNA 2310039D06 [Mus musculus] [M.musculus]

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\$09 : (D)	ELEC	Conseni Acc or Refeat ID	Model Code:	Kacwa Cene Name	eliit retevid cenerges coeginü
			H, General Core Tox Markers,		ESTs, Highly similar to
2170	18507	AI175551	General Alternate	· ·	EF1B_MOUSE Elongation factor 1-beta (EF-1-beta) [M.musculus] Rattus norvegicus Sprague-
2177	19004	AI175875	NN, 00		Dawley lipid-binding protein mRNA, complete cds
2180	6549	AI176002			ESTs, Highly similar to 2206297A folylpoly-gamma-Glu synthetase [Mus musculus] [M.musculus]
2185_	7022	AI176041	LLL, SSS, UUU		ESTs, Highly similar to PIR_MOUSE Pirin [M.musculus]
2187	5876	Al176117	υυ	HMm:pyruvate dehydrogenase (lipoamide) beta	ESTs, ESTs, Highly similar to S15892 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain - rat [R.norvegicus]
2206	15191	AI176456	C, E, L, T, W, DD, SS, WW, III, JJJ, KKK, NNN		ESTs, Highly similar to SMRT2 metallothionein II - rat [R.norvegicus]
2211	22823	AI176491	WW, BBB,		ESTs, Moderately similar to RIKEN cDNA 2310016K22; RIKEN cDNA 2310016K22 gene [Mus musculus] [M.musculus]
2241	10310	AI176961	А, В, Н	ribosomal protein, mitochondrial, L12	ribosomal protein, mitochondrial, L12
2242	16124	AI176963	บบบ	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy- terminal domain, 2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
2246	2359	Al177029	DD	tec protein tyrosine kinase	tec protein tyrosine kinase
2260	14083	AI177181	General Core Tox Markers		ESTs, Weakly similar to FYV1_MOUSE FYVE finger-containing phosphoinositide kinase (1-phosphatidylinositol-4-phosphate kinase) (PIP5K) (PtdIns(4)P-5-kinase) (p235) [M.musculus]

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(D)	(10) K/O* (GF)(GC)	Conson: Accor Reiseg ID:	(Mocal)	Known Cene Neme	ellik refeine Securence Clieter tille
				HMm:c-src tyrosine	ESTs, Highly similar to 1709363A protein Tyr kinase CSK [Rattus
2265	15251	AI177363	Z	kinase	norvegicus] [R.norvegicus]
					ESTs, Highly similar to FKB8_MOUSE 38 kDa FK-506 binding protein homolog
2275	24602	A1477742	PPP,		(FKBPR38) (FK506-binding protein 8) (muFKBP38)
2275	21603	AI177742	QQQ		[M.musculus] ESTs, Highly similar to
					TGIF_MOUSE 5'-TG-3' INTERACTING FACTOR (HOMEOBOX PROTEIN TGIF)
2284	19184	AI178025	Q, W	i	[M.musculus]
2287	13389	AI178104	KKK		ESTs, Highly similar to RIKEN cDNA 2400009B11 [Mus musculus] [M.musculus]
2201	13309	A1176104	NAN_		ESTs, Highly similar to
1 .	l				SYFB_MOUSE Phenylalanyl-
}		}		•	tRNA synthetase beta chain
1		}		HMm:phenylalanine-	(PhenylalaninetRNA ligase beta
2300	6502	AI178283	XX	tRNA synthetase-like	chain) (PheRS) [M.musculus]
				HMm:c-src tyrosine	ESTs, Highly similar to 1709363A protein Tyr kinase CSK [Rattus
2307	15252	AI178605	GG, HH	kinase	norvegicus] [R.norvegicus]
2313	2825	Al178752	ww		ESTs, Highly similar to CLN3_MOUSE CLN3 PROTEIN
2313	2023	A1170752	VVV		(BATTENIN) [M.musculus] ESTs, Highly similar to
1	ļ	}			M2A1_RAT Alpha-mannosidase II
ł					(Mannosyl-oligosaccharide 1,3-
					1,6-alpha-mannosidase) (MAN II)
					(Golgi alpha-mannosidase II)
					(Mannosidase alpha class 2A
2319	6628	AI178793	GG		member 1) [R.norvegicus]
				Chorionic	
	}			somatomammotropin	Chorionic somatomammotropin
2324	3076	AI179075	RR	hormone 1 variant; Placental lactogen-1	hormone 1 variant; Placental lactogen-1
	100,0	A113010	1313	racental lactogen-1	ESTs, Moderately similar to
					VNN1 MOUSE Pantetheinase
					precursor (Pantetheine
					hydrolase) (Vascular non-
2325	5887	Al179099	U, XX, BBB		inflammatory molecule 1) (Vanin 1) [M.musculus]

TABL		- E	A TOP OF THE	AG AG	torney Docket 44921-5093-01WQ Document No. 1985323.1
500 (D ::::	ID Not:	Consenz Accor Reference	Model Code	Known Cone Name	Unigene Sequence Cluster Title
2338	16703	AI179300	K, U, FF, LL, TT, UU, HHH, LLL, SSS, UUU, General Core Tox Markers		ESTs, Highly similar to RIKEN cDNA 1300002A08 [Mus musculus] [M.musculus]
2364	17224	AI179883	PP, QQ		ESTs, Highly similar to testis expressed gene 189 [Mus musculus] [M.musculus]
2374	2099	AI180015	R	ribosomal protein L14	ribosomal protein L14
2380	9821	Al180114	O, P, PP, QQ		ESTs, Highly similar to NIP2_MOUSE BCL2/ADENOVIRUS E1B 19- KDA PROTEIN-INTERACTING PROTEIN 2 [M.musculus]
2000	0021				ESTs, Highly similar to NUB2_MOUSE Nucleotide binding protein 2 (NBP 2)
2389	24368	AI180392	G, H, ZZ		[M.musculus] ESTs, Highly similar to ATPase,
2409	11782	Al228004	Z, AA		class 1, member h; ATPase 11A, p type; ATPase 11A, class VI [Mus musculus] [M.musculus] ESTs, Highly similar to neuronal protein 15.6 [Mus musculus]
2413	16913	AI228236	QQQ		[M.musculus] ESTs, Highly similar to
2419	22915	AI228299	L		craniofacial development protein 1 [Mus musculus] [M.musculus] ESTs, Highly similar to
2473	16093	AI229849	Т		WDR1_MOUSE WD-repeat protein 1 (Actin interacting protein 1) [M.musculus]
2479	17672	Al230074	N, PPP, QQQ	HMm:NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 casein kinase II beta	ESTs, Highly similar to NIMM_MOUSE NADH- ubiquinone oxidoreductase MWFE subunit (Complex I- MWFE) (CI-MWFE) [M.musculus]
2486	1480	AI230260	RŘ	subunit	casein kinase II beta subunit
2488	23628	Al230278	GG		ESTs, Highly similar to mitochondrial ribosomal protein S16 [Mus musculus] [M.musculus]

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1		Rakai ID : Aes or Rakai ID :		Known Cone Name	Unigane Sequence Civeter Tille
2492	14662	Al230413	z, aa		ESTs, Highly similar to ZW10_MOUSE Centromere/kinetochore protein zw10 homolog [M.musculus]
		Al230759	A, B, Z,		ESTs, Moderately similar to ornithine decarboxylase antizyme 2; ornithine decarboxylase antizyme; antizyme 2 [Mus musculus] [M.musculus]
2505 2509	15551 17720	AI230759	AA, RR I, J		ESTs, Highly similar to protein- tyrosine sulfotransferase 2 [Mus musculus] [M.musculus]
2518	2299	Al231094	GGG		ESTs, Highly similar to SAP3_MOUSE Ganglioside GM2 activator precursor (GM2-AP) (Cerebroside sulfate activator protein) (Shingolipid activator protein 3) (SAP-3) [M.musculus]
2526	22791	AI231230	SS		ESTs, Weakly similar to dual- specificity phosphatase [Mus musculus] [M.musculus] ESTs, Highly similar to
2534	22379	AI231448	X, Y, Z, RR <u>,</u> XX		G6PI_MOUSE Glucose-6- phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Neuroleukin) (NLK) [M.musculus]
2539	13092	Al231547	T, W, DD, EE, JJ, UU, KKK		ESTs, Highly similar to S14538 transition protein - mouse [M.musculus]
2542	4703	Al231606	C, KKK		ESTs, Moderately similar to RIKEN cDNA 6330579B17 [Mus musculus] [M.musculus]
2544	17297	AI231785	s		ESTs, Moderately similar to Niemann Pick type C2 [Mus musculus] [M.musculus]
2545	15171	Al231792	Q, AA		ESTs, Highly similar to BAG3_MOUSE BAG-family molecular chaperone regulator-3 (BCL-2 binding athanogene-3) (BAG-3) (Bcl-2-binding protein Bis) [M.musculus]
2551	17144	Al231921	YY	Protein-L- isoaspartate (D- aspartate) O- methyltransferase	Protein-L-isoaspartate (D- aspartate) O-methyltransferase

	31 - 1 - 1	1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5		A	tomay Docket 4/1921-5083-01/WO
	ID Kos.	Conseni Accor Reiseg ID	Model Code	Known Cene Name	Walgana Saquance Cluetar, Tille
2554	19094	Al232021	С		ESTs, Highly similar to SUI1_MOUSE Protein translation factor SUI1 homolog [M.musculus]
2561	19274	Al232135	DDD, General Alternate		ESTs, Highly similar to COG2_MOUSE Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP) [M.musculus]
2567	409	Al232268	GG	low density lipoprotein receptor- related protein associated protein 1	low density lipoprotein receptor- related protein associated protein 1
2574	15582	Al232320	U, FF, PP, QQ		Rat mitochondrial 3-hydroxy-3- methylglutaryl-CoA synthase mRNA, complete cds
2587	8709	Al232534	ZZ		ESTs, Weakly similar to DnaJ (Hsp40) homolog, subfamily B, member 3; heat shock protein, DNAJ-like 3 [Mus musculus] [M.musculus]
2592	3860	Al232703	U, LL, BBB, CCC, LLL, RRR, SSS, UUU	malonyl-CoA decarboxylase	malonyl-CoA decarboxylase
2593	12463	Al232706	L, PP	translin-associated factor X	translin-associated factor X
2611	14103	Al233172	GGG, LLL, RRR, SSS, UUU, General Core Tox Markers		ESTs, Weakly similar to A Chain A, Crystal Structure Of The Epsin N-Terminal Homology (Enth) Domain At 1.56 Angstrom Resolution [R.norvegicus]
2618	19470	Al233266	GGG, HHH		ESTs, Weakly similar to PROD_MOUSE PROLINE OXIDASE, MITOCHONDRIAL PRECURSOR (PROLINE DEHYDROGENASE) [M.musculus] ESTs, Moderately similar to
2619	10378	Al233300	K		CO5_MOUSE Complement C5 precursor (Hemolytic complement) [Contains: C5A anaphylatoxin] [M.musculus]

TABL	31			A	tomey Docket 44921-5033-01000
S09, ID::::		Lessed Desired Tesses	Model Codo	Known Cene Kame	elili, reteule concupce coeginu
2651	12736	Al233972	JJJ	Gap junction membrane channel, protein alpha 4 (connexin 37)	Gap junction membrane channel, protein alpha 4 (connexin 37)
2007	40704	A1024527	M, GG,	HMm:glutathione S- transferase, alpha 4	ESTs, Highly similar to S23433 glutathione transferase (EC 2.5.1.18) 8 - rat [R.norvegicus]
2667	16781	AI234527	<u> </u>		
2680	19057	Al235094	E	cortactin isoform B	cortactin isoform B
			Z, AA,		ESTs, Highly similar to G6PI_MOUSE Glucose-6- phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Neuroleukin)
2681	22380	Al235217	NNN	•	(NLK) [M.musculus]
2684	15004	Al235224	SS, EEE, III, JJJ, MMM	tissue inhibitor of metalloproteinase 1	tissue inhibitor of metalloproteinase 1
2687	11644	Al235282	FFF, GGG, General Alternate	HMm:low density lipoprotein receptor- related protein 1	ESTs, Highly similar to S25111 alpha-2-macroglobulin receptor precursor - mouse [M.musculus]
2698	1462	Al235585	K	cathepsin D	cathepsin D
2712	3617	Al236021	DD		ESTs, Highly similar to JC4857 hepatocarcinogenesis-related transcription factor - rat [R.norvegicus]
2716	11465	Al236084	ไ		ESTs, Moderately similar to TNR9_MOUSE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen) [M.musculus]
2717	16943	Al236097	PPP, QQQ		ESTs, Highly similar to ITMB_MOUSE Integral membrane protein 2B (E25B protein) [M.musculus]
2728	5052	Al236302	ZZ, UUU		ESTs, Weakly similar to TTHY_RAT Transthyretin precursor (Prealbumin) (TBPA) [R.norvegicus]
2740	7691	Al236611	Υ	isopentenyl- diphosphate delta isomerase	isopentenyl-diphosphate delta isomerase
2753	15850	Al236795	F, J, S, RR		ESTs; ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]

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800 ID:	id nove Gree	Lesses Le	Modely (Code)	ems/Lems mwon/	Unigene Sequence Cluster Tible
					ESTs, Moderately similar to MBNL_MOUSE Muscleblind-like protein (Triplet-expansion RNA-
2757	22176	AI236907	RR, SS		binding protein) [M.musculus]
2761	11404	Al237002	H, Z, KK, FFF, GGG, General Core Tox Markers	spermidine synthase	
2780	18854	AI237636	000		ESTs, Weakly similar to CNE6_MOUSE Copine VI (Neuronal-copine) (N-copine) [M.musculus]
2700	10034	A1237030	000	sulfotransferase	[w.musecius]
				family, cytosolic, 1C,	sulfotransferase family, cytosolic,
2792	11692	AI638982	М	member 2	1C, member 2
2794	17108	Al639017	С		ESTs, Weakly similar to T17453 ERG-associated protein ESET - mouse [M.musculus]
				HMm:transformed	ESTs, Highly similar to A42772
				mouse 3T3 cell	mdm2 protein - rat (fragments)
2828	20082	Al639488	F, II, VV	double minute 2	[R.norvegicus]
2833	23220	AJ000347	V, X, Y, HH, JJ, SS, ZZ, AAA, HHH	3'(2'),5'-bisphosphate nucleotidase	3'(2'),5'-bisphosphate nucleotidase
				tumor-associated	
0005	44000	A 1004044	14	calcium signal	tumor-associated calcium signal
2835	14332	AJ001044	11	transducer 1	transducer 1
2838	14882	D00362	O, P, NN, OO, XX, YY, BBB, DDD	Esterase 2	Esterase 2
				Serine protease	
2841	3292	D00753	NNN	inhibitor	Serine protease inhibitor
2842	1515	D10233	O, P	renin-binding protein	renin-binding protein
2846	19053	D12770	ZZ, AAA	solute carrier family 25 (mitochondrial adenine nucleotide translocator) member 4	solute carrier family 25 (mitochondrial adenine nucleotide translocator) member 4
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TABL		4.		A TANK	tomey Docket 44921-5033-01000
Seq . ID :		CONSENT ACCO ROBEQ ID	Model Code	Known Cene Name.	Unigone Sequence Ciuster Tille
			U, FF, XX, YY,	hydroxyacyl- Coenzyme A dehydrogenase/3- ketoacyl-Coenzyme A thiolase/enoyl- Coenzyme A hydratase	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl- Coenzyme A thiolase/enoyl-
2850	1728	D16479	BBB, RRR, SSS	(trifunctional protein), beta subunit	Coenzyme A hydratase (trifunctional protein), beta subunit
2853	179	D17809	GG, WW E, I, J, K,	beta-4N- acetylgalactosaminylt ransferase dynein, cytoplasmic,	beta-4N- acetylgalactosaminyltransferase
	.054	500005	RRR,	intermediate	dynein, cytoplasmic, intermediate
2862	1354	D38065	DD, EE,	polypeptide 2 cyclin G-associated	polypeptide 2
2865	1350	D38560	NNN	kinase	cyclin G-associated kinase
2868	2578	D50694	S, BBB, CCC, GGG G, H, X, Y, General	Proteasome (prosome, macropain) 26S subunit, ATPase proteasome (prosome, macropain) 26S	Proteasome (prosome, macropain) 26S subunit, ATPase proteasome (prosome, macropain) 26S subunit, ATPase,
2869	1884	D50695	Alternate	subunit, ATPase, 4	4
2870	727	D50696	Y, CCC, PPP, QQQ	protease (prosome, macropain) 26S subunit, ATPase 1 CDP-diacylglycerol inositol 3- phosphatidyltransfera	protease (prosome, macropain) 26S subunit, ATPase 1
2873	826	D82928	Z, AA, EE	se (phosphatidylinositol synthase)	CDP-diacylglycerolinositol 3- phosphatidyltransferase (phosphatidylinositol synthase)
2877	134	D87839	A, B, III, JJJ, OOO, General Core Tox Markers	4-aminobutyrate aminotransferase	4-aminobutyrate aminotransferase
2877	135	D87839	B, J, OO, RRR	4-aminobutyrate aminotransferase	4-aminobutyrate aminotransferase
2879	1218	D89340	OOO, General Alternate	dipeptidylpeptidase	dipeptidylpeptidase III

TABL	图1	25/78	· · · · · · · · · · · · · · · · · · ·		lonney Doeket 44921-5038-011W0 
500 (D)	ELEC DD Ko.	, indenda i diposish gundan	Model Code	Known Gene Name:	Unigene Sequence Cluster Ville
2888	1888	E13573	F, X, Y, LLL	BH3 interacting (with BCL2 family) domain, apoptosis agonist	BH3 interacting (with BCL2 family) domain, apoptosis agonist
2915	14266	H33842	IJ		ESTs, Weakly similar to A45988 dentin matrix acidic phosphoprotein AG1 - rat [R.norvegicus]
2920 2924	16130 1514	J01435 J02780	F, DD, EE, HH, NNN O, P, VV	unknown Glu-Pro dipeptide repeat protein Tropomyosin 4	unknown Glu-Pro dipeptide repeat protein Tropomyosin 4
2933	293	J05499	GG, VV, GGG	liver mitochondrial glutaminase C1-tetrahydrofolate	liver mitochondrial glutaminase
2934	1549	J05519	мм, ттт	synthase	C1-tetrahydrofolate synthase
2938 2945	23486 1894	K02816 L03201	FF DDD	pR-ET2 encoded oncodevelopmental protein cathepsin S	pR-ET2 encoded oncodevelopmental protein cathepsin S
2950	4144	L12380	PP, QQ,	ADP-ribosylation factor 1	ADP-ribosylation factor 1
2957	1481	L15619	N, V, ZZ, AAA, PPP, QQQ	casein kinase II beta subunit	casein kinase II beta subunit
2964	1795	L24207	K, L, N, O, P, X, NN, OO, PP, TT, LLL, UUU	Cytochrome P450, subfamily IIIA, polypeptide 3	Cytochrome P450, subfamily IIIA, polypeptide 3
2964	1796	L24207	K, L, M, N, X, TT	Cytochrome P450, subfamily IIIA, polypeptide 3	Cytochrome P450, subfamily IIIA, polypeptide 3
2967	13499	L26267	O, P, Q, R, W, NN, OO, PP, QQ	nuclear factor kappa B p105 subunit	nuclear factor kappa B p105 subunit
2970	31	L27651	XX, YY, General Alternate	solute carrier family 22 (organic anion transporter), member 7	solute carrier family 22 (organic anion transporter), member 7

TABL	롤 1 .	, i i	Tipe Co.	A	torney Docket 44921-5058-01000 Document No. 1935323.1
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			M, U, GGG, OOO, PPP, QQQ, General Core Tox Markers,	solute carrier family 22 (organic anion	
2970	32	L27651	General Alternate	transporter), member 7	solute carrier family 22 (organic anion transporter), member 7
2976	695	L41254	F	corticosteroid- induced protein	corticosteroid-induced protein
2978	11955	L48209	F	cytochrome c oxidase, subunit VIIIa	cytochrome c oxidase, subunit VIIIa
2989	24860	M13506	E, K, M, X, TT, BBB, DDD, EEE, MMM		Rat liver UDP- glucuronosyltransferase, phenobarbital-inducible form mRNA, complete cds
2994	19255	M15562	X, 00		Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)
2994	19256	M15562	M, X, OO		Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)
3000	14881	M20629	O, P, NN, OO, XX, YY, CCC	Esterase 2	Esterase 2
3008	11956	M28255	LL	cytochrome c oxidase, subunit VIIIa small nuclear	cytochrome c oxidase, subunit VIIIa
3009	1580	M29293	ZZ, AAA C, KK,	ribonucleoparticle- associated protein (snRNP) mRNA, clone Sm51	small nuclear ribonucleoparticle- associated protein (snRNP) mRNA, clone Sm51
3010	17123	M29295	FFF, GGG, HHH, General Alternate Y, FF,	small nuclear ribonucleoprotein polypeptides B and B1	small nuclear ribonucleoprotein polypeptides B and B1 Rat mitochondrial 3-hydroxy-3- methylglutaryl-CoA synthase
3014	15579 15580	M33648 M33648	RRR, SSS U, FF		mRNA, complete cds Rat mitochondrial 3-hydroxy-3- methylglutaryl-CoA synthase mRNA, complete cds

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Seq. ( ID. )	ELEC	AMESMED TO SO SO SERIES	Model Gode	Known Gene Name	Unigene Sequence Cluster IIIle
3015	16807	M33936	FF		Rat Cyp4a locus, encoding cytochrome P450 (IVA3) mRNA, complete cds
					Rat mRNA for MHC class II antigen RT1.B-1 beta-chain, Rattus norvegicus MHC class II
3021	9223	M36151	X, Y, NN, OO, PP		antigen RT1.B beta chain mRNA, partial cds
3023	17145	M38566	vv	Serine protease inhibitor	Serine protease inhibitor
3024	1246	M57507	A, B, M, FFF, HHH, KKK, NNN, OOO, General Core Tox Markers	Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase)	Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase)
	20207	M64378	RR		Rat olfactory protein mRNA, complete cds
3038	1138	M76740	RR, SS	Mucin3	Mucin3
3038	25446	M76740	D, SS S, FFF, GGG, OOO, UUU, General Core Tox	Mucin3  Ryudocan/syndecan	Mucin3
3042	1529	M81687	Markers	2	Ryudocan/syndecan 2
3044	4198	M83143	F, S, U, BB, CC, TT, III, JJJ, LLL, OOO, SSS, UUU, General Alternate		Rat beta-galactoside-alpha 2,6- sialyltransferase mRNA
3044	4199		E, F, G, U, LL, CCC, LLL, RRR, SSS, UUU		Rat beta-galactoside-alpha 2,6-sialyltransferase mRNA
3045			UU	Microtubule- associated protein 1a	Microtubule-associated protein 1a

TABL	<b>3</b> 1≥				tomey Docket 44921-5088-011WO Document No. 1985328.1
998 10		CONSERVA ACC OT A RCASCO ID	lebem	Known CeneWame	Unigana Saquanaa Cluster Titlo
2050	25467	M93297	A, B, II, WW	ornithine aminotransferase	ornithine aminotransferase
3050	3424	M94557	A, B	•	ESTs, Highly similar to SSB_RAT SINGLE-STRANDED DNA-BINDING PROTEIN, MITOCHONDRIAL PRECURSOR (MT-SSB) (MTSSB) (P16) [R.norvegicus]
3052	729	M95762	FFF FFF	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13
3053	1624	M95768	Z, AA	di-N-acetylchitobiase	di-N-acetylchitobiase
3056	1508	M97662	м	ureidopropionase, beta Hydroxy-delta-5-	ureidopropionase, beta
3086	17292	NM 012584	K, GGG	steroid dehydrogenase, 3 beta- and steroid delta-isomerase (Hsd3b), mRNA. 1/2002 Length =	Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase
3092	382	NM_012599	FF, RRR	Mannose binding protein A, serum (Mbpa), mRNA. 11/2000 Length = 717	Mannose binding protein A,
3106	17147	NM_012657	L, TT	Serine protease inhibitor (Spin2b), mRNA. 11/2002 Length = 1664	Serine protease inhibitor
3106	17148	NM_012657	нн, тт	Serine protease inhibitor (Spin2b), mRNA. 11/2002 Length = 1664	Serine protease inhibitor
3128	18730	NM_012730	N, TT	Cytochrome P450, subfamily IID2 (Cyp2d2), mRNA. 11/2000 Length = 1698	Cytochrome P450, subfamily IID2
3135	13731	NM_012755	P	Fyn proto-oncogene (Fyn), mRNA. 9/2002 Length = 1844 caspase 1 (Casp1),	Fyn proto-oncogene
3136	18068	NM_012762	P, W	mRNA. 11/2002 Length = 1209	Interleukin 1beta converting enzyme

TABU		3 2 2		AL AL	torney Docket 44921-5033-01WQ Document No. 1935323.1
S00\{ In	@LGC	(CONSIDERAL)  ACC OF (C)  BOXSON (D)	Model · ·	emely enes myronx	Unigene Sequence Cluster Title
	<u> </u>	ا بد چه روحوده	NN, OO,	Cyclin D3 (Ccnd3),	
			PP, QQ,	mRNA. 11/2002	
3137	17257	NM_012766	ZZ	Length = 1843	Cyclin D3
				Cyclin D3 (Ccnd3),	
			NN, ZZ,	mRNA. 11/2002	Overlie D2
3137	17258	NM_012766	AAA	Length = 1843	Cyclin D3
	i			Arrestin, beta 2	
	1			(Arrb2), mRNA. 11/2002 Length =	
3174	16581	NM_012911	v	1758	Arrestin, beta 2
31/4	10361	14141_012311		v-crk-associated	Arrestin, beta 2
			T. III. JJJ.	tyrosine kinase	
			KKK,	substrate (Crkas),	
			General	mRNA, 11/2002	v-crk-associated tyrosine kinase
3180	18695	NM 012931	Alternate	Length = 3335	substrate
				NADH ubiquinone	
				oxidoreductase	
				subunit B13	
				(Ndufa5), mRNA.	
				11/2000 Length =	NADH ubiquinone oxidoreductase
3187	20943	NM_012985	MM, TTT	553	subunit B13
	•			N-arginine dibasic	
			11 77	convertase 1 (Nrd1), mRNA, 11/2000	
3190	9917	NM 012993	JJ, KK, HHH	Length = 3581	N-arginine dibasic convertase 1
3190	9917	14141_012993	13(3) 1	N-arginine dibasic	14-aigilille dibasic convertase 1
				convertase 1 (Nrd1),	·
			-	mRNA. 11/2000	
3190	9918	NM_012993	JJ. KK	Length = 3581	N-arginine dibasic convertase 1
			•	phosphatidylethanola	
				mine N-	
}				methyltransferase	
				(Pemt), mRNA.	
			EE, JJ,	11/2002 Length =	Phosphatidylethanolamine N-
3194	24718	NM_013003	KK	893	methyltransferase
				Solute carrier family	
				34 (sodium	
				phosphate), member	R.norvegicus ASI mRNA for
				1 (Slc34a1), mRNA. 11/2002 Length =	mammalian equivalent of
2200	17174	NIM 012020	JJ, KK,	2440	bacterial large ribosomal subunit
3200	17174	NM_013030	ннн	[ <del>244</del> 0	protein L22

TABL	<b>ક</b> ી~્				iomey Docket 44921-5053-01WC : Document No. 1935323.1
	(1) Kid. (6) (6)	insense To soa U pezien	Model.	Known Cene Name	Unicere Sequence Suster Mile
3202	17401	NM_013043	B, L, X, Y, HH, GGG, LLL, OOO, SSS, UUU, General Core Tox Markers	Transforming growth factor beta stimulated clone 22 (Tgfb1i4), mRNA. 11/2000 Length = 1666	Transforming growth factor beta stimulated clone 22
			,	Tyrosine 3- monooxygenase/trypt ophan 5- monooxygenase activation protein, theta polypeptide (Ywhaq), mRNA. 11/2002 Length =	Tyrosine 3- monooxygenase/tryptophan 5- monooxygenase activation
3206	14423	NM_013053	O, P	2099 Ribophorin I (Rpn1),	protein, theta polypeptide
3211	19335	NM_013067	FF	mRNA. 11/2002 Length = 2214	Ribophorin I
3213	17181	NM 013073	ZZ, AAA	Protein-L- isoaspartate (D- aspartate) O- methyltransferase (Pcmt1), mRNA. 11/2002 Length = 1658	Protein-L-isoaspartate (D- aspartate) O-methyltransferase
	1521	NM 013091	C, E, Q, R, General Alternate	Tumor necrosis factor receptor (Tnfr1), mRNA. 11/2002 Length = 2130	Tumor necrosis factor receptor superfamily, member 1a
3221	1793	NM_013105	K, L, M, N, FF, TT, DDD, UUU	Cytochrome P450, subfamily IIIA, polypeptide 3 (Cyp3a3), mRNA. 11/2000 Length = 2026	Cytochrome P450, subfamily IIIA, polypeptide 3
3221	1794	NM_013105	K, L, M, N, TT, DDD, LLL, UUU	Cytochrome P450, subfamily IIIA, polypeptide 3 (Cyp3a3), mRNA. 11/2000 Length = 2026	Cytochrome P450, subfamily IIIA, polypeptide 3

TABL	<b>3</b> 1	4.57			torney Docket 44921-5038-01WO Document No. 1935323.1
S00 10: }-:	(10) (10) (10) (10) (10)	. 1656 10 20 10 10 10 10 10 10 10 10 10 10 10 10 10	Model Codo. 4	COPT CONTRACTOR PRODUCTION CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRA	Unigene Sequence Cluster Tille
3221	1797	NM_013105	Κ, L, ΤΤ, DDD	Cytochrome P450, subfamily IIIA, polypeptide 3 (Cyp3a3), mRNA. 11/2000 Length = 2026	Cytochrome P450, subfamily IIIA, polypeptide 3, Rattus norvegicus Sprague Dawley testosterone 6-beta-hydroxylase, cytochrome P450/6-beta-A, (CYP3A2) mRNA, complete cds
3223	23709	NM_013113		ATPase Na+/K+ transporting beta 1 polypeptide (Atp1b1), mRNA. 11/2000 Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
3223	23710	NM_013113	I, M, MM,	ATPase Na+/K+ transporting beta 1 polypeptide (Atp1b1), mRNA. 11/2000 Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
3223	23711	NM_013113	WW, TTT	ATPase Na+/K+ transporting beta 1 polypeptide (Atp1b1), mRNA. 11/2000 Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
3224	22582	NM_013120	A, B, G, S, GGG, OOO, General Core Tox Markers	Glucokinase regulatory protein (Gckr), mRNA. 11/2002 Length = 2156	Glucokinase regulatory protein
3225	16650	NM_013132	o, w	Annexin V (Anx5), mRNA. 11/2002 Length = 1417	Annexin V
3227	16982	NM 013144	I, J, W, MM, OOO, TTT, General Core Tox Markers	insulin-like growth factor binding protein 1 (Igfbp1), mRNA. 11/2002 Length = 1500	Insulin-like growth factor binding protein 1
3231	1258	NM_013185	VV	Hemopoietic cell tyrosine kinase (Hck), mRNA. 11/2000 Length =	Hemopoietic cell tyrosine kinase
3233	21396	NM_013198	OO, OOO, General Core Tox Markers	Monoamine oxidase B (Maob), mRNA. 11/2002 Length = 2389	Monoamine oxidase B

TABU	<b>3</b> 1;			Ω	tomey Docket 44921-5158-01W0
Seq :	OLGC OLGC	Constant Accor	Model,	දිරාදුරු දෙනේ බාග්ත්ත්ව	Unigane Sequenca Civeter Title
	U Dall Cogar.	indephased its. 1.	Good Millian	adenylate kinase 3	Confidence Creates Arres
		V		(Ak3), mRNA.	
			1	11/2002 Length =	
3239	20826	NM_013218	С. НН	1061	adenylate kinase 3
				CTL target antigen	
				(Cth), mRNA.	
			L, 00,	11/2000 Length =	
3269	18452	NM_017074	บบ	1743	CTL target antigen
				CTL target antigen	
			L, NN,	(Cth), mRNA.	
			00, 111,	11/2000 Length =	
3269	18453	NM_017074	111, 000	1743	CTL target antigen
				cytochrome P450,	•
				2c39 (Cyp2c39), mRNA. 11/2002	
3294	2967	NM 017158	uш	Length = 1731	cytochrome P450, 2c39
3234	2301	14101_017130_	1111	cytochrome P450,	Cytocarome 1 430, 2033
				2c39 (Cyp2c39),	
				mRNA. 11/2002	<u> </u>
3294	2968	NM 017158	MM, TTT	Length = 1731	cytochrome P450, 2c39
				cytochrome P450,	
ļ ·				2c39 (Cyp2c39),	
				mRNA. 11/2002	
3294	2969	NM_017158	N, TT	Length = 1731	cytochrome P450, 2c39
				cytochrome P450,	
				2c39 (Cyp2c39),	
		lass / i	N, HH,	mRNA. 11/2002	
3294	2970	NM_017158	SS	Length = 1731	cytochrome P450, 2c39
				stathmin 1 (Stmn1),	
2207	20702	NIM 017166	77 000	mRNA. 11/2002	Leukemia-associated cytosolic
3297	20702	NM_017166	ZZ, AAA	Length = 1054 6-pyruvoyl-	phosphoprotein stathmin
				tetrahydropterin	
				synthase (Pts),	
1				mRNA. 11/2002	growth and transformation-
3310	18445	NM_017220	F. L	Length = 1176	dependent protein
				iron-responsive	
				element-binding	
				protein (Ratireb),	
				mRNA. 11/2000	iron-responsive element-binding
3340	17516	NM_017321	RRR, SSS	Length = 3564	protein
				stress activated	
1			-	protein kinase alpha	
				II (SAPK), mRNA.	
0044	0.4700	NA 047000		11/2000 Length =	stress activated protein kinase
3341	24766	NM_017322	EE	2622	alpha II

TABL	图 9				10 mey Docket 44921-5033-01W0 Document No. 1985328.1
S0013	GLGC.	Reserved ID	Model A	Kinowa Gene Neme	Vinigana Sequence Cluster Villa
3341	24767	NM_017322	A, B, L	stress activated protein kinase alpha II (SAPK), mRNA. 11/2000 Length = 2622	stress activated protein kinase alpha II
3343	24247	NM_017332	v	fatty acid synthase (Fasn), mRNA. 11/2002 Length = 9136	fatty acid synthase
3346	16382	NM_017343	v	myosin regulatory light chain (MRLCB), mRNA. 6/2001 Length = 1139 muscarinic	myosin regulatory light chain
3348	20146	NM_017362	l, J	acetylcholine receptor M5 (Chrm5), mRNA. 11/2002 Length = 2733	muscarinic acetylcholine receptor M5
3349	20778	NM_019124	E, K, L, KKK, NNN, OOO, General Alternate	rabaptin 5 (LOC54190), mRNA. 11/2002 Length = 3465	rabaptin 5
	24392	NM_019129	D, Z, AA	Insulin (Ins1), mRNA. 11/2000 Length = 333	Insulin
3358	17304	NM_019144	GG	Acid phosphatase 5, tartrate resistant (Acp5), mRNA. 11/2002 Length = 1381	Acid phosphatase 5, tartrate resistant
3387	10015	NM_019289	B, I, J, O, P, NN,	Actin-related protein complex 1b (Arpc1b), mRNA. 11/2000 Length = 1430	Actin-related protein complex 1b
3387	10016	NM_019289	00, VV	Actin-related protein complex 1b (Arpc1b), mRNA. 11/2000 Length = 1430	Actin-related protein complex 1b
3391	17507	NM_019299		clathrin, heavy polypeptide (Hc) (Cltc), mRNA. 11/2002 Length = 6071	clathrin, heavy polypeptide (Hc)

TABL	≣1-			344 % 444.	formay Dockat 44921-5033-011WO Document No. 1995323.1
800 ID :	id ka erec	Gensenk Acc or Refseq ID	Model Code	Known Cene Neme	Unigene Sequence Civeter Tide
3394	24757	NM_019317	D, Z, AA	Mucosal vascular addressin cell adhesion molecule 1 (Madcam1), mRNA. 11/2000 Length = 1279	Mucosal vascular addressin cell adhesion molecule 1
3399	3775	NM_019354	M, VV	Uncoupling protein 2, mitochondrial (Ucp2), mRNA. 11/2000 Length = 1575	Uncoupling protein 2, mitochondrial
3400	4592	NM_019356	D, PPP, General Alternate	eukaryotic translation initiation factor 2, subunit 1 (alpha ) (Eif2s1), mRNA. 11/2000 Length = 1377	eukaryotic translation initiation factor 2, subunit 1 (alpha)
3404	20057	NM_019370		alkaline phosphodiesterase (LOC54410), mRNA. 11/2000 Length =	alkaline phosphodiesterase
3405	15066	NM_019373	PPP, QQQ	apolipoprotein M (Apom), mRNA. 11/2002 Length = 757	apolipoprotein M
3410	24066	NM_019384	υυ	CTD-binding SR-like (rA1), mRNA. 11/2000 Length = 3851 cytochrome P450,	CTD-binding SR-like rA1
3411	20716	NM 019623	N, EEE, HHH, MMM, PPP, QQQ, General Alternate	subfamily IVF, polypeptide 14 (leukotriene B4 omega hydroxylase) (Cyp4f14), mRNA. 11/2002 Length =	cytochrome P450 4F1
3416	18702	NM_020080	T, MM,	nuclear protein E3-3 orf1 (LOC56769), mRNA. 11/2000 Length = 721	nuclear protein E3-3 orf1
3419	13486	NM_020306	O, P	a disintegrin and metalloproteinase domain 17 (Adam17), mRNA. 11/2002 Length = 4128	a disintegrin and metalloproteinase domain 17

TABL	<b>3</b> 1* ****		The second second	AV AV	ionney, Doedrat 44921-5033-011WO
Seq :		(671-571) Acc or - Re(829 [D,	Model Code	Knova Cene Neme	Unigéne Sequence Civeter IIIle
3424	18727	NM_021577	A, B, I, J, L, MM, WW, BBB, KKK, OOO, TTT, General Alternate	argininosuccinate Iyase (AsI), mRNA. 11/2002 Length = 1574	argininosuccinate lyase
3426	17324	NM_021593	L, GG, EEE, GGG, KKK, LLL, MMM, UUU, General Core Tox Markers	kynurenine 3- hydroxylase (Kmo), mRNA. 11/2002 Length = 1733	kynurenine 3-hydroxylase
3432	19710	NM 021744	II, KKK	CD14 antigen (Cd14), mRNA. 11/2002 Length = 1591	CD14 antigen
3432	19711	NM_021744	N, GG	CD14 antigen (Cd14), mRNA. 11/2002 Length = 1591	CD14 antigen
3434	19824	NM_021750	A, B, JJ, HHH, General Alternate	cysteine-sulfinate decarboxylase (Csad), mRNA. 11/2000 Length = 2413	cysteine-sulfinate decarboxylase
3434	19825	NM_021750	B, I, J, JJ, HHH, General Alternate	cysteine-sulfinate decarboxylase (Csad), mRNA. 11/2000 Length = 2413	cysteine-sulfinate decarboxylase
3436	17885	NM_021765	X, Y, SS	beta prime COP (Copb), mRNA. 11/2000 Length = 3025 jun B proto-oncogene	beta prime COP
3439	20161	NM_021836	CC, DD, EE, II, NNN	(Junb), mRNA. 11/2002 Length = 1035 Hexokinase 3 (Hk3),	jun B proto-oncogene
3445	17100	NM_022179	F	mRNA. 12/2000 Length = 3692	Hexokinase 3

TABL			April Serie	A	Cotiney Docker 44921-5133-91WO *** Document No. 1995323.1
809. D: 5	(10 K)2	CONLINE AGE OF ROSSON	Model Code	Known Cene Neine	Unigene Sequence Civeter Title
3445	17101	NM_022179	JJ, KK, FFF, HHH	Hexokinase 3 (Hk3), mRNA. 12/2000 Length = 3692	Hexokinase 3
				insulin receptor- related receptor (Insrr), mRNA. 11/2002 Length =	
3448	20266	NM_022212	D, SS	1410 G protein-coupled	insulin receptor-related receptor
2440	20070	,		receptor 5-1 (Gpcr5- 1), mRNA. 12/2000	0
3449	20276	NM_022216	SS	Length = 1062	G protein-coupled receptor 5-1
			A, B, Y, FFF, GGG, HHH, LLL, PPP, QQQ, General Core Tox	L-gulono-gamma- lactone oxidase (Gulo), mRNA. 12/2000 Length =	
3450	20299	NM_022220	Markers	1323	L-gulono-gamma-lactone oxidase
3451	20385	NM_022229	G, H, S, T, U	heat shock protein 60 (liver) (Hsp60), mRNA. 12/2000 Length = 2175	heat shock protein 60 (liver)
3454	760	NM_022245	LL	cytochrome b5 (Cyb5), mRNA. 12/2000 Length = 751	cytochrome b5
3454	762	NM_022245	K, GG, PP, QQ, TT	cytochrome b5 (Cyb5), mRNA. 12/2000 Length = 751	cytochrome b5
3455	6263	NM 022251	EEE, III, JJJ, MMM, OOO, General Core Tox Markers, General Alternate	aminopeptidase A (Enpep), mRNA. 12/2000 Length = 4075	aminonostidaco A
J400	0203	TAINI_022231	Allemate	connective tissue growth factor (Ctgf), mRNA. 11/2002	aminopeptidase A
3456	6585	NM_022266	Α	Length = 2345	connective tissue growth factor

TABL	<b>国们</b> 。"		5. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	A	lorney Docker 44221-5033-91000 
509 <u>.</u> ID	id ke. Gree	Consenia Accor Respond	Model Codo	Known Cone Kame	elitt rejevið senevþez sússinÚ
				alpha-tubulin (Tuba1), mRNA. 12/2000 Length =	·
3461	17158	NM_022298	O, P	1617	alpha-tubulin
2464	47464	NIA 022209	W VV VV	alpha-tubulin (Tuba1), mRNA. 12/2000 Length =	alaha tuhulia
3461	17161	NM_022298	V, XX, YY	1617	alpha-tubulin
3465	12082	NM_022389	KKK, NNN, General Alternate	7-dehydrocholesterol reductase (Dhcr7), mRNA. 11/2002 Length = 2427	7-dehydrocholesterol reductase
2465	42002	NIA 022200	KKK, NNN, General	7-dehydrocholesterol reductase (Dhcr7), mRNA. 11/2002	7. debudraek desteral redustano
3465	12083	NM_022389	Alternate	Length = 2427 quinoid	7-dehydrocholesterol reductase
			III, JJJ,	dihydropteridine reductase (Qdpr), mRNA. 11/2002	quinoid dihydropteridine
3466	13479	NM_022390	KKK E, XX,	Length = 1307 quinoid	reductase
3466	13480	NM 022390	YY, III, JJJ, General Alternate	dihydropteridine reductase (Qdpr), mRNA. 11/2002 Length = 1307	quinoid dihydropteridine reductase
				dopa/tyrosine sulfotransferase (LOC64305), mRNA. 11/2002 Length =	
3475	2384	NM_022513	X, Y	1279 transcobalamin II	dopa/tyrosine sulfotransferase
3480	7505	NM_022534	N ·	precursor (Tcn2p), mRNA. 11/2002 Length = 1808	transcobalamin II precursor
3460	7303	14W_022334		peroxiredoxin 3	transcobalariii ii precursor
3484	9240	NM_022540	E, BBB, CCC	(Prdx3), mRNA. 11/2002 Length = 1433	peroxiredoxin 3
				peroxiredoxin 3 (Prdx3), mRNA. 11/2002 Length =	
3484	9241	NM_022540	KK	1433 steroid sensitive	peroxiredoxin 3
2407	11020	NINA 000540	G, General	gene 1 (Ssg1), mRNA. 11/2002	ataraid agaitive sons 4 protein
3487	11039	NM_022543	Alternate	Length = 3719	steroid sensitive gene-1 protein

TABL	<b>3</b> ()			A	lomey Docket 44921-5033-01WO Document No. 1995323.1
	1	COMBONIX			F. * Thoramiting Way (1886)
<b>ම</b> ර්ග	ଞାଞ୍ଚ	Accor	Model		
(D)	ID No.	Rosson ID	Codo :	Known Cone Neme:	Unigana Sequena Cluster 71110
B. St. Maries Co.				transketolase (Tkt),	
	× .			mRNA. 11/2002	
3494	20802	NM_022592	J, Y, FF	Length = 2098	transketolase
				transketolase (Tkt),	
			J, X, BB,	mRNA. 11/2002	
3494	20803	NM_022592	CC, HH	Length = 2098	transketolase
				transketolase (Tkt),	
			l	mRNA. 11/2002	
3494	20804	NM_022592	×	Length = 2098	transketolase
			===	cathepsin B (Ctsb),	
2407	00044	NIM 000507	W, EEE,	mRNA. 11/2002	anthonoin P
3497	20944	NM_022597	МММ	Length = 1904 cellular nucleic acid	cathepsin B
i				binding protein	·
i	1			(Cnbp), mRNA.	
	1			11/2002 Length =	cellular nucleic acid binding
3498	20959	NM 022598	D	1640	protein
0-100	20000			cellular nucleic acid	
				binding protein	
1				(Cnbp), mRNA.	
		-		11/2002 Length =	cellular nucleic acid binding
3498	20960	NM_022598	D	1640	protein
				serine threonine	
į				kinase pim3 (Pim3),	
				mRNA. 1/2001	
3499	21115	NM_022602	JJ, KK	Length = 2133	serine threonine kinase pim3
					ESTs, Highly similar to 148404
l				germinal histone H4	histone H4 (55AA) (1 is 3rd base
3504	6121	NM_022686	GG	gene (Hist4), mRNA. 1/2001 Length = 377	in codon) - mouse (fragment) [M.musculus]
3504	0121	14W 022000	00	transcription factor	[IVI.ITIUSCUIUS]
		·		HES-3 (Hes3),	
ļ				mRNA. 1/2001	
3505	20507	NM 022687	F	Length = 964	transcription factor HES-3
1				synaptosomal-	
				associated protein,	
				23 kD (Snap23),	
				mRNA. 1/2001	synaptosomal-associated protein,
3506	20509	NM_022689	VV	Length = 633	23 kD
				small GTP-binding	
1	1			protein rab5 (Rab5a),	
				mRNA. 1/2001	
3507	20303	NM_022692	Q, R	Length = 649	small GTP-binding protein rab5
1		1	ļ	p105 coactivator	
			<u>'</u>	(U83883), mRNA.	
2500	17500	NIM 000004	VV	8/2001 Length =	a 105 gagativator
3508	17586	NM_022694	KK	3166	p105 coactivator

TABL	<b>ສ</b> ິ່ງ :			THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND THE PARTY AND TH	tomay Doctat 44921-5058-011WO Document No. 1985323.1
S39 (D.:::	.eki di	Kenseni Ace or Refseg ID	Modd Code	Known, Cene Name	Unigene Sequence Cluster Tille
				bcl-2 associated death agonist (Bad), mRNA. 1/2001	,
3510	17757	NM_022698	YY	Length = 1015	bcl-2 associated death agonist
3511	17809	NM 022699	O, P, XX,	ribosomal protein L30 (Rpl30), mRNA. 11/2002 Length ≃ 392	ribosomal protein L30
3311	17009	14IM_022699	11	nucleolar	mbosomai protein C30
				phosphoprotein p130 (Nopp140), mRNA. 1/2001 Length =	
3517	24283	NM_022869	SS	3609 nucleolar	nucleolar phosphoprotein p130
			C, AAA, General Core Tox	phosphoprotein p130 (Nopp140), mRNA. 1/2001 Length =	,
3517	24284	NM_022869	Markers	3609	nucleolar phosphoprotein p130
3522	15697	NM_022939	PP, QQ, UU	syntaxin 12 (Stx12), mRNA. 11/2002 Length = 819	syntaxin 12
3524	18107	NM 022949	General Alternate	ribosomal protein L14 (Rpl14), mRNA. 11/2002 Length = 715	ribosomal protein L14
3324	10107	14141_022949	Alternate	putative protein	nbosoniai protein £14
				phosphatase 1 nuclear targeting subunit (Ppp1r10), mRNA. 1/2001	putative protein phosphatase 1
3525	21491	NM_022951	ZZ, AAA	Length = 4131	nuclear targeting subunit
	4 = 2 : 2			phosphatidylinositol 3 kinase (Pik3c3), mRNA. 1/2001	
3527	15743	NM_022958	нн	Length = 2752	phosphatidylinositol 3-kinase
3529	1053	NM_022962	E	CL1BA protein (CL1BA), mRNA. 1/2001 Length = 5579	CL1BA protein
2524	9360	NINA 000400	N 66 77	alpha(1)-inhibitor 3, variant I (Mug1), mRNA. 2/2001	
3531	8266	NM_023103	N, SS, IT	Length = 4620 alpha(1)-inhibitor 3,	alpha(1)-inhibitor 3, variant I
2524	0007	<b>NIMA</b> 000400	General ·	variant I (Mug1), mRNA. 2/2001	
3531	8267	NM_023103	Alternate	Length = 4620	alpha(1)-inhibitor 3, variant I

TABL	<b>3</b> 1				tormey Doctat 44921-5053-01W0
Seq.		CONSERVA ACCON ROSSOQUD	Model Code	Kinowa Gene Name	Unigene Sequence Cluster Title
3531	8269	NM_023103	RR, WW	alpha(1)-inhibitor 3, variant I (Mug1), mRNA. 2/2001 Length = 4620	alpha(1)-inhibitor 3, variant l
3539	17517	NM 024151	LL, UU	ADP-ribosylation factor 4 (Arf4), mRNA. 11/2002 Length = 1608	ADP-ribosylation factor 4
3541	1161	NM 024153	D	adrenodoxin reductase (Fdxr), mRNA. 2/2001 Length = 1786	adrenodoxin reductase
3544	4504	NM 024159	PP	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (Dab2), mRNA. 5/2002 Length = 3170	disabled homolog 2, mitogen- responsive phosphoprotein (Drosophila)
	20770	NM 024160	w	cytochrome b558 alpha-subunit (Cyba), mRNA. 2/2001 Length = 709	cytochrome b558 alpha-subunit
3546	15779	_ NM 024163	RR	brain-enriched guanylate kinase- associated (BEGAIN), mRNA. 2/2001 Length = 2640	brain-enriched guanylate kinase- associated
3552	15623	- NM 024369		follistatin-related protein (Frp), mRNA. 11/2002 Length = 1370	follistatin-related protein precursor
3553	23489	NM_024375	RR	prepro bone inducing protein (Gdf10), mRNA. 3/2001 Length = 2411 peroxisomal	prepro bone inducing protein
3555	9929	NM_024392	U, EE, XX, YY, RRR, SSS	multifunctional enzyme type II (Hsd17b4), mRNA. 3/2001 Length = 2535	peroxisomal multifunctional enzyme type II
3555	9931	NM_024392	U, RRR, SSS	peroxisomal multifunctional enzyme type II (Hsd17b4), mRNA. 3/2001 Length = 2535	peroxisomal multifunctional enzyme type II

TABL	<b>3</b> 1,,				They Docket 44921-5058-01W0 Document No. 1985323.1
Seq ID	10 Ko:}:			Knovn Cene Name	Unigane Sequence Civeter Title
3555	25070	NM_024392	U, FF, LL, CCC, RRR, SSS	peroxisomal multifunctional enzyme type II (Hsd17b4), mRNA. 3/2001 Length = 2535	peroxisomal multifunctional enzyme type II
3558	13633	NM 024403	W	activating transcription factor ATF-4 (Atf4), mRNA. 3/2001 Length = 1173	activating transcription factor ATF-
3558	13634		м	activating transcription factor ATF-4 (Atf4), mRNA. 3/2001 Length = 1173	activating transcription factor ATF-
3566	10306	NM_030835	BB, CC	ribosome associated membrane protein 4 (RAMP4), mRNA. 4/2001 Length = 2335	ribosome associated membrane protein 4
3566	10308	NM 030835	LL	ribosome associated membrane protein 4 (RAMP4), mRNA. 4/2001 Length = 2335	ribosome associated membrane protein 4
	1221	 NM_030845	A, E, BB, CC, DD, EE, NN, OO, PP, EEE, III, KKK, MMM,	gro (Gro1), mRNA. 4/2001 Length = 929	gro
3568	18023	NM_030846	s	growth factor receptor bound protein 2 (Grb2), mRNA. 11/2002 Length = 2099	growth factor receptor bound protein 2
3568	18728	NM_030846	N, MM, PPP, QQQ, TTT	growth factor receptor bound protein 2 (Grb2), mRNA. 11/2002 Length = 2099	growth factor receptor bound protein 2
3569	21509	NM_030847	O, P	epithelial membrane protein 3 (Emp3), mRNA. 11/2002 Length = 737	epithelial membrane protein 3

TABL	<b>3</b> 1				torney Docket 44921-5033-01000 Document No. 1935328.1
Seq.; 100 † ;	ejec. D.Ko.:	Consoni Ace or Refseq ID	(1990) (1 (1990)	enel lene) avoal	Unigene Sequence Cluster Title
				Bradykinin receptor B1 (Bdkrb1), mRNA. 5/2002 Length =	
3570	1035	NM_030851	l, J	1312 DNA ligase I (Lig1),	Bradykinin receptor B1
3571	9594	NM_030855	RR	mRNA. 11/2002 Length = 3112	DNA ligase I
3578	8815	NM_030991	w	synaptosomal- associated protein (Snap25), mRNA. 11/2002 Length = 2100	ESTs, Highly similar to LAS1_MOUSE LIM AND SH3 DOMAIN PROTEIN 1 (LASP-1) (MLN 50) [M.musculus]
				aldo-keto reductase family 1, member A1 (Akr1a1), mRNA. 11/2002 Length =	aldo-keto reductase family 1,
3580	23109	NM_031000	G, H H, II, VV, EEE, FFF, LLL, MMM, UUU, General	dihydropyrimidine dehydrogenase (Dpyd), mRNA. 11/2002 Length =	member A1 (aldehyde reductase)
3584	6911	NM_031027	X, Y, II, VV, XX,	4358 dihydropyrimidine dehydrogenase (Dpyd), mRNA. 11/2002 Length =	dihydropyrimidine dehydrogenase
3584	6912	NM_031027	YY	GTP-binding protein (G-alpha-i2) (Gnai2), mRNA. 4/2001	dihydropyrimidine dehydrogenase
3586	15886	NM_031035	ZZ, AAA HH, XX, General	Length = 1748 glutamic-pyruvate transaminase (alanine aminotransferase) (Gpt), mRNA. 11/2002 Length =	GTP-binding protein (G-alpha-i2) glutamic-pyruvate transaminase
3587	21094	NM_031039	Alternate	1744 glutamic-pyruvate transaminase (alanine aminotransferase) (Gpt), mRNA. 11/2002 Length =	(alanine aminotransferase) glutamic-pyruvate transaminase
3587	21096	NM_031039	М	1744	(alanine aminotransferase)

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UALE.		1 Oak Broken	NOTE OF		Document No. 1995828.1
S09 (D)	elec .	Conseni Accor Reisog (D)	Model Gode	3473	Unicing Sequence Civeter Title
				general transcription	
				factor IIB (Gtf2b),	
0.500			TT, ZZ,	mRNA. 11/2002	
3588	20899	NM_031041	AAA	Length = 1227	general transcription factor IIB
1				glycogenin (Gyg), mRNA. 11/2002	
3589	17727	NM 031043	O, P, VV	Length = 1624	glycogenin
		<del></del>		neurotrophin-3	
				(HDNF/NT-3) (Ntf3),	
				mRNA. 4/2001	
3595	24508	NM_031073	UU, KKK	Length = 1020	neurotrophin-3 (HDNF/NT-3)
				phosphatidylinositol 4	
	]			kinase (Pik4cb), mRNA. 11/2002	
3597	4683	NM_031083	N. Z. AA	Length = 3205	phosphatidylinositol 4-kinase
-			, , _, , , , ,	#NAME? (Rala),	pricepriditayiii conor y ninacc
				mRNA. 11/2002	
3599	15201	NM_031093	F	Length = 952	#NAME?
			l :	#NAME? (Rala),	
2500	15202	NNA 024002	V, LL, WW	mRNA. 11/2002	40100453
3599	15202	NM_031093	VVVV	Length = 952 ribosomal protein L5	#NAME?
1				(Rpl5), mRNA.	
1				11/2002 Length =	
3600	12638	NM_031099	Τ	1069	ribosomal protein L5
		-	H, S, II,	ribosomal protein L5	
[			FFF,	(Rpl5), mRNA.	
3600	12639	NM 031099	General Alternate	11/2002 Length = 1069	ribosomal protein L5
3000	12039	14141_031099	Alternate	ribosomal protein S9	inbosomai protein L3
				(Rps9), mRNA.	
				11/2002 Length =	
3606	16929	NM_031108	Н	688	mRNA for ribosomal protein S9
				ribosomal protein	
			u pp	S10 (Rps10), mRNA.	
3607	16847	NM 031109	U, RR, FFF	11/2002 Length = 610	ribosomal protein S10
3007	10047	14101_031109	G, I, J,		nibusumai proteiit 310
			000,		
[			PPP,		
			QQQ,		
			General		
				sulfite oxidase	
			Markers, General	(Suox), mRNA. 11/2002 Length =	
3613	14970	NM_031127	Alternate	1777	sulfite oxidase

TABL	EQ.			Z.M	tomey/Docket 44921-5038-01W0
Seq ;	CLEC.		Model	Known Cene Name.	Unicana Sequence Cluster Title
3614	6525	NM 031129	F	transcription elongation factor B (SIII) polypeptide 2 (18kD, elongin B) (TCEB2), mRNA. 4/2001 Length = 357	transcription elongation factor B (SIII) polypeptide 2 (18kD, elongin B)
3014	0525	14101_031129		thymosin beta-4 (Tmsb4x), mRNA.	5)
3615	15052	NM_031136	O, P, Z,	4/2001 Length = 686	thymosin beta-4
3618	15185	NM_031140	AA, NN, OO, VV, EEE, MMM	vimentin (Vim), mRNA. 11/2002 Length = 1796	vimentin
3620	20862	NM 031154	A, B, GGG, HHH, General Alternate	glutathione S- transferase, mu type 3 (Yb3) (Gstm3), mRNA. 4/2001 Length = 1208	glutathione S-transferase, mu type 3 (Yb3)
3625	18597	NM 031325	E, S,	UDP-glucose dehydrogeanse (Ugdh), mRNA. 4/2001 Length =	UDP-glucose dehydrogeanse
0020	10007		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	proteasome (prosome, macropain) 26S subunit, non- ATPase,4 (Psmd4), mRNA. 4/2001	proteasome (prosome, macropain) 26S subunit, non-
3627	18375	NM_031331	G, H, S	Length = 1334 proteasome (prosome, macropain) 26S subunit, non- ATPase,4 (Psmd4), mRNA. 4/2001	proteasome (prosome, macropain) 26S subunit, non-
3627	18376	NM_031331	ss	Length = 1334 organic anion transporter (LOC83500), mRNA.	ATPase,4
3628	12682	NM_031332	М	4/2001 Length = 2157	organic anion transporter
3629	6672	NM_031333	L, LLL, SSS	cadherin 2 (Cdh2), mRNA. 11/2002 Length = 4350 cadherin 2 (Cdh2),	cadherin 2, type 1, N-cadherin (neuronal)
3629	6673	NM_031333	GGG, LLL	mRNA. 11/2002 Length = 4350	cadherin 2, type 1, N-cadherin (neuronal)

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: :	(Alama) Ama			Document No. 1985323.1
erec Erce	Accor.		emen eneo avoida	Unigeno Sequence Clusier Tille
18539	NM_031353	кк	voltage-dependent anion channel 1 (Vdac1), mRNA. 11/2002 Length = 1818	voltage-dependent anion channel
4.4022	NINA 024522		Androsterone UDP- glucuronosyltransfera se (Ugt2b2), mRNA. 5/2001 Length =	Androsterone UDP-
14633	NM_031533	K	1593	glucuronosyltransferase  B cell lymphoma 2 like, ESTs,
445	NM_031535	I, J	B cell lymphoma 2 like (Bcl2I), mRNA. 5/2001 Length = 1748	Moderately similar to ilvB (bacterial acetolactate synthase)- like; acetolactate synthase homolog [Homo sapiens] [H.sapiens]
15024	NM_031572	GG	Cytochrom P450 15- beta gene (Cyp2c12), mRNA. 11/2002 Length = 1714	Cytochrom P450 15-beta gene
20765	NM 031643	11	mitogen activated protein kinase kinase 1 (Map2k1), mRNA. 11/2002 Length =	mitogen-activated protein kinase kinase 1
	NM 031643	P	mitogen activated protein kinase kinase 1 (Map2k1), mRNA. 11/2002 Length = 2136	mitogen-activated protein kinase kinase 1
20502	_	A, N	solute carrier family 21, member 10 (Slc21a10), mRNA. 11/2002 Length = 3212	solute carrier family (organic anion transporter) member 10
			ribosomal protein S12 (Rps12), mRNA. 11/2002 Length =	
16918	NM_031709	F	499	ribosomal protein S12
20724	NIM 031753		cell adhesion molecule (Alcam), mRNA. 11/2002	activated leukocyte cell adhesion
	18539 14633 445 20765 20767	ELEC Resegile.  18539 NM_031353  14633 NM_031533  445 NM_031535  15024 NM_031572  20765 NM_031643  20767 NM_031643  20502 NM_031650  16918 NM_031709	©LGC AGG OF ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID NO. ROSOGID: COCOMID N	Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code   Code

TABL	39 : = };			AT AT	torney Docket 44921-5038-011WO Document No. 1985328.1
 Seq ID	id ko Grec	Consont Accor Reference	Model Code	emski eneg mygiki	Onigane Sequence Cluster Title
				ATP-binding cassette, sub-family B (MDR/TAP), member 11 (Abcb11), mRNA.	
3685	4314	NM 031760	II, VV, DDD	11/2002 Length = 5036	ATP-binding cassette, sub-family B (MDR/TAP), member 11
3003	4314			guanine deaminase (Gda), mRNA. 11/2002 Length =	
3687	14184	NM_031776	ν, υυ	1568 guanine deaminase	guanine deaminase
3687	14185	NM 031776	V, NN	(Gda), mRNA. 11/2002 Length =	guanine deaminase
		_		transaldolase 1 (Taldo1), mRNA. 11/2002 Length =	
3692	16039	NM_031811	J, FF	1057	transaldolase 1
3701	11170	NM_031833	O, P, General Alternate	nucleoside diphosphate kinase (Nme2), mRNA. 5/2001 Length = 631	ESTs, nucleoside diphosphate kinase
3704	10176	NM_031837	ww, kkk	E-septin (LOC83788), mRNA. 5/2001 Length = 3061	E-septin
3713	1475	NM_031971	A, B, Q	Heat shock protein 70-1 (Hspa1a), mRNA. 5/2001 Length = 2455	ESTs, Highly similar to S10A_RAT S-100 protein, alpha chain [R.norvegicus], Heat shock protein 70-1
3714	24644	NM_031972	GG	Aldehyde dehydrogenase family 3, subfamily A1 (Aldh3a1), mRNA. 11/2002 Length = 1725	Aldehyde dehydrogenase class 3
3715	16257	NM 031975	N, General Alternate	parathymosin (Ptms), mRNA. 11/2002 Length = 936	parathymosin
3715	17556	NM_031975	N, S, V	parathymosin (Ptms), mRNA. 11/2002 Length = 936	parathymosin
3718		NM_031980	PP, QQ,	UDP- glucuronosyltransfera se (Ugt2b12), mRNA. 5/2001 Length = 1846	

TABL	<b>3</b> 1			A A	Comey Docket 44921-5033-01WO Document No. 1935323.1
	(10 kg. :	ingentalis Assor Restent	Model : Code :	Knovn Cene Keine	Unigana Sequence Cluster Tille
				UDP- glucuronosyltransfera se (Ugt2b12),	·
3718	17806	NM_031980	RRR	mRNA. 5/2001 Length = 1846	UDP-glucuronosyltransferase
3719	15265	NM_031981	Q, R	p47 protein (p47), mRNA. 11/2002 Length = 1451	p47 protein
3719	15266	NM 031981	Q, R	p47 protein (p47), mRNA. 11/2002 Length = 1451	p47 protein
3719	15267	NM 031981	ww	p47 protein (p47), mRNA. 11/2002 Length = 1451	p47 protein
3720	18899	NM_031985	·	S6 kinase (Rps6kb1), mRNA. 5/2001 Length = 2287	S6 kinase
3724	20793	NM 032058	UU	eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (Eif2b2), mRNA. 5/2001 Length = 1474	eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD)
3725	9106	 NM 032066	BBB CCC	smooth muscle- specific 17 beta- hydroxysteroid dehydrogenase type 3 (LOC84013), mRNA. 5/2001 Length = 1830	smooth muscle-specific 17 beta- hydroxysteroid dehydrogenase type 3
				LIM and SH3 protein 1 (Lasp1), mRNA. 11/2002 Length =	ESTs, ESTs, Highly similar to LAS1_MOUSE LIM AND SH3 DOMAIN PROTEIN 1 (LASP-1)
3729	8817	NM_032613		Protein phosphatase type 1B (formely 2C), Mg-dependent, beta isoform (Ppm1b), mRNA. 7/2001	(MLN 50) [M.musculus]  Protein phosphatase type 1B (formely 2C), Mg-dependent, beta
3733	25529 2577	NM_033096 NM_033236	R, VV	Length = 3257 Proteasome (prosome, macropain) 26S subunit, ATPase (Psmc2), mRNA. 8/2001 Length = 1403	Proteasome (prosome, macropain) 26S subunit, ATPase

TABL					Tormey Docket 44921-5038-01000
Seq ි	GLGC:	CONSINI ACCO ROSCO LD	Model (code	Movin Gene Wine	Unigane Sequence Ciuster Tille
3742	16364	NM_053019	A, B, H, I, GG, OOO, General Core Tox Markers	arginine vasopressin receptor 1A (Avpr1a), mRNA. 10/2002 Length = 1606	Vasopressin receptor V1a
3752	15791	NM_053341	D	regulator of G-protein signaling 19 interacting protein 1 (Rgs19ip1), mRNA. 11/2002 Length = 1607	regulator of G-protein signaling 19
2755	44240		НН	beta-catenin (Catnb), mRNA. 11/2002	beta-catenin
3755	11319	NM_053357	GG, ZZ,	Length = 2650 nerve growth factor receptor (TNFRSF16) associated protein 1 (Ngfrap1), mRNA. 11/2002 Length =	·
3759	16018 6962	NM_053401 NM_053404	AAA LL	519 dynactin 4 (Dctn4), mRNA. 11/2002 Length = 2573	brain expressed X-linked 3 ESTs, Moderately similar to C54354 calnexin precursor - rat [R.norvegicus]
				acyl- CoA:dihydroxyaceton ephosphate acyltransferase (Gnpat), mRNA. 11/2001 Length =	acyl- CoA:dihydroxyacetonephosphate
3763	6774	NM_053410	CC	zinc finger protein 103 (Zfp103), mRNA. 11/2002 Length =	acyltransferase
3765 3767	5561 4621	NM_053438 NM_053463	JJ, KK	3258 nucleobindin (Nucb), mRNA. 11/2002 Length = 2303	zinc finger protein 103 nucleobindin
3767	4622	NM_053463	JJ, KK H, FFF,	nucleobindin (Nucb), mRNA. 11/2002 Length = 2303 spermidine synthase	nucleobindin
3768	11403	NM_053464	General Core Tox Markers	(Srm), mRNA. 11/2002 Length = 1268	spermidine synthase

TABL	國 ()	The second			iomicy/Docket 44921-5188-01W0 :
		Carena Ace or Referred	Coda Model	Known Cene Name	elili reteule concupe Signi
				integral membrane protein Tmp21-I (p23) (Tmp21), mRNA. 11/2001	integral membrane protein Tmp21
3769	23274	NM_053467	O, P, FF	Length = 1314 integral membrane protein Tmp21-I (p23) (Tmp21), mRNA. 11/2001	I (p23) integral membrane protein Tmp21-
3769	23276	NM_053467	V	Length = 1314 protein tyrosine phosphatase type	I (p23)
3772	9573	NM_053475	ZZ, AAA	IVA, member 2 (Ptp4a2), mRNA. 11/2002 Length = 1095	protein tyrosine phosphatase type IVA, member 2
				peroxisomal membrane protein Pmp26p (Peroxin-11) (Pex11a), mRNA. 11/2001 Length =	peroxisomal membrane protein
3774	4290	NM_053487	ввв	1194	Pmp26p (Peroxin-11)
3775	9307	NM_053491	N, XX, YY	plasminogen (Plg), mRNA. 11/2002 Length = 2737	plasminogen
3775	25443	NM 053491	GGG, HHH, PPP, QQQ, UUU, General Alternate	plasminogen (Plg), mRNA. 11/2002 Length = 2737	plasminogen
			OO, III, JJJ, KKK, General Core Tox	expressed in non- metastatic cells 3, protein (nucleoside diphosphate kinase) (Nme3), mRNA. 11/2001 Length =	expressed in non-metastatic cells 3, protein (nucleoside diphosphate kinase)
3776	23558	NM_053507	Markers	peroxiredoxin 4 (Prdx4), mRNA. 11/2002 Length =	ырпоѕрнате ктаѕе)
3777	7219	NM_053512	F PP, WW,	965	peroxiredoxin 4
3778	16125	NM_053514	DDD, General Alternate	lin-7-Ba (Veli1), mRNA. 11/2001 Length = 660	lin-7-Ba

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TABL	<b>₹</b> 1		10000000000000000000000000000000000000		Omey Docket 44921-5033-01W0 ***********************************
\$69 D:	erec Bros	CONSINI AGG OT ROSSOJ ID	Code.	Known Cene Name	Unidene Sequence Cluster Title
3779	16134	NM_053516	III, JJJ	unknown Glu-Pro dipeptide repeat protein (LOC85383), mRNA. 11/2001 Length = 1876	unknown Glu-Pro dipeptide repeat protein
3779	16135	NM_053516	L, S, DD, EE, HH	unknown Glu-Pro dipeptide repeat protein (LOC85383), mRNA. 11/2001 Length = 1876	unknown Glu-Pro dipeptide repeat protein
3780	19205	NM_053522	Q, R	ras-like protein (Tc10), mRNA. 11/2002 Length = 3873	ras-like protein
3783	14199	NM_053538	O, P	lysosomal-associated protein transmembrane 5 (Laptm5), mRNA. 11/2001 Length = 1309	lysosomal-associated protein transmembrane 5
3784	8358	NM 053540	X, Y	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast) (Cox17), mRNA. 11/2001 Length = 229	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)
3785	12496	NM_053541	XX, YY, RRR	low density lipoprotein receptor- related protein 3 (Lrp3), mRNA. 11/2001 Length = 3891	low density lipoprotein receptor- related protein 3
3787	15829	NM_053551	ZZ, AAA	pyruvate dehydrogenate kinase 4 (Pdk4), mRNA. 11/2002 Length = 1435	pyruvate dehydrogenase kinase, isoenzyme 4
3788	11843	 NM_053555	ZZ, AAA	vesicle-associated membrane protein 5 (Vamp5), mRNA. 11/2001 Length = 309.	vesicle-associated membrane protein 5
3790	4327	NM_053563	R	nuclear RNA helicase, DECD variant of DEAD box family (Ddxl), mRNA. 11/2001 Length = 1511	nuclear RNA helicase, DECD variant of DEAD box family

TABL				AV .	tomey Docket 44921-5033-011WO
S00 :	id ko: Gree	Conseni Assor Reisign ID	Model Code	rianovan Cono Nama.	Unicine Sequence Cluster Title
3792	21940	NM_053568	KKK, NNN		phosphate cytidylyltransferase 2, ethanolamine
3792	21941	NM_053568	т, хх, ккк	phosphate cytidylyltransferase 2, ethanolamine (Pcyt2), mRNA. 11/2001 Length = 1846	phosphate cytidylyltransferase 2, ethanolamine
2705	21424	NIM 053586	vv vv	cytochrome c oxidase subunit Vb (Cox5b), mRNA. 11/2001 Length = 485	cytochrome c oxidase subunit Vb
3795	21424	NM_053586	XX, YY	485	cytochrome c oxidase subunit vo
3797	20842	NM_053590	X, Y, RR, UUU	proteasome (prosome, macropain) subunit, beta type 1 (Psmb1), mRNA. 11/2001 Length = 799	proteasome (prosome, macropain) subunit, beta type 1
3798	20896	NM_053592	U, NNN	Deoxyuridinetriphosp hatase (dUTPase) (Dut), mRNA. 5/2002 Length = 952	Deoxyuridinetriphosphatase (dUTPase)
			PP, QQ,	Endothelin- converting enzyme 1 (Ece1), mRNA. 5/2002 Length =	
3800	21708	NM_053596	UU, WW	4469 Endothelin-	Endothelin-converting enzyme 1
3800	21709	NM 053596	MM, PP, UU, III, JJJ, TTT, UUU	converting enzyme 1 (Ece1), mRNA. 5/2002 Length =	Endothelin-converting enzyme 1
3801	11830	NM_053598	M, DD, SS, TT, FFF, General Core Tox Markers, General Alternate	diphosphoinositol polyphosphate phosphohydolase type II (Nudt4), mRNA. 11/2001 Length = 2954	diphosphoinositol polyphosphate phosphohydolase type II

TABL	<b>≧</b> 1		3		tomey Docket 44921-5068-01WO Document No. 1986323.1
Seq.	id no.	(697) 577) Ass or	Model Codo		Unigéne Seguence Civeter Itile
3801	18795	NM_053598	E, DD, JJ, KK, MM, UU, FFF, KKK, NNN, TTT, General Alternate	diphosphoinositol polyphosphate phosphohydolase type II (Nudt4), mRNA. 11/2001 Length = 2954	diphosphoinositol polyphosphate phosphohydolase type II
	23192		N, GG, JJ, KK, General	diphosphoinositol polyphosphate phosphohydolase type II (Nudt4), mRNA. 11/2001	diphosphoinositol polyphosphate
3801	1127	NM_053598 NM_053626	Alternate	Length = 2954 D-amino acid oxidase (Dao1), mRNA. 11/2001 Length = 1646	phosphohydolase type II  D-amino acid oxidase
3808	9055	NM 053631	Х, Ү, UUU	Breakpoint cluster region protein, uterine leiomyoma, 1; barrier to autointegration factor (Bcrp1), mRNA. 11/2001 Length = 733	Breakpoint cluster region protein, uterine leiomyoma, 1; barrier to autointegration factor
3811	3454	NM_053662	Q, R, W	cyclin L (Ccnl), mRNA. 11/2001 Length = 2092	cyclin L
3811	3455	NM_053662	Q, R	cyclin L (Ccnl), mRNA. 11/2001 Length = 2092	cyclin L
3812	24204	NM_053670	c, uu	calcitonin gene- related peptide- receptor component protein (Crcp), mRNA. 11/2002 Length = 1408	calcitonin gene-related peptide- receptor component protein
3813	16123	NM_053698	F, DD, EE	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (Cited2), mRNA. 11/2001 Length = 1155	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2

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TABL	ਵਿ <b>ੀ</b> :				termey Docket 4/1921-5033-01/1/0 
(D) (C)	id kjo" erec:		Model Code	Knovin Cene Leme.	Unigene Sequence Civisia, Tille
3814	14795	NM_053699	JJ, KK	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4 (Cited4), mRNA. 11/2001 Length = 897 embigin (Emb),	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4
3815	5798	NM_053719	Т	mRNA. 11/2001 Length = 1458	embigin
3816	15269	NM 053739	PP, QQ, DDD, HHH	beclin 1 (coiled-coil, myosin-like BCL2- interacting protein) (Becn1), mRNA. 11/2001 Length = 1908	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)
3827	25625	NM_053783	PP, QQ	interferon gamma receptor (Ifngr), mRNA. 11/2001 Length = 1860	interferon gamma receptor
3828	25594	NM_053799	М	aspartyl-tRNA synthetase (Dars), mRNA. 11/2001 Length = 2143 thioredoxin (Txn),	aspartyl-tRNA synthetase
3829	15615	NM_053800	DDD .	mRNA. 11/2002 Length = 330	thioredoxin
3831	4361	NM_053812	О, Р	BCL2- antagonist/killer 1 (Bak1), mRNA. 11/2001 Length = 1923	BCL2-antagonist/killer 1
3834	15002	NM_053819		tissue inhibitor of metalloproteinase 1 (Timp1), mRNA. 11/2001 Length = 740	tissue inhibitor of metalloproteinase 1
3836	17154	NM_053835	K, Q, R, BBB, CCC, LLL, RRR, SSS		clathrin, light polypeptide (Lcb)
3836	17155	NM_053835	H, LLL, UUU, General Alternate	clathrin, light polypeptide (Lcb) (Cltb), mRNA. 11/2002 Length = 982	clathrin, light polypeptide (Lcb)

TABL	<b>3</b> 1		. 53.5	e de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de l	torney Dockst 44921-5093-01W0 Document No. 1995323.1
Seq .	GLGC:	Conseni Ace or Refer ID	Model :	Known Cene Name	enerija senerpes sacējuu
3837	17299	NM_053842	PPP, QQQ	mitogen activated protein kinase 1 (Mapk1), mRNA. 11/2002 Length = 1467	mitogen activated protein kinase 1
3839	19018	NM 053849	C, FF	protein disulfide isomerase related protein (calcium- binding protein, intestinal-related) (Erp70), mRNA. 11/2001 Length = 2398	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)
3840	16362	NM 053853	C, W	N-acetyltransferase 1 (arylamine N- acetyltransferase) (Nat1), mRNA. 11/2002 Length = 2533	N-acetyltransferase 1 (arylamine N-acetyltransferase)
3848	15934	NM 053904	w	5-oxoprolinase (ATP- hydrolysing) (Oplah), mRNA. 11/2001 Length = 4003	5-oxoprolinase (ATP-hydrolysing)
3850	15718	NM_053907	HH, General Alternate	deoxyribonuclease I- like 3 (Dnase1l3), mRNA. 11/2001 Length = 1417	deoxyribonuclease I-like 3
3851	8152	NM_053908	0	protein tyrosine phosphatase, non- receptor type 6 (Ptph6), mRNA. 11/2001 Length = 2176	protein tyrosine phosphatase, non- receptor type 6
3855	14591	NM_053961	DD, EE, NNN	endoplasmic retuclum protein 29 (Erp29), mRNA. 11/2001 Length = 4529	ESTs, Moderately similar to N- acetyl galactosaminidase, alpha [Mus musculus] [M.musculus]
3855	16553	NM_053961	I, J	endoplasmic retuclum protein 29 (Erp29), mRNA. 11/2001 Length = 4529	endoplasmic retuclum protein 29
3856	24778	NM_053962	C, MM, FFF, TTT	Serine dehydratase (Sdh), mRNA. 11/2002 Length = 1444	serine dehydratase

TABL	31				omey Docket 44921-5063-011WO
(r: Sog: ID;	erec.	CONSTRUCTION ACCOUNTY ACCOUNTY	Model: Code:		Unicero Sequence Civeter Ville
3856	24779	NM_053962	C, MM, TTT	Serine dehydratase (Sdh), mRNA. 11/2002 Length = 1444	serine dehydratase
3856	25321	NM_053962	MM, FFF,	Serine dehydratase (Sdh), mRNA. 11/2002 Length = 1444	serine dehydratase
3859	15135	NM_053971	G, H, FFF	ribosomal protein L6 (Rpl6), mRNA. 11/2001 Length = 963	ribosomal protein L6
3859	15136	NM_053971	M, X, Y, KK, HHH, General Core Tox Markers	(Rpl6), mRNA. 11/2001 Length = 963	ribosomal protein L6
3860	18798	NM 053978	ннн	RAB28, member RAS oncogene family (Rab28), mRNA. 11/2001 Length = 1483	RAB28, member RAS oncogene family
2002	45042	NIM OFZOGE	000,	H3 histone, family 3B (H3f3b), mRNA. 11/2001 Length =	H3 histone, family 3B
3863	15642	NM_053985	TTT	H3 histone, family 3B (H3f3b), mRNA. 11/2001 Length =	no historie, family ob
3863	15643	NM_053985	W	1107 H3 histone, family 3B (H3f3b), mRNA. 11/2001 Length =	H3 histone, family 3B
3863	15645	NM_053985	w	1107 progestin induced protein (dd5), mRNA.	H3 histone, family 3B
3865	18025	NM_053989	ZZ, AAA	11/2001 Length = 3180	progestin induced protein

TABL	ਵ਼0	N. 81	1 (20.00 20.00 (20.00)		iomey Docket 44921-5033-01WO Document No. 1985323.1
Seq (D)	elec. Eolo	Consonia Accor Refeed ID	Model ;;; Gode	Knowa Gene Reine	Vilgone Sequence Cluster Tille
			B, W, BB, CC, DD, EE, JJ, NN, OO, PP, HHH, III, KKK, NNN, General Core Tox Markers, General	protein tyrosine phosphatase, non- receptor type 2 (Ptpn2), mRNA. 11/2002 Length =	protein tyrosine phosphatase, non
3866	16809	NM_053990	Alternate	proline transporter	receptor type 2
3868	24430	NM_053996	Z, AA	(Prot), mRNA. 11/2001 Length = 2722	proline transporter
3870	16964	NIM 053000	ОВ	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform (Ppp2r2a), mRNA. 11/2001 Length = 2142	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
	·	NM_053999	Q, R	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform (Ppp2r2a), mRNA. 11/2001	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52),
3870	16965	NM_053999 ,	Q, R B, OO, General	Length = 2142  CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (Cd36i2), mRNA. 11/2001 Length =	alpha isoform  CD36 antigen (collagen type I receptor, thrombospondin
3871	21066	NM_054001	Alternate	1938 unr protein (unr),	receptor)-like 2
3872	17431	NM_054006	LL	mRNA. 11/2001 Length = 3755 unr protein (unr),	unr protein
3872	17433	NM_054006	N, UU	mRNA. 11/2001 Length = 3755	unr protein
3880	15391	NM_057114	U, LLL	peroxiredoxin 1 (Prdx1), mRNA. 11/2001 Length = 882	peroxiredoxin 1

TABL	39	1 2		A.	tomey Docket 44921-5033-91WO Document No. 1935323.1
(D)	ID KJO.	Constant Acc or Roßog ID	Model Code	Known Cene Name	eill teleule concoccionil
3883	15151	NM 057131	E	phosphoribosyl pyrophosphate synthetase- associated protein 2 (Prpsap2), mRNA. 11/2001 Length = 1612	phosphoribosyl pyrophosphate synthetase-associated protein 2
3885	8592	NM 057137	G, WW, General Alternate	phenylalkylamine Ca2+ antagonist (emopamil) binding protein (Ebp), mRNA. 11/2001 Length =	
3888	12331	NM 057155	A, B, General Core Tox Markers	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound (Xpnpep2), mRNA. 11/2001 Length = 2828	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-
3888	12332	NM 057155	General Core Tox Markers	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound (Xpnpep2), mRNA. 11/2001 Length = 2828	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane- bound
3893	14125	NM_057208	vv	tropomyosin 3, gamma (Tpm3), mRNA. 11/2001 Length = 1101	R.norvegicus mRNA for tropomyosin isoform 6, Rattus norvegicus nonmuscle tropomyosin 5 (Tpm5) isoforms NM 5 and NM 6 mRNA, partial cds
3894	24459	NM_057209	υυ	myosin light chain kinase 2, skeletal muscle (Mylk2), mRNA. 11/2001 Length = 2799 phosphatidylinositol-4	myosin light chain kinase 2, skeletal muscle
3899_	15764	NM_080480	к	phosphate 5-kinase, type II, gamma (Pip5k2c), mRNA. 12/2001 Length = 2669	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma
3903	18004	NM_080688	EE, NNN	phospholipase C, delta 4 (Plcd4), mRNA. 11/2002 Length = 2696	phospholipase C, delta 4

TABL			43 V V 1 3 4 V	¥* A	tomay Docket 44921-5033-01000
809 ID : :	@r@c⊹	Ressen Legison: Consoni	Model Code	Known Cene Name	Unicaio Secrence Cretor Tillo
3904	17662	NM_080697	GG	dynein light chain-2 (Dlc2), mRNA. 1/2002 Length = 510	dynein light chain-2
3905	23550	NM_080698	D	fibromodulin (Fmod), mRNA. 11/2002 Length = 2960	fibromodulin
				thioredoxin-like (32kD) (Txnl), mRNA. 1/2002	
3910	18902	NM_080887	A, B	Length = 1061	ESTs, thioredoxin-like (32kD)
3911	13799	NM 080888	L, Z	BCL2/adenovirus E1B 19 kDa- interacting protein 3- like (Bnip3l), mRNA. 1/2002 Length = 3219	BCL2/adenovirus E1B 19 kDa- interacting protein 3-like
2044	10005	NIM 000000	7	BCL2/adenovirus E1B 19 kDa- interacting protein 3- like (Bnip3l), mRNA. 1/2002 Length =	BCL2/adenovirus E1B 19 kDa-
3911	19605 23033	NM_080888 NM_080888	1, J, E, Z	BCL2/adenovirus E1B 19 kDa- interacting protein 3- like (Bnip3l), mRNA. 1/2002 Length = 3219	interacting protein 3-like  BCL2/adenovirus E1B 19 kDa- interacting protein 3-like
3912	6143	NM 080892	K, GG, HH, NN, OO	selenium binding protein 2 (Selenbp2), mRNA. 1/2002 Length = 1685	selenium binding protein 2
3913	16267	NM_080896	P, Q, R	heterogeneous nuclear ribonucleoprotein H1 (Hnrnph1), mRNA. 11/2002 Length = 1967 reticulon 3 (Rtn3),	heterogeneous nuclear ribonucleoprotein H1 Rattus norvegicus CaM-kinase II
3915	17413	NM 080909	т	mRNA. 11/2002 Length = 2773	inhibitor alpha mRNA, complete cds, reticulon 3
3916	11421	NM_130405		src associated in mitosis, 68 kDa (Sam68), mRNA. 1/2002 Length = 2655	src associated in mitosis, 68 kDa

TABU			- F11 A - 7	M	torney Docket 44921-5033-011WC Document No. 1985328.1
509 ID	(1) No.	COMBANI ACCOT ROISON ID	Model	Kapowa Cene Neme	Unigene Sequence Cluster Tide
2046	40005	NIA 420405		src associated in mitosis, 68 kDa (Sam68), mRNA. 1/2002 Length =	
3916	12035	NM_130405	O, P	2655	src associated in mitosis, 68 kDa
3919	19316	NM_130411	<b>~</b>	coronin, actin binding protein 1A (Coro1a), mRNA. 1/2002 Length = 1386	coronin, actin binding protein 1A
				acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3- oxoacyl-Coenzyme A thiolase) (Acaa2), mRNA. 1/2002	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3
3923	18293	NM_130433	LL	Length = 1619 stellate cell activation	oxoacyl-Coenzyme A thiolase)
3925	15961	NM 130744	E, III, JJJ	associated protein (Staap), mRNA. 11/2002 Length =	stellate cell activation associated protein
				citrate synthase (Cs), mRNA. 2/2002	
3926	18846	NM 130755	F .	Length = 1498	citrate synthase
			I, J, U, FF, XX,	hydroxyacyl- Coenzyme A dehydrogenase/3- ketoacyl-Coenzyme A hiolase/enoyl- Coenzyme A hydratase (trifunctional protein), alpha subunit (Hadha), mRNA. 2/2002 Length =	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl- Coenzyme A hiolase/enoyl- Coenzyme A hydratase (trifunctional protein), alpha
3929	16767	NM_130826	YY, RRR	2775	subunit
3929	16768	NM_130826		hydroxyacyl- Coenzyme A dehydrogenase/3- ketoacyl-Coenzyme A hiolase/enoyl- Coenzyme A hydratase (trifunctional protein), alpha subunit (Hadha), mRNA. 2/2002 Length =	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl- Coenzyme A hiolase/enoyl- Coenzyme A hydratase (trifunctional protein), alpha subunit

TABL	<b>≣</b> 1	:			torney Docket 44921-5033-01W0 Document No. 1995323.1
600 (D		Keiseg ID	Model Code	Kijova Cere Kame	Unigene Sequence Cluster Thie
			WW BBB	hydroxyacyl- Coenzyme A dehydrogenase/3- ketoacyl-Coenzyme A hiolase/enoyl- Coenzyme A hydratase (trifunctional protein), alpha subunit (Hadha), mRNA. 2/2002 Length =	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl- Coenzyme A hiolase/enoyl- Coenzyme A hydratase (trifunctional protein), alpha
3929	16769	NM_130826	ccc	2775	subunit
3931	20707	NM_131906	K, M, N, X, BB, CC, GG, TT, FFF, GGG, UUU, General Core Tox Markers	solute carrier family 21 (organic anion transporter), member 5 (Slc21a5), mRNA. 2/2002 Length = 3622	solute carrier family 21 (organic anion transporter), member 5
3941	17634	NM_133418	PP, QQ	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 (Slc25a10), mRNA. 3/2002 Length = 1946	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10
3941	17635	NM_133418	GG	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 (Slc25a10), mRNA. 3/2002 Length = 1946	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10
				dapit (LOC171069), mRNA. 3/2002	
3946	19613	NM_133544	Q, R, XX	Length = 322 cell division cycle	dapit
3951	1827	NM_133572	NN, OO	25B (Cdc25b), mRNA. 3/2002 Length = 2804 protein phosphatase	cell division cycle 25B
3955	24352	NM_133589	L	V (LOC171121), mRNA. 3/2002 Length = 1270	protein phosphatase V

TABL	31			A. A.	ionney Docket 4/921-5053-01000 Document No. 1935323.1
Seq :	id ko: Græc	ESSECTION & COLORS	Model) Codo	Known Cene Name	Unificia Scquence Civister Title
3956	1546	NM_133595	KKK, PPP, QQQ, General Alternate	GTP cyclohydrolase I feedback regulatory protein (Gchfr), mRNA. 3/2002 Length = 676 lectin, galactoside- binding, soluble, 2	GTP cyclohydrolase I feedback regulatory protein
3957	15637	NM_133599	xx	(galectin 2) (Lgals2), mRNA. 3/2002 Length = 624	lectin, galactoside-binding, soluble, 2 (galectin 2)
3958	17758	NM 133606	G, U, FF, LL, XX, YY, BBB, CCC, FFF, RRR, SSS, UUU, General Alternate	enoyl-Coenzyme A, hydratase/3- hydroxyacyl Coenzyme A dehydrogenase (Ehhadh), mRNA. 11/2002 Length = 3097	enoyl-Coenzyme A, hydratase/3- hydroxyacyl Coenzyme A dehydrogenase
3960	19706	NM 134329	M, U	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide (Adh7), mRNA. 3/2002 Length =	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3961	16456	NM_134346	, O	RAP1B, member of RAS oncogene family (Rap1b), mRNA. 3/2002 Length = 1874	RAP1B, member of RAS oncogene family
3961	16457	NM_134346	A, B, O, P, VV	RAP1B, member of RAS oncogene family (Rap1b), mRNA. 3/2002 Length = 1874 calcium-independent	RAP1B, member of RAS oncogene family
3966	2643	NM_134408	Z, AA, RR	alpha-latrotoxin receptor homolog 2 (Cirl2), mRNA. 3/2002 Length = 5602 PKC-delta binding	calcium-independent alpha- latrotoxin receptor homolog 2
3969	2802	NM_134449	A	protein (SRBC), mRNA. 3/2002 Length = 1049	PKC-delta binding protein

Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semilarik   Semi	TABL	31	17			tomey Docket 4A921-5038-01WO Document No. 1935323.1
3975   24672   NM_138517   SS   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 925   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830   Length = 1830			Acc or		enjek eneë awoak	Unigene Sequence Cluster VIIIe
3975   24672   NM   138517   SS   Length = 925   complete cds						
expressed in non-metastatic cells   (Nme1), mRNA.   11/2002 Length =   737   vacuole Membrane   Protein 1 (Vmp1), mRNA.   11/2002 Length =   1/3002   vacuole Membrane   Protein 1 (Vmp1), mRNA.   11/2002   Length =   1830   vacuole Membrane   Protein 1 (Vmp1), mRNA.   11/2002   Length =   1830   vacuole Membrane   Protein 1 (Vmp1), mRNA.   11/2002   Length =   1830   vacuole Membrane   Protein 1 (Vmp1), mRNA.   11/2002   Length =   1830   vacuole Membrane   Protein 1   (vgtochrome b-5)   reductase) (Dia1), mRNA.   4/2002   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Length =   1893   Leng					1	1' ' '
metastatic cells 1 ((Nme1), mRNA. 11/2002 Length = 737	3975	24672	NM_138517	SS		complete cds
Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   Common   C					1 .	·
11/2002 Length =   1, protein (NM23A) (nucleoside diphosphate kinase)   11/2002 Length =   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NM23A) (nucleoside diphosphate kinase)   1, protein (NADH) (cytochrome b-5 reductase) (NADH) (cytochrome b-5 reductase) (Dia1), mRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diap	İ					expressed in non-metastatic cells
3979   20999   NM_138548   I, J   737   diphosphate kinase)	l					
3984   23166   NM_138839   Alternate   R, BB, CC, JJ, ROND   Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Control (Con	3979	20999	NM 138548	l. J	<b>1</b>	
3984   23166   NM_138839   Alternate   Length = 1830   Vacuole Membrane Protein 1				<del></del>	vacuole Membrane	
3984   23166		ļ		B, WW,	Protein 1 (Vmp1),	
R, BB, CC, JJ, (cytochrome b-5 reductase) (Dia1), mRNA. 4/2002 Length = 1893    17530				General	mRNA. 11/2002	·
CC, JJ, KK, General	3984	23166	NM_138839			Vacuole Membrane Protein 1
KK, General   RNA. 4/2002   Length = 1893   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Length = 1893   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Length = 1893   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Length = 1893   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Length = 1893   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Length = 1893   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Length = 1893   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Length = 1893   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), General   MRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase (NADH) (cytochrome b-5 reductase) (Diaphorase		[				
Seed   17530						
3986   17530   NM_138877   Alternate   Length = 1893   b-5 reductase)					, , , , ,	Disabassa (NADII) (sutasbussas
Diaphorase (NADH)	2000	47500	NINA 420077		1	
Cytochrome b-5   reductase) (Dia1),   mRNA. 4/2002   Length = 1893   b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b	3986	17530	138877	Alternate		b-5 reductase)
Reductase   (Dia1), mRNA. 4/2002   Length = 1893   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (						
See   17531					1, -	
3986   17531   NM_138877   Alternate   Length = 1893   b-5 reductase)				General		Diaphorase (NADH) (cytochrome
Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), mRNA. 4/2002 Length = 1893 b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (cytochrome b-5 reductase)   Diaphorase (NADH) (c	3986	17531	NM 138877		E .	
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KK,   reductase) (Dia1),   mRNA. 4/2002   Diaphorase (NADH) (cytochrome b-5 reductase)   Best5 protein   (Best5), mRNA. 4/2002 Length =   3987   4593   NM_138881   W   3628   Best5 protein						
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TABL	<b>E</b> 1		3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	A	tomey Docket 44921-5033-01W0
S09 (D) ;-:	ID No. Grec	Centenk Acc or Refsee ID	Cocia Mocial	Known Cene Name	Willigene Sequence Cluster Title
3988	7394	NM 138883	DDD	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (Atp5o), mRNA. 4/2002 Length = 707	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
3989	14964	NM_138884	EEE, MMM	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid- 5-beta-reductase) (Akr1d1), mRNA. 4/2002 Length = 3189	
3989	14965	NM 138884	RR	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid- 5-beta-reductase) (Akr1d1), mRNA. 4/2002 Length = 3189	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid 5-beta-reductase)
3993	18867	NM_138900		complement component 1, s subcomponent (C1s), mRNA. 11/2002 Length = 2908	complement component 1, s subcomponent
4000	809	NM 139089	w	small inducible cytokine B subfamily (Cys-X-Cys), member 10 (Cxcl10), mRNA. 11/2002 Length = 1133	small inducible cytokine B subfamily (Cys-X-Cys), member 10
4004	17684	NM_139102		dimethylglycine dehydrogenase precursor (Dmgdh), mRNA. 5/2002 Length = 2574	dimethylglycine dehydrogenase precursor

TABL	国 9			A A	tofficy Docket 44921-5033-01WC
	ID No.	Centeni Acc or Refseg ID ::	Model Code	1 (1) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4	Unicene Sequence Cluster Title
4006	18450	NM_139106	LL, CCC, RRR	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (Atp5d), mRNA. 5/2002 Length = 811	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit
4010	1301	NM_139192	s, xx	stearoyl-Coenzyme A desaturase 1 (Scd1), mRNA. 5/2002 Length = 4689	stearoyl-Coenzyme A desaturase 1
4014	8719	NM 139333	GG	neuronal differentiation-related gene (LOC246216), mRNA. 11/2002 Length = 1853	neuronal differentiation-related gene
4019	23682	_	нн, ss	protein phosphatase 2A B regulatory subunit delta isoform (LOC246255), mRNA. 11/2002 Length = 2034	Rattus norvegicus protein phosphatase 2A B regulatory subunit delta isoform mRNA, complete cds
4027	24657	NM_145774	L, OOO, General Alternate	Rab38, member of RAS oncogene family (Rab38), mRNA. 11/2002 Length = 1405	Rattus norvegicus rab-related GTP-binding protein mRNA, complete cds
4028	16278	NM_145782	x	cytochrome P450, 3a18 (Cyp3a18), mRNA. 11/2002 Length = 2005 cytochrome c	R.norvegicus CYP3 mRNA
4029	1448	NM_145783	U	oxidase, subunit Va (Cox5a), mRNA. 10/2002 Length = 600	Rat CoxVa mRNA for mitochondrial cytochrome c oxidase subunit Va
				protein phosphatase 1G (formerly 2C), magnesium- dependent, gamma isoform (Ppm1g), mRNA. 11/2002	ESTs, Weakly similar to JC2524 phosphoprotein phosphatase (EC 3.1.3.16) 1A-beta - rat
4035 4036	16963	NM_147209 NM_147214	U F, SS, NNN	Length = 1629 alpha-2u globulin PGCL1 (LOC259246), mRNA. 11/2002 Length = 878	[R.norvegicus] Caldesmon 1, protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform

TABL	≣ 0 ∵∵			Au	tomay Doctat 44921-6033-011WO Document No. 1936323.1
S09:		instend Acc or Refer ID.	ල්ලේට :: (Moල්ල්)	Movan Cene Name	ellit retevid sonsijos sassinu
4037	16969	NM_147215	O, P	alpha-2u globulin PGCL4 (LOC259247), mRNA. 11/2002 Length = 1003	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
			C, H, JJ, KK, PP, QQ, ZZ, AAA, HHH, PPP, QQQ, General Core Tox	outer mitochondrial membrane receptor rTOM20 (LOC266601), mRNA. 11/2002	Rattus norvegicus outer mitochondrial membrane receptor
4041	10544	NM_152935	Markers C, FFF,	Length = 976	rTOM20 mRNA, complete cds
4041	10545	NM_152935	GGG, HHH, PPP, QQQ, General Core Tox Markers	outer mitochondrial membrane receptor rTOM20 (LOC266601), mRNA. 11/2002 Length = 976	Rattus norvegicus outer mitochondrial membrane receptor rTOM20 mRNA, complete cds
4042	12700	NM_152936	F	pancreatic secretory trypsin inhibitor type II (PSTI-II) (LOC266602), mRNA. 11/2002 Length = 379	Rat pancreatic secretory trypsin inhibitor type II (PSTI-II) mRNA, complete cds
4043	9176	NM_153303	нн	dystonia 1, torsion (autosomal dominant; torsin A) (Dyt1), mRNA. 10/2002 Length = 1254	ESTs, Highly similar to TO1A_MOUSE Torsin A precursor [M.musculus]
4046	1130	NM_153313	Т	cytochrome P450 2D1 (CYP2D1), mRNA. 10/2002 Length = 1630	Rat cytochrome P450CMF1b mRNA, complete cds
4047	14346	NM_153314	N.	UDP- glucuronosyltransfera se 2B3 precursor, microsomal (UDPGT), mRNA. 10/2002 Length = 1716	Rat UDP-glucuronosyltransferase mRNA, complete cds

TABL	2				torney Docket 44921-5033-01000 Document No. 1935323.1
Seq (D:	elec Solu	<u>Fot</u> Seq ID : ∴ Conson:	Model ::	Knovn Cene Name.	ellii retzulD esneupeS eneginU
4047	14347	NM_153314	K, QQ, UU	UDP- glucuronosyltransfera se 2B3 precursor, microsomal (UDPGT), mRNA. 10/2002 Length = 1716	
4047	14632	NM_153314	MM, TTT	UDP- glucuronosyltransfera se 2B3 precursor, microsomal (UDPGT), mRNA. 10/2002 Length = 1716	Androsterone UDP- glucuronosyltransferase
4048	1753	NM_153318	II, III, JJJ, KKK, General Core Tox Markers	cytochrome P450 4F6 (CYP4F6), mRNA. 10/2002 Length = 1782	Rattus norvegicus cytochrome P450 4F6 (CYP4F6) mRNA, complete cds
4074	21981	S75019	V		ESTs, Highly similar to B54676 antiquitin - rat (fragment) [R.norvegicus]
4077	24469	S77858	J, Q, R, GG, II, EEE, FFF, HHH, MMM		ESTs, Highly similar to MLES_RAT Myosin light chain alkali, smooth-muscle isoform (MLC3SM) [R.norvegicus]
4080	16131	S79304	LL, YY	unknown Glu-Pro dipeptide repeat protein	unknown Glu-Pro dipeptide repeat protein
4082	14121	S82383	O, P, VV		R.norvegicus mRNA for tropomyosin isoform 6
4084	13520	S87522	KK, PP, QQ	HMm:leukotriene A4 hydrolase corticotropin-	ESTs, Highly similar to S20444 leukotriene-A4 hydrolase (EC 3.3.2.6) - rat [R.norvegicus]
4102	53	U16253	К	releasing factor receptor subtype 2	corticotropin-releasing factor receptor subtype 2
4104 4104	17999 18000	U19485 U19485	BBB, CCC CCC	spp-24 precursor spp-24 precursor	spp-24 precursor spp-24 precursor Rattus norvegicus lamina-
4105	1948	U19614	L		associated polypeptide 1C (LAP1C) mRNA, complete cds

TABU	ਵੀ:				Corney Docket 44921-5033-01000 Document No. 1935328.1
Seq.	GLEC	COMBERNA AGG OF ROSSON	Model Code	Amiski energianyonish	Unicono Sequence Cluster Tille
<u> </u>	(12) iceo'i	Independent in the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second seco	H, K, DD,		(Pingeno eegesnes eccess. 1805)
			EE, UUU, General		Rattus norvegicus complement
4107	228	U20194	Alternate		C8 beta (C8b) mRNA, partial cds
		;	S, Z, AA, BBB, CCC, PPP, QQQ,		Rattus norvegicus complement
4107	229	U20194	RRR		C8 beta (C8b) mRNA, partial cds
4119	21488	U32575	GG, PP, QQ		ESTs, Weakly similar to I49523 tumor necrosis factor alpha- induced protein 2 - mouse [M.musculus]
71.10	21100	002010	F, FFF,		Rattus norvegicus cytochrome
4126	255	U39206	General Alternate		P450 4F4 (CYP4F4) mRNA, complete cds
				complement	
4139	358	U52948	вв, сс	component 9 serine (or cysteine)	complement component 9
-			D, E, BB, GG, NN, III, JJJ,	proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin),
4144	699	U55765	RRR	10	member 10
44.47	4007	1157745		FGF receptor	
4147	1337 1731	U57715 U58858	C D, KKK	activating protein 1 unction plakoglobin	FGF receptor activating protein 1 unction plakoglobin
4150	990	U60096	RR	Integrin, beta 4	Integrin, beta 4
4151	1283	U61729	Z, AA, LL		Rattus norvegicus proline rich protein mRNA, complete cds
4153	1547	U66471	MM, TTT	cell growth regulatory with ring finger domain	cell growth regulatory with ring finger domain
4154	870	U66478	PP, QQ	MAD (mothers against decapentaplegic, Drosophila) homolog	MAD (mothers against decapentaplegic, Drosophila) homolog 1
4157	953	U67915	D	mast cell protease 1	mast cell protease 1
	20386	U68562	Q, R, S, T, BBB, CCC	heat shock protein 60 (liver)	heat shock protein 60 (liver)
4165	16398	U75392	CCC	B-cell receptor- associated protein 37	B-cell receptor-associated protein 37
4170	1602	U76379	C, T, TT, EEE, MMM	Organic cation transporter	Organic cation transporter

TABL	≣9:				tomay Docket 44921-5033-011WO Document No. 1935323.1
Seq .	@L@C	Content ;	Model -		
(D.		Roßeg ID	Coolo	Known Cene Name	eliit referiO concupce CaegiaU
4187	428	X03468	T	Apolipoprotein A-II	Apolipoprotein A-II
4195	672	X13722	JJ	, фолрорископии	Rat mRNA for LDL-receptor
1	<u> </u>			NADH ubiquinone	
l		]		oxidoreductase	NADH ubiquinone oxidoreductase
4198	15653	X14210	CC, II	subunit B13	subunit B13
					ESTs, Highly similar to
			вв, сс,		RL26_RAT 60S RIBOSOMAL
4200	18541	X14671	RR		PROTEIN L26 [R.norvegicus]
					ESTs, Highly similar to
1					RL7A_HUMAN 60S ribosomal
1					protein L7a (Surfeit locus protein
4202	19244	X15013			3) (PLA-X polypeptide) [R.norvegicus]
4202	19244	X13013	G, H, JJJ		[[K.norvegicus]
				Myxovirus (influenza)	
				resistance, homolog	
	İ			of murine Mx (also	
	1			interferon-inducible	
ľ				protein IFI78),	
				myxovirus (influenza	myxovirus (influenza virus)
4213	517	X52713	RR	virus) resistance 3	resistance 3
			G, H, CC, DDD, GGG,	-	
1	Ì		HHH,		ESTa Highly similar to
			General Core Tox		ESTs, Highly similar to RL12 RAT 60S RIBOSOMAL
4216	18606	X53504	Markers	•	PROTEIN L12 [R.norvegicus]
7210	10000	7.00004	Warkers	trans-golgi network	1 TO TENTE 12 [Killor vegicus]
4217	1899	X53565	ww	protein 1	trans-golgi network protein 1
					ESTs, Highly similar to R6RTP2
					acidic ribosomal protein P2,
			C, F, K,		cytosolic [validated] - rat
4220	24577	X55153	DDD		[R.norvegicus]
1			II, JJ, KK,		R.norvegicus ASI mRNA for
			FFF,		mammalian equivalent of
1227	17175	V59390	GGG,		bacterial large ribosomal subunit protein L22
4227	17175	X58389	ННН		R.norvegicus ASI mRNA for
					mammalian equivalent of
					bacterial large ribosomal subunit
4233	17176	X60212	LL, SS		protein L22
			BB, CC,		
			GG, HH,		
	]		NN, OO,		Rattus norvegicus interferon-
			PP, QQ,		inducible protein variant 10
4235	21657	X61381	LLL		mRNA, complete cds

TABL					(Omey Docker 44921-5033-011WO ***
309 309	id ko: :: erec	Refer (D.)	Code Model	emisk ened nwenkl	Unicene Sequence Civeter Title
4242	16780	X62660	X, GG, II, XX, YY	HMm:glutathione S- transferase, alpha 4	ESTs, Highly similar to S23433 glutathione transferase (EC 2.5.1.18) 8 - rat [R.norvegicus]
4249 4250	1391 602	X66366 X68101	C, XX, YY ZZ, AAA	Gephyrin	Gephyrin R.norvegicus trg mRNA
4252 4255	588 16300	X69834 X70706	H, O, P, GG, PPP, QQQ DDD	plastin 3 (T-isoform)	R.norvegicus mRNA for serine protease inhibitor 2.4 plastin 3 (T-isoform)
4258	16725	X73371	V, X, Y, LL, ZZ, AAA, LLL		R.norvegicus mRNA for Fc gamma receptor
4259	768	X74549	General Alternate	leuserpin-2 Organic cation	leuserpin-2
4264	1603	X78855	TT	transporter	Organic cation transporter
4271	1764	X83399	R	initiation factor 4E	eukaryotic translation initiation factor 4E
4272	463	X83579	S, PPP, QQQ	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase) R.norvegicus mRNA for Trihydroxycoprostanoyl-CoA
4280	853	X95189	M, XX, YY	Social australia	Oxidase
4282	17146	Y07534	J	Serine protease inhibitor	Serine protease inhibitor
1846	2069	Al103616	vv	HHs:ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	ESTs, Weakly similar to ras-like protein [Rattus norvegicus] [R.norvegicus]
2362	23120	Al179857	S	HHs:huntingtin interacting protein 2	ESTs, Weakly similar to ubiquitin- conjugating enzyme E2D 2 [Rattus norvegicus] [R.norvegicus]
2616	5778	Al233246	G, H	HHs:polymerase (RNA) II (DNA directed) polypeptide B (140kD) heterogeneous	ESTs, Weakly similar to RNA polymerase I (127 kDa subunit) [Rattus norvegicus] [R.norvegicus]
3	2417	AA684857	w	nuclear ribonucleoprotein K	heterogeneous nuclear ribonucleoprotein K
408 412	18578 17110	AA859980 AA860062	L, FF Z, AA	T-complex 1 Albumin	T-complex 1 Albumin

TABL	<b>31</b>		2. 大道 3. 大道		omey Doctot 44921-5088-01W0 ***********************************
Seq (D)	id kari Grec	Constant Acc or Roßeg ID	Modol	Known Cene Name	Unigene Sequence Cluster Title
412	17111	AA860062	S, SS	Albumin	Albumin
445	18897	AA875207	C, T, Z, AA	Hemoglobin, beta	Hemoglobin, beta
535	4259	AA892123	JJ, KK, FFF, GGG	ribosomal protein L36	ribosomal protein L36
588	12118	AA892775	OO, VV, XX, YY	Lysozyme	Lysozyme
593	17080	AA892814	М	calpain, small subunit 1	calpain, small subunit 1
628	20985	AA893242	H, BBB, CCC, RRR, General Alternate	fatty acid Coenzyme A ligase, long chain 2	fatty acid Coenzyme A ligase, long chain 2
			A, B, BBB, CCC, FFF, General	fatty acid Coenzyme	fatty acid Coenzyme A ligase,
628	20986	AA893242	Alternate	A ligase, long chain 2	long chain 2
673	6377	AA894273	υU	dimethylarginine dimethylaminohydrol ase 1	dimethylarginine dimethylaminohydrolase 1
699	23778	AA899854	U	topoisomerase (DNA) Il alpha	topoisomerase (DNA) II alpha
785	22843	AA925473	VV	cell division cycle 42	cell division cycle 42
845	1682	AA943555	SS	linker of T-cell receptor pathways	linker of T-cell receptor pathways
854	19425	AA943842	N F, DD,	dimethylarginine dimethylaminohydrol ase 1 serum-inducible	ESTs, dimethylarginine dimethylaminohydrolase 1
855	2655	AA943886	PP	kinase	serum-inducible kinase
889	22504	AA944827	Q, R	bone morphogenetic protein 2	bone morphogenetic protein 2
902	19421	AA945152	S, NNN	dimethylarginine dimethylaminohydrol ase 1 Acyl-Coa	dimethylarginine dimethylaminohydrolase 1
1008	16722	AA956311	ccc	dehydrogenase, Very long chain	Acyl-Coa dehydrogenase, Very long chain
1023	23919	AA956992	D	secretory carrier membrane protein 3	secretory carrier membrane protein 3
1064	2329	AA964157	ss	SMC (segregation of mitotic chromosomes 1)-like 1 (yeast)	SMC (segregation of mitotic chromosomes 1)-like 1 (yeast)
1083	1322	AA964628	w	Glucose-6- phosphatase	Glucose-6-phosphatase

TABL	로이	\$ .			tomey Docket 44921-5038-011W0 Document No. 1985323.1
S00 [D	10 Ko. 61.66	Constant : Acc or Rowseq ID :	Model Code		Unigene Sequence Cluster Tille
1153	1437	AA997844	V	Cd63 antigen	Cd63 antigen
			BBB,		
1205	3512	AB006607	CCC, RRR	choline kinase-like	choline kinase-like
			BBB,		
1205	3513	AB006607		choline kinase-like	choline kinase-like
1209	17962	AB012230	General Alternate	nuclear factor I/B	nuclear factor I/B
1210	47000	AB012231	FFF, General Core Tox Markers, General	footon I/D	
1210	17963	ABU12231	Alternate	nuclear factor I/B Nuclear factor I/X	nuclear factor I/B
				(CCAAT-binding	Nuclear factor I/X (CCAAT-
1211	24414	AB012234	D, SS	transcription factor)	binding transcription factor)
12.1		7.5012201	2, 00	contactin associated	Silvening it directly the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
1215	954	AF000114	D	protein 1	contactin associated protein 1
1244	25211	AF087839	sss, uuu		ATP-binding cassette, sub-family C (CFTR/MRP), member 9
1359	16521	Al010470	FF	Ceruloplasmin (ferroxidase)	Ceruloplasmin (ferroxidase)
1442	12300	AI013333	N	aldehyde dehydrogenase 2, mitochondrial	aldehyde dehydrogenase 2, mitochondrial
1480	2866	Al029058	Z, AA	Cyclin D1	Cyclin D1
1515	7665	AI030668	General Core Tox Markers, General Alternate	nucleosome assembly protein 1- like 1	nucleosome assembly protein 1- like 1
1558	1431	Al044610	II, General Alternate	Dopa decarboxylase (aromatic L-amino acid decarboxylase)	Dopa decarboxylase (aromatic L- amino acid decarboxylase)
1566	20983	A1044900	A, FF, JJ, KK, LL, FFF, HHH, SSS, General Core Tox Markers, General Alternate	fatty acid Coenzyme A ligase, long chain 2	
1583	169	Al045171	E	calsequestrin 2	calsequestrin 2

TABU	፭ ባ <i>ነ ነ</i> ∙.	F	1	ACC	iomey Docket 44921-5033-91W0 ; Document No. 1935323.1
	erec Grec	Lesses Seguines Reserting			Unigené Sequence Cluster Tille
1870	18277	AI104399	т, ннн	Triosephosphate isomerase 1	Triosephosphate isomerase 1
1887	17171	Al105137	M, V, JJ, KK	Somatostatin	ESTs, Highly similar to GTK1_RAT Glutathione S- transferase, mitochondrial (GST 13-13) (Glutathione S-transferase subunit 13) (GST class-kappa) [R.norvegicus], Somatostatin
1928	1841	Al113289	O, P, Q, R, V, DD, NN, OO, PP, QQ, III, JJJ, General Alternate	protein tyrosine phosphatase, non- receptor type 1	protein tyrosine phosphatase, non receptor type 1 zinc finger protein 36, C3H type-
1939	20920	AI136891	w	C3H type-like 1	like 1
1958	16510	Al137583	L, T	Inhibitor of DNA binding 2, dominant negative helix-loop- helix protein branched chain keto	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein branched chain keto acid
				acid dehydrogenase	dehydrogenase E1, beta
1990 2033	8213	AI168942 AI169883	WW F, PP, QQ, XX, YY, LLL, UUU	E1, beta polypeptide  ferritin light chain 1	polypeptide  ferritin light chain 1
2104	8215	Al171692	CC, GG, HH, EEE, III, JJJ, MMM, General Core Tox Markers, General Alternate	ferritin light chain 1	ESTs, Highly similar to S66270 kynurenineoxoglutarate transaminase (EC 2.6.1.7) / glutaminephenylpyruvate transaminase (EC 2.6.1.64) mitochondrial precursor [validated] - rat [R.norvegicus], ferritin light chain 1
2163	12614	Al175294	т	ribosomal protein L21	ribosomal protein L21
			Y, LLL, General Core Tox Markers, General		
2209	24763	AI176488	Alternate	nuclear factor I/B ALG-2 interacting	nuclear factor I/B
2296	5459 18907	Al178246 Al178971	RR T	protein 1 Hemoglobin, alpha 1	ALG-2 interacting protein 1 Hemoglobin, alpha 1
2323	18907	Al178971	T	Hemoglobin, alpha 1	Hemoglobin, alpha 1

TABL	e 1			A	tomey Decket 44921-5033-011WC Document No. 199323.1
809 (D r )	ELEC	Keiseg (D	Modal Code	Known Cene Name	Unigene Sequence Cluster Title
				dimethylarginine	
			EE, PP,	dimethylaminohydrol	dimethylarginine
2349	19427	Al179510	QQ, YY	ase 1	dimethylaminohydrolase 1
2370	1687	AI179971	T	Hemoglobin, alpha 1	Hemoglobin, alpha 1
2403	22845	Al227887	К	cell division cycle 42	cell division cycle 42
			JJ, XX,		
2429	18612	Al228624	YY, HHH	ribosomal protein L29	ribosomal protein L29
2512	1688	Al230970	T	Hemoglobin, alpha 1	Hemoglobin, alpha 1
				prolactin regulatory	prolactin regulatory element
2638	22866	AI233754	E, HH	element binding	binding
2699	8440	Al235611	T	ZAP 36/annexin IV	ZAP 36/annexin IV
2731	1689	Al236360	T, XX, YY	Hemoglobin, alpha 1	Hemoglobin, alpha 1
				heterogeneous	
				nuclear	heterogeneous nuclear
	2416	Al237051	LL	ribonucleoprotein K	ribonucleoprotein K
2845	1375	D12573	Z, AA	hippocalcin	hippocalcin
2849	25041	D14014	E, HH	Cyclin D1	Cyclin D1
				proteasome	ESTs, Highly similar to S60038
				(prosome,	multicatalytic endopeptidase
				macropain) subunit,	complex (EC 3.4.99.46) alpha
2860	9029	D30804	WW, SSS	alpha type 7	chain RC6-I - rat [R.norvegicus]
				LIM motif-containing	LIM motif-containing protein
2861	1351	D31874	RRR	protein kinase 2	kinase 2
1					ESTs, Highly similar to
]		ł			PSB5_RAT Proteasome subunit
ł					beta type 5 precursor
				•	(Proteasome epsilon chain)
ł		1			(Macropain epsilon chain)
l					(Multicatalytic endopeptidase
1					complex epsilon chain)
1					(Proteasome subunit X)
				proteasome beta	(Proteasome chain 6)
2867	9135	D45247	N, RRR	type subunit 5	[R.norvegicus]
}			U, FF,		
			FFF,		
1			ННН,		
	0000	D0040-	General		fatty acid Coenzyme A ligase,
2881	20984	D90109	Alternate	A ligase, long chain 2	
2917	26368	H34047	E	T-complex 1	T-complex 1
			N, BB,		
			CC, DD,		
1			HH, III,		
			JJJ, KKK,		
			NNN,	B-cell translocation	
000-			General		B-cell translocation gene 1, anti-
2968	19	L26268	Alternate	proliferative	proliferative

TABL	E1			A A	tomey Docket 44921-5093-011WO Document No. 1935323.1
Seq : (D: 14	ELEC:	Refsed ID &	Model Code	Kijown Cene Name.	Unigene Seguence Cluster Title
2968 2979	20 427	L26268 M00001	BB, CC, DD, LL, UU, III, JJJ, KKK, NNN, General Alternate CCC	B-cell translocation gene 1, anti- proliferative Apolipoprotein A-I	B-cell translocation gene 1, anti- proliferative Apolipoprotein A-I
2980	17472	M10934	HH, SS	Retinol binding protein 4	ESTs, Highly similar to RETB_RAT Plasma retinol- binding protein precursor (PRBP) (RBP) [R.norvegicus]
2990	1466	M14050	LL	Heat shock 70kD protein 5	ESTs, Heat shock 70kD protein 5
3001	16427	M21354	M, II	procollagen, type III, alpha 1	procollagen, type III, alpha 1 ESTs, Highly similar to A33792 phosphoglycerate kinase (EC
3012	1312	M31788	I, J, LLL DD, ZZ,	phosphoglycerate kinase 1 protein tyrosine	2.7.2.3) - rat [R.norvegicus], phosphoglycerate kinase 1
3016	1843	M33962	AAA, III, JJJ, KKK	phosphatase, non- receptor type 1	protein tyrosine phosphatase, non- receptor type 1
3016	1844	M33962	E, DD, ZZ, AAA, III, JJJ	protein tyrosine phosphatase, non- receptor type 1	ESTs, protein tyrosine phosphatase, non-receptor type 1
3029	1973		I, J, Y, FF, KKK, LLL, OOO, RRR, SSS, General Core Tox Markers, General Alternate	protein tyrosine phosphatase, receptor-type, F	protein tyrosine phosphatase, receptor-type, F
				hypoxanthine guanine phosphoribosyl	ESTs, Moderately similar to ICA2_MOUSE Intercellular adhesion molecule-2 precursor (ICAM-2) (CD102) (Lymphocyte function-associated AG-1 counterreceptor) [M.musculus], hypoxanthine guanine
3033		M75168	С	transferase HLA-B associated transcript 1A	phosphoribosyl transferase  HLA-B associated transcript 1A
3039			RR	adenylyl cyclase 2	adenylyl cyclase 2

TABL	<b>E 1</b>			A	tomay Doctet 44921,5033-011W0 Document No.:1935323.1
Seq.	ELEC	Censoni Acc or Resseq ID	Model (Code);	Known Cene Neme	ekii weten Sequence Sineta Tike
2040	21670	M90601	C	programmed cell death 2	areas amond call death 2
3046	1430	M80601 M84648	TT, DDD, General Core Tox Markers, General Alternate	Dopa decarboxylase (aromatic L-amino acid decarboxylase)	Dopa decarboxylase (aromatic Lamino acid decarboxylase)
3057	22512	NM_012488	BB, NN, EEE, MMM	alpha-2- macroglobulin (A2m), mRNA. 11/2002 Length = 4595	Alpha-2-macroglobulin
3057	22513	NM_012488	A, E, W, BB, UU, EEE, MMM	alpha-2- macroglobulin (A2m), mRNA. 11/2002 Length = 4595	Alpha-2-macroglobulin
3057	22514	NM_012488	BB, NN, UU	alpha-2- macroglobulin (A2m), mRNA. 11/2002 Length = 4595	Alpha-2-macroglobulin
3057	22515	NM 012488	E, W, BB, NN, OO, EEE, III, JJJ, KKK, MMM	alpha-2- macroglobulin (A2m), mRNA. 11/2002 Length = 4595	Alpha-2-macroglobulin
3059	23942	NM_012493	General Alternate	Alpha-fetoprotein (Afp), mRNA. 11/2000 Length = 1990	Alpha-fetoprotein
3065	563	NM_012516	BB, JJ, KK	Complement component 4 binding protein, alpha (C4bpa), mRNA. 11/2000 Length = 1882	Complement component 4 binding protein, alpha
3068	16214	NM_012523	O, P	CD53 antigen (Cd53), mRNA. 11/2002 Length = 1699	Leukocyte antigen (Ox-44)
3072	16519		BB, CC, NN, SSS,	Ceruloplasmin (ferroxidase) (Cp), mRNA. 11/2002 Length = 3700	Ceruloplasmin (ferroxidase)

				-229-	
TABL	31 ·	1		A	tomey Doctet 44921-5088-91W0 Document No. 1995328.1
Seq	@L@C	COMEDIA	Model :	(c) (c) (c) (c) (c) (c) (c) (c) (c) (c)	and the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of th
(D)	ID Ko.	Raiseg (D).	Codo	Kinewn Cene Name	Unigene Sequence Cluster Title
ιω	תש ועשי	livenesed in	G000 . **		Company exclusiones empera fings
				Ceruloplasmin	
		1		(ferroxidase) (Cp), mRNA, 11/2002	
3072	16520	NM 012532	вв, сс	Length = 3700	Ceruloplasmin (ferroxidase)
3072	10020	NIVI_012332	BB, CC	Enolase 1, alpha	Cerdiopiasmin (terroxidase)
			Ì	(Eno1), mRNA.	
				11/2000 Length =	
3076	19407	NM 012554	G, H, W	1725	Enolase 1, alpha
	10.00		., .,	Ets avian	
	]	]		erythroblastosis virus	1
1				E2 oncogene	
		1	1	homolog 1 (tumor	
		İ	į.	progression locus 1)	
				(Ets1), mRNA.	Ets avian erythroblastosis virus
			O, P, PP,		E2 oncogene homolog 1 (tumor
3077	21836	NM_012555	QQ	4991	progression locus 1)
				Interferon regulatory	Interferon regulatory factor 1,
				factor 1 (Irf1), mRNA.	sirtuin 2 (silent mating type
0000	00400		<b>-</b>	11/2002 Length =	information regulation 2,
3089	20126	NM_012591	T, W	2078	homolog) 2 (S. cerevisiae)
				Lipoprotein lipase	
1			O, P, EEE,	(LpI), mRNA. 11/2002 Length =	
3091	18385	NM 012598	MMM	3617	Lipoprotein lipase
000.	10000	1111_0.2000		Nerve growth factor	Lipoproton npago
	l			receptor, fast (Ngfr),	
				mRNA. 11/2000	
3095	1299	NM_012610	V	Length = 3259	Nerve growth factor receptor, fast
				steroid sulfatase	
	l	1		(Sts), mRNA.	
				11/2002 Length =	
3107	21087	NM_012661	FFF	2472	Steroid sulfatase
	·			lipase A, lysosomal	
			T 00	acid (Lipa), mRNA.	
3129	10250	NM 012732	T, GG,	10/2002 Length = 3144	Chalantaral anterna (amazz atia)
3129	10260	1411/1_012/32	HH, LL	lipase A, lysosomal	Cholesterol esterase (pancreatic)
		1		acid (Lipa), mRNA.	
]				10/2002 Length =	
3129	25563	NM 012732	DD, EE	3144	Cholesterol esterase (pancreatic)
			<b></b>	Dipeptidyl peptidase	Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
				4 (Dpp4), mRNA.	
].			BB, CC,	11/2000 Length =	
3140	7784	NM_012789	11, 00	4835	Dipeptidyl peptidase 4

TABL		:		A	iomey Docket 44921-5033-01W0 Document No. 1935323.1
Seq 10	ELEC:	COMBONIA ACCOT ROSSON	Model :		Unigeno Segueneo Civeter Tide
			A, GG, II, TT, III, JJJ, LLL, SSS, UUU, General Core Tox	Flavin-containing monooxygenase 1 (Fmo1), mRNA. 11/2000 Length =	Flavin-containing
3141	23445	NM_012792	Markers	2042 ATP-binding	monooxygenase 1
3145	21729	NM_012804	WW, RRR, SSS	cassette, sub-family D (ALD), member 3 (Abcd3), mRNA. 10/2002 Length = 3324	ATP-binding cassette, sub-family D (ALD), member 3
0.145	04700			ATP-binding cassette, sub-family D (ALD), member 3 (Abcd3), mRNA. 10/2002 Length =	ATP-binding cassette, sub-family
3145	21730	NM_012804	K, U, FF	O-acetyltransferase Milk fat glolbule membrane protein (Mfge8), mRNA. 11/2000 Length =	D (ALD), member 3  O-acetyltransferase Milk fat
3146	17992	NM_012811	XX, YY	1969 Cytochrome c oxidase subunit VIa polypeptide 2 (heart) (Cox6a2), mRNA. 11/2000 Length =	glolbule membrane protein  Cytochrome c oxidase subunit
3147	20605	NM_012812	вв, сс	395 Lysosomal associated membrane protein 1 (120 kDa) (Lamp1), mRNA. 11/2000	VIa polypeptide 2 (heart)  Lysosomal associated membrane
3160	18770	NM_012857	EE	Length = 2006	protein 1 (120 kDa)
3168	16721	NM_012891	ccc,	Acyl-Coa dehydrogenase, Very long chain (Acadvl), mRNA. 10/2002 Length = 2117	Acyl-Coa dehydrogenase, Very long chain
3175	24431	 NM_012912		Activating transcription factor 3 (Atf3), mRNA. 11/2002 Length = 1893	Activating transcription factor 3

	TABLE 1 Attorney Docket 44921-5093-017 Document No. 199532							
509 ID , .	@L@C 	Reservant Acc or Reservant	Model Model	Kinown Cene Neme	Unigene Sequence Civeter Title			
3178	20755	NM_012923	F, R, II, VV, General Alternate	Cyclin G1 (Ccng1), mRNA. 11/2002 Length = 3169	Cyclin G1			
3178	20757	NM_012923	F, II, FFF, General Core Tox Markers	Cyclin G1 (Ccng1), mRNA. 11/2002 Length = 3169	Cyclin G1			
3192	24263	NM_012999	вв, сс	Subtilisin - like endoprotease (Pace4), mRNA. 10/2001 Length = 4153	Subtilisin - like endoprotease			
3192	24264	NM_012999	MM, TTT	Subtilisin - like endoprotease (Pace4), mRNA. 10/2001 Length = 4153	Subtilisin - like endoprotease			
3196	20926	NM_013013	PP, QQ	Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator) (Psap), mRNA. 11/2000 Length = 2175	Peroxisomal enoyl hydratase-like protein, Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator)			
3200	18078	NM 013030	RR	Solute carrier family 34 (sodium phosphate), member 1 (Slc34a1), mRNA. 11/2002 Length = 2440	Rattus norvegicus mRNA for NaPi-2 alpha, complete cds, Solute carrier family 17 (sodium/hydrogen exchanger), member 2			
3201	730	_		ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (Abcc9), mRNA. 4/2002 Length = 6628	ATP-binding cassette, sub-family C (CFTR/MRP), member 9			
3204	20535	NM_013049	l, J	tumor necrosis factor superfamily, member 4 (Tnfrsf4), mRNA. 11/2002 Length = 1017 Hemoglobin, alpha 1	tumor necrosis factor receptor superfamily, member 4			
3217	1684	NM_013096		(Hba1), mRNA. 11/2000 Length = 556	Hemoglobin, alpha 1			

TABL	E1			A	iomay Docket 44921-5033-011WO Document No. 1985323.1
Seq. D:::	ID Ko-:	(COM: 2011) ACC OT RESEQUE	Model Code	Known Cone Name	Unigane Sequence Cluster Title
				Glucose-6- phosphatase (G6pc), mRNA. 11/2000	
3218	1321	NM_013098	L	Length = 2237	Glucose-6-phosphatase
				Glutamate	
1	1			oxaloacetate	
1				transaminase 2,	
`			1	mitochondrial (aspartate	
1		1		aminotransferase 2)	
1	į			(Got2), mRNA.	Glutamate oxaloacetate
1			General	11/2000 Length =	transaminase 2, mitochondrial
3230	17628	NM_013177	Alternate	2325	(aspartate aminotransferase 2)
1				acid phosphatase 2	
				(Acp2), mRNA.	
3242	24649	NM_016988	CC HIL	11/2002 Length = 12009	Asid phasphatase 2 has year
3242	24043	14141_010900	GG, FIF	Complement	Acid phosphatase 2, lysozymal
				component 3 (C3),	·
				mRNA. 11/2002	
3246	1958	NM_016994	L, S, HH	Length = 5066	Complement component 3
				Diaphorase	
				(NADH/NADPH)	
]			K S GG	(Dia4), mRNA. 11/2000 Length =	
3247	1698	NM 017000	HH, GGG		Diaphorase (NADH/NADPH)
			F, K, M,		
		}	N, GG,	glutathione-S-	
1			HH, TT, DDD,	transferase, alpha	
				type2 (Gsta2),	
i			ммм,	mRNA. 11/2002	Glutathione-S-transferase, alpha
3250	18989	NM_017013	UUU	Length = 831	type (Yc?)
				Phosphoglucomutase	
				1 (Pgm1), mRNA.	
3256	24861	NM_017033	т	11/2002 Length = 1842	Phosphoglucomutase 1
5230	27001	14141_017033	-	Phosphoglucomutase	r nospriogiucomutase i
				1 (Pgm1), mRNA.	
				11/2002 Length =	
3256	24862	NM_017033	HH, UU	1842	Phosphoglucomutase 1
			0 1/	Transferrin (Tf),	
3263	14533	NM_017055	S, V, NNN	mRNA. 11/2002 Length = 2275	Transferrin
5203	17000	14141_017055	IAIAIA	Transferrin (Tf),	Transferrin
		4	s, tt,	mRNA. 11/2002	
3263	14534		NNN	Length = 2275	Transferrin

TABL	TABUE 1 Altomay Docket 44921-5058-01 Document No. 19353					
509 (D	id kið Grec	CERIZANI ACCOT RCISCO ID	Model Code	Known Gene Name	Unigana Sequance Cluster Tilla	
3271	1262	NM_017077	R, MM, NN, OO, TTT	Hepatocyte nuclear factor 3 gamma (Hnf3g), mRNA. 11/2000 Length = 1497	Hepatocyte nuclear factor 3 gamma	
3272	23660	NM_017080	T, U, RRR, SSS	Hydroxysteroid dehydrogenase, 11 beta type 1 (Hsd11b1), mRNA. 11/2000 Length = 1265	Hydroxysteroid dehydrogenase, 11 beta type 1	
3278	4391	NM_017101	11	Peptidylprolyl isomerase A (cyclophilin A) (Ppia), mRNA. 11/2002 Length = 743	Peptidylprolyl isomerase A (cyclophilin A)	
3278	4392	NM 017101	XX, YY	Peptidylprolyl isomerase A (cyclophilin A) (Ppia), mRNA. 11/2002 Length = 743	Peptidylprolyl isomerase A (cyclophilin A)	
3287	10503	NM_017143	VV, FFF, GGG, General Alternate	coagulation factor 10 (F10), mRNA. 11/2002 Length =	coagulation factor X	
3287	10504	NM_017143	S, GG, VV, PPP, QQQ	coagulation factor 10 (F10), mRNA. 11/2002 Length = 1497	coagulation factor X	
3291	5351	NM_017150	KK, FFF, HHH	ribosomal protein L29 (Rpl29), mRNA. 11/2002 Length = 630	ribosomal protein L29	
3296	17686	NM_017165	I, J, LL	glutathione peroxidase 4 (Gpx4), mRNA. 11/2002 Length = 872	glutathione peroxidase 4	
3299	8182	NM_017170	GGG,	serum amyloid P- component (Sap), mRNA. 11/2002 Length = 931	serum amyloid P-component	
3300	20919	NM_017172	L	zinc finger protein 36, C3H type-like 1 (Zfp36l1), mRNA. 5/2002 Length = 2741	zinc finger protein 36, C3H type- like 1	

TABL	<b>፪</b> 1	1,		AY	tomay Docket 44921-5033-01000 Document No. 1995323.1
S0 <b>9</b> :	@L@@	Centenii Aec or	Modal : .		AND THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF T
(D)	id kie" .	RefSeq ID	ලිලල්ල :	Known Cone Name	Unigene Sequence Cluster Title
				fumarylacetoacetate	
				hydrolase (Fah),	
			PPP,	mRNA. 11/2002	
3302	23961	NM_017181	QQQ	Length = 1386	fumarylacetoacetate hydrolase
				Myelin-associated	
		1	1	glycoprotein (Mag),	
1			l	mRNA. 11/2002	
3304	24437	NM_017190	D	Length = 2475	Myelin-associated glycoprotein
				signal sequence	
į				receptor 4 (Ssr4),	
			NN, OO,	mRNA. 11/2002	
3306	9124	NM_017199	XX, YY	Length = 757	signal sequence receptor, delta
				signal sequence	
ļ			U, NN,	receptor 4 (Ssr4),	
2206	0405	NIM 017400	00, XX,	mRNA. 11/2002	
3306	9125	NM_017199	YY	Length = 757 signal sequence	signal sequence receptor, delta
				receptor 4 (Ssr4),	
	ł			mRNA. 11/2002	
3306	9126	NM 017199	Z, AA	Length = 757	signal sequence receptor, delta
3300	3120	14141_017100	2, 74	Longin - 101	signal sequence receptor, della
			A, D, E,		
				lipopolysaccharide	
				binding protein (Lbp),	3
			III, JJJ,	mRNA. 11/2002	
3309	20529	NM_017208	ммм	Length = 2622	lipopolysaccharide binding protein
				solute carrier family	
				20, member 2	
1				(Slc20a2), mRNA.	
			,	11/2002 Length =	
3312	16263	NM_017223	Z, AA	2287	solute carrier family 20, member 2
				phosphatidylinositol	
Ì	Ì			transfer protein	
				(Pitpn), mRNA.	
2242	24500	NINA 047004	<b></b>	11/2002 Length =	phosphatidylinositol transfer
3313	24598	NM_017231	Τ	1638	protein
				eukaryotic translation	
	ł			elongation factor 2	
				(Eef2), mRNA.	
				11/2002 Length =	eukaryotic translation elongation
3316	17561	NM 017245	N, RR	2626	factor 2
			<u> </u>		
1				eukaryotic translation	
				elongation factor 2	
				(Eef2), mRNA.	eukaryotic translation elongation
				11/2002 Length =	factor 2, mitogen activated protein
3316	17562	NM_017245	W	2626	kinase kinase 2

TABL	TABLE 1 : Altomay Docket 4/921-5033-011 Document No. 193532							
899 (D)	ELEC	Conson: Acc or Rasson ID	Model Code	Known Cene Name	Unigene Sequence Cluster Title			
3316	17563	NM_017245	E	eukaryotic translation elongation factor 2 (Eef2), mRNA. 11/2002 Length = 2626	eukaryotic translation elongation factor 2			
3317	15012	NM_017248	v	heterogeneous nuclear ribonucleoprotein A1 (Hnrpa1), mRNA. 11/2002 Length = 1696	ESTs, Highly similar to DDRT helix-destabilizing protein - rat [R.norvegicus], heterogeneous nuclear ribonucleoprotein A1			
3317	17502	NM_017248	O, P, JJ, KK, VV, HHH	heterogeneous nuclear ribonucleoprotein A1 (Hnrpa1), mRNA. 11/2002 Length = 1696	heterogeneous nuclear ribonucleoprotein A1			
3328	15535	NM 017283	S, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 6 (Psma6), mRNA. 11/2002 Length = 932	proteasome (prosome, macropain) subunit, alpha type 6			
3328	15538	NM_017283	NNN	proteasome (prosome, macropain) subunit, alpha type 6 (Psma6), mRNA. 11/2002 Length = 932	proteasome (prosome, macropain) subunit, alpha type 6			
3330	12523	NM_017285	G, H,	proteasome (prosome, macropain) subunit, beta type 3 (Psmb3), mRNA. 11/2002 Length = 828	proteasome (prosome, macropain) subunit, beta type, 3			
3330	12524	NM_017285	G, н, s, X, Y, GGG,	proteasome (prosome, macropain) subunit, beta type 3 (Psmb3), mRNA. 11/2002 Length = 828	proteasome (prosome, macropain) subunit, beta type, 3			

TABU	ਵੇਂ 1	1		A	torney Docket 44921-5038-01W0 Document No. 1935328.1
Seq ID ::	CLCC (CLCC)	Consonk Acc or Refseq ID	Model Code : ; ;	Known Cene Name	Unigene Sequence Cluster Title
3336	23130	NM_017307	V, FF	solute carrier family 25, member 1 (Slc25a1), nuclear gene encoding mitochondrial protein, mRNA. 11/2002 Length = 1575	solute carrier family 25 (mitochondrial carrier; citrate transporter) member 1
3353	15977	NM_019132	S	Guanine nucleotide- binding protein G-s, alpha subunit, Genbank no U51565 (Gnas), mRNA. 11/2002 Length = 1738	Guanine nucleotide-binding protein G-s, alpha subunit
3354	24785	NM_019133	SS	synapsin 1 (Syn1), mRNA. 11/2002 Length = 2400	Synapsin I
3372	2632	NM_019213	S	jumping translocation breakpoint (Jtb), mRNA. 11/2002 Length = 897	jumping translocation breakpoint
3374	15347	NM_019222	Р, Т	coronin, actin-binding protein, 1B (Coro1b), mRNA. 11/2002 Length = 1800	coronin, actin binding protein 1B
3374	15348	NM_019222	X, Y	coronin, actin-binding protein, 1B (Coro1b), mRNA. 11/2002 Length = 1800	coronin, actin binding protein 1B
3377	15503	NM_019237	NN, EEE, MMM	procollagen C- proteinase enhancer protein (Pcolce), mRNA. 11/2002 Length = 1547	procollagen C-proteinase enhancer protein
3377	15504	NM_019237	NN	procollagen C- proteinase enhancer protein (Pcolce), mRNA. 11/2002 Length = 1547	procollagen C-proteinase enhancer protein
3379	17908	NM_019242	Q, W, MM, QQ, TTT	interferon-related developmental regulator 1 (Ifrd1), mRNA. 5/2002 Length = 1736	interferon-related developmental regulator 1

TABL	31 T. 12 T.			A	tomey Docket 44921-5033-011W0 Document No. 1935323.1
999 999	@L@G:	knsenk Ace or Resen ID::::	Modal :	Known Cene Name	Unigene Sequence Cluster Title
3388	15057	NM_019291	IJ	carbonic anhydrase 2 (Ca2), mRNA. 11/2002 Length = 1459	carbonic anhydrase 2
3412	574	NM 019905	O, VV, EEE, MMM	calpactin I heavy chain (Anxa2), mRNA. 11/2002 Length = 1395	calpactin I heavy chain, hydroxyacid oxidase 3 (medium- chain), unknown Glu-Pro dipeptide repeat protein
3417	12087	NM_020082	B, LLL,	ribonuclease, RNase A family 4 (Rnase4), mRNA. 11/2002 Length = 546	ribonuclease 4
3428	19679	NM 021653	CCC, LLL, RRR,	deiodinase, iodothyronine, type 1 (Dio1), mRNA. 11/2002 Length = 2106	Thyroxine deiodinase, type I
3446	23782		ww	topoisomerase (DNA) 2 alpha (Top2a), mRNA. 11/2002 Length = 6052	
3473	8211	NM_022500	N, MM, DDD, TTT	ferritin light chain 1 (Ftl1), mRNA. 11/2002 Length = 552	ferritin light chain 1
3473	8212	NM_022500	TT, YY,	ferritin light chain 1 (Ftl1), mRNA. 11/2002 Length = 552	ferritin light chain 1
3493	20762	NM_022588	YY	metastasis associated 1 (Mta1), mRNA. 1/2001 Length = 2741	metastasis associated 1
3495	20925	NM_022594	CCC,	enoyl coenzyme A hydratase 1 (Ech1), mRNA. 11/2002 Length = 1097	Peroxisomal enoyl hydratase-like protein
3521 ·	16184	NM_022935	z, aa	Amiloride binding protein 1 (Abp1), mRNA. 11/2002 Length = 2668 ZAP 36/annexin IV	amiloride binding protein 1
3542	8439	NM_024155	O, P	(Anxa4), mRNA. 2/2001 Length = 960	ZAP 36/annexin IV

TABL	₹1 :: .		ing files on the second		tomey Docket 44921-5038-01000
	id ko Grec		Modol Godo	Ennell enem nevent	Chil relevia concuped checking
	as.gos .	المعاقفون المجالات	9000	Glutathione	
				peroxidase 1 (Gpx1),	
			MM, TT,	mRNA. 11/2002	
3564	1853	NM_030826	TTT	Length = 1539	ESTs, Glutathione peroxidase 1
				Proteolipid protein	
				(Pelizaeus- Merzbacher disease,	
		:		spastic paraplegia 2,	
				uncomplicated) (Plp),	Proteolipid protein (Pelizaeus-
		:		mRNA. 11/2002	Merzbacher disease, spastic
3577	20410	NM_030990	SS	Length = 3019	paraplegia 2, uncomplicated)
<u> </u>				guanine nucleotide	
				binding protein, alpha	·
				12 (Gna12), mRNA.	
				11/2002 Length =	guanine nucleotide binding
3585	690	NM_031034	RR	1423	protein (G protein) alpha 12
	İ		G, II,	-:	
			FFF, GGG,	ribosomal protein L13 (Rpl13), mRNA.	
		i i	General	11/2002 Length =	
3601	23854	NM 031101	Alternate	722	ribosomal protein L13
3001	20004	14147_001101	Atternate	ribosomal protein L19	independent E re
•	İ			(Rpl19), mRNA.	
	l		*	11/2002 Length =	·
3603	16938	NM_031103	F, H, II	703	ribosomal protein L19
				S6 protein kinase	
				(Rsk-1) (Rps6ka1),	:
2005	17200	NINA 024407	KKK	mRNA. 4/2001	S6 protoin kingga (Bak 1)
3605	17300	NM_031107	NNN	Length = 3131 ribosomal protein	S6 protein kinase (Rsk-1)
			F II FFF	S27a (Rps27a),	
			General	mRNA. 4/2001	
3610	20839	NM 031113	Alternate	Length = 552	ribosomal protein S27a
				S-100 related protein,	
1				clone 42C	
				(S100A10), mRNA.	
3611	19040	NM_031114	O, VV	2/2002 Length = 573	S-100 related protein, clone 42C
				Glutathione-S-	1
				transferase, alpha type (Ya) (Gsta1),	
			GKTT	mRNA. 5/2001	Glutathione-S-transferase, alpha
3634	18990	NM 031509	SSS	Length = 1178	type (Yc?)
			Q, R,	Isocitrate	
			GG, PPP,	dehydrogenase 1,	
			QQQ,	soluble (Idh1),	
			General	mRNA. 5/2001	Isocitrate dehydrogenase 1,
3635	17427	NM_031510	Alternate	Length = 1719	soluble

TABL	<b>≣</b> 1 .			A	torney Docket 44921-5033-01WO Document No. 1935328.1
S99 [D:-:::	ELEG GLEG	Kefseg ID	Model Code	Knova Ceas Name	Unigene Sequenee Cluster Tille
3639	20448	NM_031530	W, II, EEE, MMM	small inducible cytokine A2 (Scya2), mRNA. 11/2002 Length = 780	Small inducible gene JE
				small inducible cytokine A2 (Scya2), mRNA. 11/2002	
3639	20449	NM_031530		Length = 780 ribosomal protein S7 (Rps7), mRNA. 11/2002 Length =	Small inducible gene JE
3649	9620	NM_031570	Alternate	650	ribosomal protein S7
3649	9621	NM_031570	В, ЈЈ, ОО, ННН	ribosomal protein S7 (Rps7), mRNA. 11/2002 Length = 650	ribosomal protein S7
3655	14295	NM_031599	ZZ, AAA, PPP, QQQ	eukaryotic translation initiation factor 2 alpha kinase 3 (Eif2ak3), mRNA. 11/2002 Length = 4510	eukaryotic translation initiation factor 2 alpha kinase 3
3658	21586	NM 031620	G	3-phosphoglycerate dehydrogenase (Phgdh), mRNA. 11/2002 Length = 1803	3-phosphoglycerate dehydrogenase
3659	14956	NM 031622	C	mitogen-activated protein kinase 6 (Mapk6), mRNA. 11/2002 Length = 3662	mitogen-activated protein kinase
3659	14957	NM 031622	С, ТТ	mitogen-activated protein kinase 6 (Mapk6), mRNA. 11/2002 Length = 3662	mitogen-activated protein kinase
3668	20743	NM_031684	I, J, KKK, General Alternate	solute carrier family 29, member 1 (Slc29a1), mRNA. 11/2002 Length = 1766	solute carrier family 29 (nucleoside transporters), member 1
3669	19727	NM_031687	N	ubiquitin A-52 residue ribosomal protein fusion product 1 (Uba52), mRNA. 11/2002 Length = 467	ubiquitin A-52 residue ribosomal protein fusion product 1

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nivasia.					Dogument No. 1985828.1
		KINGENGO	00 0		
Seq .	id ko Grec	Accor	Model Code	Marama Garas Maras	Mickey Common Charles
	ייפואי ואוויי.	Refseq ID ·	Goog		Unigene Sequence Cluster Title
				claudin 1 (Cldn1),	
3671	13706	NM 031699	QQ	mRNA. 11/2002 Length = 893	claudin 1
3071	13700	14101_031099	uu -	coated vesicle	Claddii1
		Ĭ		membrane protein	
			ļ	(Rnp24), mRNA.	
		ł		11/2002 Length =	
3677	12052	NM_031722	CC, WW	716	coated vesicle membrane protein
				1.1	
				solute carrier family	
				27 (fatty acid transporter), member	
	]			32 (Slc27a2), mRNA.	
			U, FF,	11/2002 Length =	solute carrier family 27 (fatty acid
3680	17554	NM 031736	GG	2963	transporter), member 2
				sulfotransferase	
	İ	}		family 1A, phenol-	
	ļ			preferring, member 1	
•				(Sult1a1), mRNA.	
			GGG,	1/2002 Length =	sulfotransferase family 1A, phenol
3702	4748	NM_031834	SSS	1227 sulfotransferase	preferring, member 1
				family 1A, phenol-	
İ				preferring, member 1	Aryl sulfotransferase cytosolic,
				(Sult1a1), mRNA.	1A, phenol-preferring, member 3,
				1/2002 Length =	sulfotransferase family 1A, phenol
3702	4749	NM_031834	Υ	1227	preferring, member 1
				farensyl diphosphate	
				synthase (Fdps),	
2707	45000	NINA 004040	General	mRNA. 11/2002	
3707	15069	NM_031840	Alternate	Length = 1271 farensyl diphosphate	Farnesyl diphosphate synthase
				synthase (Fdps),	
				mRNA. 11/2002	
3707	15070	NM_031840	I, T	Length = 1271	Farnesyl diphosphate synthase
				farensyl diphosphate	
				synthase (Fdps),	
				mRNA. 11/2002	
3707	25460	NM_031840	1, J, T	Length = 1271	Farnesyl diphosphate synthase
			U, LL,		
1			RR, SS,		
1			BBB,	Prohibitin (Phb),	
]			CCC, LLL,	mRNA. 11/2002	
3708	15601	NM_031851	RRR, SSS	Length = 1688	Prohibitin

TABL		: ;		A	tomey Docket 44221-5056-01WO ************************************
Seq : ID :	(10 Kg.	CONSERVA ASS OF F	ഗ്രൻവ 🙄 🗀	Known Cene Name	Officenc Sequence Cluster Tills
3727	18492	NM 032079	ННН	DnaJ (Hsp40) homolog, subfamily A, member 2 (Dnaja2), mRNA. 11/2002 Length = 1518	DnaJ (Hsp40) homolog, subfamily A, member 2
3727	18494	NM 032079	PPP, QQQ	DnaJ (Hsp40) homolog, subfamily A, member 2 (Dnaja2), mRNA. 11/2002 Length = 1518	DnaJ (Hsp40) homolog, subfamily A, member 2
3728	12299	NM_032416	N, YY	aldehyde dehydrogenase 2 (Aldh2), mRNA. 11/2002 Length = 1889	aldehyde dehydrogenase 2, mitochondrial
3734	17829	NM_033234	T, HH, NNN	Hemoglobin, beta (Hbb), mRNA. 12/2001 Length = 620 Hemoglobin, beta	Hemoglobin, beta
3734	17832	NM_033234	Т	(Hbb), mRNA. 12/2001 Length = 620 Hemoglobin, beta	Hemoglobin, beta
3734	25468	NM_033234	K, T, HH, XX, YY	(Hbb), mRNA. 12/2001 Length = 620	Hemoglobin, beta
3738	24420	NM_033539	нн	eukaryotic translation elongation factor 1 alpha 2 (Eef1a2), mRNA. 11/2002 Length = 1404	eukaryotic translation elongation factor 1 alpha 1
3748	23597	NM_053323	Υ	degenerative spermatocyte homolog (Drosophila) (Degs), mRNA. 11/2002 Length = 1390	degenerative spermatocyte homolog (Drosophila)
3750	14925	NM_053330	K, Z, AA, KK	ribosomal protein L21 (Rpl21), mRNA. 11/2002 Length = 554 ribosomal protein L21	ribosomal protein L21
3750	14926	NM_053330	V, Z, AA	(Rpl21), mRNA. 11/2002 Length = 554	ribosomal protein L21

TABL	₹1			AC CONTRACTOR	tomay Dockat 44921-5093-011WO Document No. 1935323.1
Seq.		CONSTRUCT ACCO RC(Seq ID.)		Known Cene Name	Unigene Sequence Cluster Title
3750	14927	NM_053330	v	ribosomal protein L21 (Rpl21), mRNA. 11/2002 Length ≃ 554	ribosomal protein L21
3750	14929	NM_053330	O, P, W	ribosomal protein L21 (Rpl21), mRNA. 11/2002 Length = 554	ribosomal protein L21
3753	14042	NM_053348	N, YY	fetuin beta (Fetub), mRNA. 11/2002 Length = 1392 Cdc42-binding	fetuin beta
3805	1178	NM_053620	PP, QQ	protein kinase beta (Cdc42bpb), mRNA. 11/2002 Length = 5333	Cdc42-binding protein kinase beta
3845	17728	NM_053867	FF	tumor protein, translationally- controlled 1 (Tpt1), mRNA. 11/2001 Length = 794	tumor protein, translationally- controlled 1
3864	17653	NM_053986	C, SS, WW, SSS, UUU	myosin lb (Myo1b), mRNA. 11/2002 Length = 3607	myosin IB
3874	23250	NM_057097	ZZ, AAA	vesicle-associated membrane protein 3 (Vamp3), mRNA. 11/2002 Length = 1742	vesicle-associated membrane protein 3
3876	25290	NM_057100	E, BB, JJ		growth arrest specific 6
3895	8640	NM_057211	KKK	Kruppel-like factor 9 (Klf9), mRNA. 11/2002 Length = 2721	Kruppel-like factor 9
3895	8641	NM_057211	C, DD, EE, SS	Kruppel-like factor 9 (Klf9), mRNA. 11/2002 Length = 2721	Kruppel-like factor 9
3896	10498	NM_078617	F	ribosomal protein S23 (Rps23), mRNA. 11/2002 Length = 432	ribosomal protein S23
3937	656	NM_133380	Υ	Interleukin 4 receptor (II4r), mRNA. 3/2002 Length = 3576	Interleukin 4 receptor

TABL	31		Jul 1499	A	tomey Docket 44921-5033-011W0 Document No. 1935323.1
Scq (D	elec Ean	CONSONI ACC OF RESSON ID.::	ලලේම (Nලල්ම)		Uhiganë Sequence Cluster Tille
3959	17109	NM_134326	M, S, DD, EE, SS, TT	Albumin (Alb), mRNA. 3/2002 Length = 1956	Albumin
3959	17112	NM_134326	S, HH	Albumin (Alb), mRNA. 3/2002 Length = 1956 collagen, type V,	Albumin, Glutathione peroxidase
3970	25237	NM_134452	NNN .	alpha 1 (Col5a1), mRNA. 11/2002 Length = 5551	collagen, type V, alpha 1
3982	15189	NM_138826	C, E, L, T, W, BB, DD, KKK, NNN	Metallothionein (Mt1a), mRNA. 11/2002 Length = 389	Metallothionein
3982	15190	NM_138826	C, E, L, T, DD, SS, WW, KKK, NNN	Metallothionein (Mt1a), mRNA. 11/2002 Length = 389	Metallothionein
3994	1858	NM_138907	FF, LL	mitochondrial acyl- CoA thioesterase 1 (Mte1), mRNA. 4/2002 Length = 1711	acyl-CoA thioesterase 1, cytosolic, mitochondrial acyl-CoA thioesterase 1
4054	19428	R47028	НН	dimethylarginine dimethylaminohydrol ase 1	dimethylarginine dimethylaminohydrolase 1
4063	8210	S61960	BB, CC, MM, UU, TTT, General Alternate	ferritin light chain 1	ferritin light chain 1
4079	9687	S79214	G, H	Collagen type X alpha 1	Collagen type X alpha 1
4096	1392	U10188	V	Polo-like kinase homolog	Polo-like kinase homolog
4099	1639	U11685	W, DD, EE, KKK, NNN, General Alternate	nuclear receptor subfamily 1, group H, member 3	nuclear receptor subfamily 1, group H, member 3
4117	14535	U31866	J, S	Transferrin	Rattus norvegicus Nclone10 mRNA, Transferrin
4141	17078	U53859	М	calpain, small subunit	calpain, small subunit 1
4141	17079	U53859	M MAA SS	calpain, small subunit  1 cationia amino acid	calpain, small subunit 1
4143	25608	U53927	MM, SS, TTT	cationic amino acid transporter-2A	cationic amino acid transporter- 2A

TABL	<b>E</b> 1		:	Δ	tomey Docket 44921-5033-01W0 : Document No. 1935323.1
	id kig Grec	Consons Accor Resson ID	Cocio Model	Known Cene Neme	Unigene Sequence Cluster Title
				tight junction protein	
4168	1279	U75916	A	2	tight junction protein 2
4176	1084	U89514	UU	calpain 9 (nCL-4)	calpain 9 (nCL-4)
					ESTs, Highly similar to RS3_MOUSE 40S ribosomal
4208	10819	X51536	H	ribosomal protein S3	protein S3 [R.norvegicus]
4210	18250	X51706	F, V, EEE, MMM	ribosomal protein L9	ESTs, Highly similar to RL9_RAT 60S RIBOSOMAL PROTEIN L9 [R.norvegicus]
			S, HH,		[
4212	1959	X52477	MM, SS,	Complement component 3	Complement component 3
				Transporter 1, ABC	
4223	1037	X57523	l II	(ATP binding	Transporter 1, ABC (ATP binding
4223	1037	A57525	BB, CC,	cassette)	cassette)
4226	18611	X58200	II, WW, EEE, MMM, General Alternate	ribosomal protein L29	ribosomal protein L29
4236	1435	X61654	O, P	Cd63 antigen	Cd63 antigen
					ESTs, Highly similar to RL8_HUMAN 60S ribosomal
4237	15875	X62145	F	ribosomal protein L8	protein L8 [R.norvegicus]
4243	20821	X62671	F, T	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)	ESTs, Highly similar to UBIM_RAT UBIQUITIN-LIKE PROTEIN FUBI [R.norvegicus]
4040	550	V0.4000	V, NN,		
4246	556	X64336	00	Protein C procollagen, type III,	Protein C
4254	16426	X70369	M, II	alpha 1	procollagen, type III, alpha 1
4256	1548	X70900	V, General Alternate	hepsin	hepsin
4261	1955	X76453	М	Hras-revertant gene 107	Hras-revertant gene 107
4263	11260	X77934	ww	Amyloid protein precursor-like protein 2	Amyloid protein precursor-like protein 2
4285	1818	Y11283	D, E, S, CC, MM, TTT	inter-alpha-inhibitor H4 heavy chain	inter-alpha-inhibitor H4 heavy chain

TABL	<b>3</b> 1	1.		A	tomey Docket 44921-5033-01W0 Document No. 1935323.1
\$99 10	id koj. Greć	Conson: Accor Rosseq ID:	Model , Code •	Kinowa Ceno Namo	Unigene Sequence Cluster Title
23	17613	AA799511	B, JJ, WW, DDD, HHH, General Alternate		ESTs, Weakly similar to DDRT helix-destabilizing protein - rat [R.norvegicus]
26	18981	AA799523	I, Z, AA, LL	·	ESTs, Weakly similar to ROA1_RAT Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP) [R.norvegicus]
					ESTs, Weakly similar to KEAP_RAT Kelch-like ECH- associated protein 1 (Cytosolic inhibitor of Nrf2) (INrf2)
30	17599	AA799539	Q, R		[R.norvegicus] ESTs, Highly similar to TBB1_RAT TUBULIN BETA CHAIN (T BETA-15)
39	18361	AA799591	U, V, GG	ubiquitin conjugating	[R.norvegicus]
42	17380	AA799612	MM, TTT	enzyme	ubiquitin conjugating enzyme
52	21679	AA799691	DD, EE, KKK, NNN, OOO		ESTs, Moderately similar to T31432 K-Cl cotransport protein 2, furosemide-sensitive - rat [R.norvegicus]
67	20998	AA799803	T, U, JJ, KK, WW, BBB, GGG, PPP, QQQ, RRR		ESTs, Weakly similar to JC6554 complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - rat [R.norvegicus]
70	21042	AA799814	MM, TTT	HMm:MAP kinase- activated protein kinase 2	ESTs, Weakly similar to A34366 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II delta chain - rat [R.norvegicus]
71	1607	AA799879	C		ESTs, Moderately similar to SNG1_RAT SYNAPTOGYRIN 1 (P29) [R.norvegicus]
80 100	16653 6892	AA799996 AA800551	Z, AA Q	DnaJ-like protein	ESTs, Weakly similar to GBG5_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-5 subunit [R.norvegicus] DnaJ-like protein

				A	tomey Docket 4/921-5033-91WO 
809 (D		Conlant Acc or Refseg ID	Model Code	Known Gene Name	Valgene Sequence Cluster Title
128	5934	AA817695	A, I, J, FFF, OOO, General Core Tox Markers		ESTs, Highly similar to 2008147A protein RAKb [Rattus norvegicus] [R.norvegicus]
136	1822	AA817843	LLL, UUU	CCAAT binding transcription factor of CBF-B/NFY-B	CCAAT binding transcription factor of CBF-B/NFY-B
139	2109	AA817887	W	profilin	profilin
143	2544	AA817968	LLL, SSS, UUU, General Alternate	ectonucleotide pyrophosphatase/pho sphodiesterase 1	ectonucleotide pyrophosphatase/phosphodiester ase 1
152	3016	AA818069	EE	polyubiquitin	polyubiquitin
160	6016	AA818163	B, H, GG, HHH, PPP, General Core Tox Markers		ESTs, Weakly similar to PON1_RAT Serum paraoxonase/arylesterase 1 (PON 1) (Serum aryldiakylphosphatase 1) (A- esterase 1) (Aromatic esterase 1) [R.norvegicus]
163	17771	AA818224	AA		Rat mRNA for beta-tubulin T
103		77.010224			EST, Moderately similar to ISI1_RAT Insulin-induced protein 1 (Insulin-induced growth response protein CL-6) (Immediate-early protein CL-6)
178	6236	AA818627	K, L, UU	V	[R.norvegicus] ESTs, Weakly similar to latexin
209	6237	AA819288	H, S		[Rattus norvegicus] [R.norvegicus]
224	15668	AA819643	к	AMP-activated protein kinase	AMP-activated protein kinase
233	19433	AA819776	K, XX, YY		ESTs, Weakly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
240	17614	AA848306	SS		ESTs, Weakly similar to DDRT helix-destabilizing protein - rat [R.norvegicus]
278	21310	AA850055	E		ESTs, Weakly similar to solute carrier family 27 (fatty acid transporter), member 2 [Rattus norvegicus] [R.norvegicus]

TABL	<b>E</b> 1				iomey Docket 44921-5033-01W0 Document No. 1935323.1
509 [D::	ELEC	(CONSINX ACC OT ROBERT	Codo Model	Knewn Cene Name	Unigene Sequence Cluster Title
					ESTs, Moderately similar to S21348 probable pol polyprotein- related protein 4 - rat
284	14324	AA850402	E		[R.norvegicus]
325	13772	AA851926	C, J		ESTs, Weakly similar to A57514 RNA helicase HEL117 - rat [R.norvegicus]
		44050500			ESTs, Highly similar to 2008109A set gene [Rattus norvegicus]
334	17461	AA858528	MM, TTT	heat shock protein 60	[R.norvegicus] Rattus norvegicus CDK110 mRNA, heat shock protein 60
345	14987	AA858640	G, H, U	(liver)	(liver)  ESTs, Highly similar to NFM_RAT
					Neurofilament triplet M protein (160 kDa neurofilament protein) (Neurofilament medium polypeptide) (NF-M)
367	6443	AA859150	000		[R.norvegicus]
					ESTs, Weakly similar to HG17_RAT NONHISTONE CHROMOSOMAL PROTEIN
368	19105	AA859230	III, JJJ,		HMG-17 [R.norvegicus]
070	0.1005		OOO, General Core Tox	synaptojanin 2	
370	21025	AA859241	Markers	binding protein	synaptojanin 2 binding protein ESTs, Weakly similar to
377	6342	AA859458	Z, AA		KPCG_MOUSE Protein kinase C, gamma type (PKC-gamma) [R.norvegicus]
					ESTs, Weakly similar to DJA1_MOUSE DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2)
390	16318	AA859648	Q		[R.norvegicus]
407	23301	AA859975	вв, сс	2-oxoglutarate carrier	2-oxoglutarate carrier
414	4462	AA866264	General Alternate		ESTs, Weakly similar to PE2R_RAT 20-alpha- hydroxysteroid dehydrogenase (20-alpha-HSD) (HSD1) [R.norvegicus]

TABL	<b>E1</b>			A	tomey Docket 44921-5033-01WO Document No. 1935323.1
509 10:	ID Ko. ©L©©	EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	Modaj Code :	Known Cone Name	Unigene Sequence Cluster Title
434	16327	AA875050	DD, EE, JJ, OO, III, JJJ, OOO, General Core Tox Markers		ESTs, Weakly similar to KICE_RAT Choline/ethanolamine kinase [Includes: Choline kinase (CK); Ethanolamine kinase (EK)] [R.norvegicus]
435	20701	AA875097	E, V, W, Z, AA, BB, CC, OO, PP, SS, UU, EEE, III, KKK, LLL, MMM, UUU		EST, Highly similar to FIBA_RAT Fibrinogen alpha/alpha-E chain precursor [R.norvegicus]
448	15933	AA875253	PP, QQ	ADP-ribosylation factor-like 1	ADP-ribosylation factor-like 1
463	6079	AA891037	טט	I AUTOI-IINE I	ESTs, Moderately similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus]
472	9136	AA891226	G, H, X, Y, GGG, LLL		ESTs, Highly similar to PSB5_RAT Proteasome subunit beta type 5 precursor (Proteasome epsilon chain) (Macropain epsilon chain) (Multicatalytic endopeptidase complex epsilon chain) (Proteasome subunit X) (Proteasome chain 6) [R.norvegicus]
473	18397	AA891242	ккк		ESTs, Weakly similar to MLRV_RAT Myosin regulatory light chain 2, ventricular/cardiac muscle isoform (MLC-2) [R.norvegicus]
				sarcosine	
497	2753 18269	AA891589 AA891769	RR D, N	dehydrogenase	ESTs, sarcosine dehydrogenase ESTs, Weakly similar to SC65 synaptonemal complex protein [Rattus norvegicus] [R.norvegicus]
				polypyrimidine tract	polypyrimidine tract binding
513 548	3902 24295	AA891901 AA892260	JJ, KK R	binding protein	protein ESTs, Highly similar to JC5386 steroidogenic acute regulatory protein - rat [R.norvegicus]

TABL	<b>E</b> 1			A	torney Docket 44921-5033-01W0
509 ID .	GLEC BLOC.	Centeni Ace or . Refer ID :	Model Gode:	Known Cene Name	Unigane Sequence Cluster Title
556	13647	AA892367	B, XX, YY, HHH		ESTs, Highly similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus]
	1000				ESTs, Weakly similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD)
561	19226	AA892394 AA892394	ZZ, AAA		(Hu-antigen D) [R.norvegicus] ESTs, Weakly similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) [R.norvegicus]
			C, H, S,		ESTs, Highly similar to S03644
567	9254 11992	AA892470 AA892485	OOO MM, TTT	dihydrolipoamide acetyltransferase	histone H2A.Z - rat [R.norvegicus] dihydrolipoamide acetyltransferase
570	24873	AA892498	N, O, P		ESTs, Weakly similar to CD63_RAT CD63 antigen (AD1 antigen) [R.norvegicus]
580	15876	AA892582	F, G, H		ESTs, Highly similar to RL8_HUMAN 60S ribosomal protein L8 [R.norvegicus]
592	22537	AA892799	S	HMm:glyoxylate reductase/hydroxypyr uvate reductase	ESTs, Weakly similar to 3- phosphoglycerate dehydrogenase [Rattus norvegicus] [R.norvegicus]
592	22538	AA892799	М	HMm:glyoxylate reductase/hydroxypyr uvate reductase	ESTs, Weakly similar to 3- phosphoglycerate dehydrogenase [Rattus norvegicus] [R.norvegicus]
598	7148	AA892842	L		ESTs, Weakly similar to CAZ3_RAT F-actin capping protein alpha-3 subunit (CAPZ alpha-3) [R.norvegicus]
609	3438	AA892921	K, V		ESTs, Weakly similar to A55143 calpain (EC 3.4.22.17) light chain rat (fragment) [R.norvegicus]
640	1562	AA893552	A, F, G, V, SSS, General Alternate		Rattus norvegicus kallistatin mRNA, complete cds
644	3465	AA893611	ZZ, AAA		ESTs, Moderately similar to MXI1_RAT MAX interacting protein 1 (MXI1 protein) [R.norvegicus]

TABL	E1		:	A A	torney Doctot 44221-5033-91W0 Document No. 1915323.1
509 ID .	@L@G;	CONSINX ACCOT RCISCO ID	Modal Codo :	Known Caro	Unigene Sequence Cluster Title
٠ . العلق	ווא וצופינו	lycagogal in:	ROGED : 1:	rotein carrying the	
			XX, YY,	RING-H2 sequence	rotein carrying the RING-H2
662	7637	AA894089	ZZ, AAA	motif	sequence motif
1002	1.00.	701054005	LL, 7001	mour	ESTs, Weakly similar to
					2019243A amyloid precursor-like
		·	1		protein 2 [Rattus norvegicus]
666	18419	AA894130	s		[R.norvegicus]
				ubiquitin-conjugating	
i		1	,	enzyme E2D 3	ubiquitin-conjugating enzyme
1				(homologous to yeast	E2D 3 (homologous to yeast
672	15274	AA894258	L, HH	UBC4/5)	UBC4/5)
				ubiquitin-conjugating	
	ļ			enzyme E2D 3	ubiquitin-conjugating enzyme
			i.		E2D 3 (homologous to yeast
704	15275	AA900187	D	UBC4/5)	UBC4/5)
					ESTs, Highly similar to
				HMm:carbon	A2MG_RAT ALPHA-2-
		ļ	7	catabolite repression	MACROGLOBULIN
706	4725	AA900290	Z, MM,	4 homolog (S.	PRECURSOR (ALPHA-2-M)
706	4725	AA900290	III	cerevisiae)	[R.norvegicus] ESTs, Weakly similar to JQ0866
l					T-complex protein 1 - rat
710	17849	AA900460	GGG	, i	[R.norvegicus]
1.10	11045	701300100			ESTs, Weakly similar to
			1		OBRG RAT Leptin receptor gene-
					related protein (OB-R gene
					related protein) (OB-RGRP)
711	6483	AA900461	RR		[R.norvegicus]
			000,		ESTs, Weakly similar to
	1		General		HE47_RAT Probable ATP-
	i		Core Tox		dependent RNA helicase p47
716	3822	AA900863	Markers		[R.norvegicus]
	1				ESTs, Weakly similar to DnaJ-
l					like protein [Rattus norvegicus]
753	5003	AA924691	UU		[R.norvegicus]
1	İ				
	ļ			siah binding protein	
				1; FBP interacting	sigh hinding protein 4: CBD
ŀ				repressor; pyrimidine tract binding splicing	siah binding protein 1; FBP
				factor; Ro	interacting repressor; pyrimidine tract binding splicing factor; Ro
		!	SS, ZZ,	ribonucleoprotein-	ribonucleoprotein-binding protein
775	10666	AA925212	AAA	binding protein 1	1
<del></del>				zog protont 1	ESTs, Weakly similar to
l	1		D, U, FF,		1701410A choline
			ввв,	HMm:carnitine	acetyltransferase [Rattus
777	21010	AA925306		acetyltransferase	norvegicus] [R.norvegicus]
				<del></del>	ESTs, Weakly similar to A57514
					RNA helicase HEL117 - rat
836	22142	AA943066	KK		[R.norvegicus]

TABL	E 1			A	iomey Docket 44921-5063-01W0 Document No. 1935323.1
<u> </u>	22.22	Consens, ;		12AP	
	. 99J9	Acc or Reference	Code Modeli	Known Cene Name	Makana Garana Ghrana Tillh
	الاهالاي المال	Managard (m)	Goog :	Minewi Cente Menue	Unigene Sequence Cluster Title
					ESTs, Moderately similar to
				11114	HS9B_RAT Heat shock protein
076	20705	A A A A A A A A A A A A A A A A A A A		HMm:heat shock	HSP 90-beta (HSP 84)
876	20795	AA944397	K	protein, 86 kDa 1	[R.norvegicus]
					TOT- West State
i					ESTs, Weakly similar to
1				]	FCN2_RAT Ficolin 2 precursor
					(Collagen/fibrinogen domain-
	ļ				containing protein 2) (Ficolin-B)
000	4.700	A A O 4 4 4 O 4	l <u>-</u> -		(Ficolin B) (Serum lectin P35)
882	14763	AA944481	FF		(EBP-37) (Hucolin) [R.norvegicus]
ì					ESTs, Weakly similar to R6RT37
l	10000	4 4 4 4 5 9 9			ribosomal protein L37, cytosolic
884	12228	AA944536	ZZ, AAA		[validated] - rat [R.norvegicus]
l					ESTs, Weakly similar to
	l	1			ROD_RAT Heterogeneous
1					nuclear ribonucleoprotein D0
					(hnRNP D0) (AU-rich element
					RNA-binding protein 1)
890	2893	AA944833	VV		[R.norvegicus]
1					ESTs, Weakly similar to
	1				ARG2_RAT Arginase II,
					mitochondrial precursor (Non-
1					hepatic arginase) (Kidney-type
915	22606	AA945580	W		arginase) [R.norvegicus]
1	1				ESTs, Weakly similar to
i					ARG2_RAT Arginase II,
					mitochondrial precursor (Non-
					hepatic arginase) (Kidney-type
915	22607	AA945580	W		arginase) [R.norvegicus]
					ESTs, Weakly similar to A34162
İ					NAD(P)H dehydrogenase
					(quinone) (EC 1.6.99.2) - rat
920	22612	AA945624	000		[R.norvegicus]
Ì					ESTs, Weakly similar to solute
j	1				carrier family 25
İ					(carnitine/acylcarnitine
					translocase), member 20 [Rattus
922	20904		ZZ, AAA		norvegicus] [R.norvegicus]
			J, GG,		
	i		нн,		
	1		General		
			Core Tox	retinoid X receptor	
966	23584	AA955071	Markers	gamma (	retinoid X receptor gamma (
1					ESTs, Weakly similar to
·					GRB2_HUMAN Growth factor
					receptor-bound protein 2 (GRB2
		Į			adapter protein) (SH2/SH3
					adapter GRB2) (ASH protein)
978	23542	AA955389	AA		[R.norvegicus]

TABL	<b>3</b> 1	72 <del>1</del> 2 1	- 1945 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 - 1975 -	A. A.	tomey Docket 44921-5033-011WO Document No. 1935323.1
		Gewrenyz .	. 7.7	चें ने नवंदर्वे स्थान	en en en en en en en en en en en en en e
	Gree .		model		
W.G.	(D) Klo.	RefSeq ID	(cooo	Myowy Gave Marve	Ufigene Sequence Cluster Title
					ESTs, Weakly similar to
		Ì			LIS1_MOUSE Platelet-activating
		1			factor acetylhydrolase IB alpha
	1		1		subunit (PAF acetylhydrolase 45
	ŀ		\		kDa subunit) (PAF-AH 45 kDa
	1			Ì	subunit) (PAF-AH alpha) (PAFAH
000	40400	4.055700			alpha) (Lissencephaly-1 protein)
993	12426	AA955760	YY		(LIS-1) [R.norvegicus]
			ННН,		ESTs, Weakly similar to JQ0866
1,005	44050		General		T-complex protein 1 - rat
1005	11050	AA956164	Alternate		[R.norvegicus]
					ESTs, Weakly similar to
1			ĺ		TERA_RAT TRANSITIONAL
		1	<u> </u>		ENDOPLASMIC RETICULUM
1					ATPASE (TER ATPASE) (15S
					MG(2+)-ATPASE P97 SUBUNIT)
		†			(VALOSIN CONTAINING
1010	25442	A A O E C 4 2 7	DD 66		PROTEIN) (VCP) [CONTAINS:
1010	25112	AA956437	BB, CC		VALOSIN] [R.norvegicus]
	i				ESTs, Highly similar to
					FCEG_RAT High affinity
					immunoglobulin epsilon receptor
					gamma-subunit precursor
	1				(FcERI) (IgE Fc receptor gamma-
1030	24040	AA957422	P, VV		subunit) (Fc-epsilon RI-gamma) [R.norvegicus]
1030	24040	77331422	r, vv		ESTs, Weakly similar to JC5567
			General		lamin B receptor - rat
1031	23080	AA957423	Alternate		[R.norvegicus]
1001	20000	701307420	Atternate		ESTs, Weakly similar to
ŀ					TXTP RAT Tricarboxylate
1					transport protein, mitochondrial
}					precursor (Citrate transport
	Ì				protein) (CTP) (Tricarboxylate
1042	23541	AA957999	ww		carrier protein) [R.norvegicus]
F					ESTs, Moderately similar to
	Į (				A53770 growth factor-responsive
					protein, vascular smooth muscle -
1049	16577	AA963286	V		rat [R.norvegicus]
					ESTs, Weakly similar to
					HS9B_RAT Heat shock protein
					HSP 90-beta (HSP 84)
1058	18648	AA963782	ss		[R.norvegicus]
					ESTs, Highly similar to
					ACTB_HUMAN Actin,
1					cytoplasmic 1 (Beta-actin)
1075	18830	AA964496	T, W		[R.norvegicus]
					Kelch-like ECH-associated
1145	13330	AA997716	X, Y	associated protein 1	protein 1

TABL				A	torney Docket 44921-5036-01000 Document No. 1986323.1
809 (D	ELEC É	Centiani Ace or Reference	Model Gode	Known Gene Name	Unigene Sequence Cluster Title
1174	3773	AA998356	A, B, E, CC, DD, EE, PP, QQ, III, JJJ, KKK, NNN		ESTs, Weakly similar to S68418 protein phosphatase 1M chain M110 isoform - rat (fragment) [R.norvegicus]
1197	1962	AB000199	D	CCA2 protein retinoid X receptor	CCA2 protein
1222	19649	AF016387	XX, YY	gamma (	retinoid X receptor gamma (
1223	1308	AF022774	ннн	rabphilin 3A-like (without C2 domains) stathmin-like-protein	rabphilin 3A-like (without C2 domains)
1225	18072	AF026529	FF	RB3	stathmin-like-protein RB3
1233	1995	AF038870	C, NN, OO, DDD	betaine- homocysteine methyltransferase	betaine-homocysteine methyltransferase
1241	20741	AF084186	A, Q, R, JJ, KK, WW, FFF, GGG, HHH, PPP, QQQ	alpha-fodrin	alpha-fodrin
1243	20133	AF087697	XX, YY	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)
1248	2947	AF099093	D.	ubiquitin-conjugating enzyme UBC7	ubiquitin-conjugating enzyme UBC7
1248	20511	AF099093	Υ	ubiquitin-conjugating enzyme UBC7	ubiquitin-conjugating enzyme UBC7
1249	4014	Al007645	J, Z, AA		ESTs, Weakly similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus] ESTs, Weakly similar to JC4647
1251	11251	AI007666	EE		KW8 protein - rat [R.norvegicus]
1254	8368	Al007808	DD, EE	·	ESTs, Highly similar to A37056 AMP deaminase (EC 3.5.4.6), brain - rat (fragment) [R.norvegicus] ESTs, Weakly similar to S40468
1262	22230	AI007920	EE	•	proteasome subunit RC10-li - rat [R.norvegicus]
1279	4098	AI008642	vv		ESTs, Weakly similar to LANP_RAT Leucine-rich acidic nuclear protein [R.norvegicus]

TABU	इ.१	1		A	tomey Docket 44921-5093-011W0 ::: Document No. 1935323.1
\$39 ID	id ko Grec	(G97:577). Ace or RefSeq (D	(Codo	emen keme	Unigana Saguanca Cluster Titla
1280	949	AI008687	ww		ESTs, Highly similar to WASL_RAT Neural Wiskott- Aldrich syndrome protein (N- WASP) [R.norvegicus]
1286	344	Al008865	UU, III, JJJ C,	Signal transducer and activator of transcription 3	Signal transducer and activator of transcription 3
1300	21838	AI009131	General Alternate I, J, MM,	laminin, gamma 1	laminin, gamma 1
1328	22545	AI009747	TTT	ERBB2, 1	transducer of ERBB2, 1
1360	163	AI010480	X, Y	dehydrogenase mitochondrial	malate dehydrogenase mitochondrial
1360	164	AI010480	1	malate dehydrogenase mitochondrial	malate dehydrogenase mitochondrial
1382	16112	AI011706	c		ESTs, Weakly similar to SFR5_RAT Splicing factor, arginine/serine-rich 5 (Pre-mRNA splicing factor SRP40) (Insulin-induced growth response protein CL-4) (Delayed-early protein HRS) [R.norvegicus]
1404	21796	Al012221	II, 00, VV		ESTs, Weakly similar to intracellular chloride ion channel protein p64H1 [Rattus norvegicus] [R.norvegicus]
1408	3417	Al012337	General Alternate		ESTs, Highly similar to NHPX_RAT NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27) [R.norvegicus]
1414	7120	Al012393	Т		ESTs, Weakly similar to JE0343 terf protein - rat [R.norvegicus]
1423	20817	Al012589	G	glutathione S- transferase, pi 2 kinesin family	glutathione S-transferase, pi 2
1441	1205	AI013107	D, V C, G, H, General Core Tox	member 3C	kinesin family member 3C ESTs, Weakly similar to cold inducible RNA-binding protein [Rattus norvegicus]
1466 1469	7299 15904	Al013911 Al013971	Markers QQ	neurofascin	[R.norvegicus] neurofascin
1525	23949	Al031019	C, E	translation initiation factor eIF-2B alpha- subunit	translation initiation factor eIF-2B alpha-subunit

TABL	<b>E</b> 1			A	iomay Docket 4X921-5033-91WO Document No. 1935323.1
509 ID	id nó. Grec	ENGLINE AGE OF ROSESSESS	Code Model	Known Cene Keine	Unigene Sequence Cluster Title
		1	R, PPP,	translation initiation factor eIF-2B alpha-	translation initiation factor eIF-2B
1525	23950	AI031019	QQQ	subunit	alpha-subunit
1.020	-	1			ESTs, Weakly similar to
1	1				FIBA RAT Fibrinogen
				j	alpha/alpha-E chain precursor
1536	7891	AI043759	N		[R.norvegicus]
1.000	1.001	7.110-107-00	<del>  `                                   </del>		ESTs, Weakly similar to
1					TC17_RAT Zinc finger protein
1	1				354A (Transcription factor 17)
1	]				(Renal transcription factor Kid-1)
}					(Kidney, ischemia, and
ł					developmentally regulated protein-
1545	7961	AI044042	lww		, , , , , ,
1545	7901	A1044042	10000		1) [R.norvegicus] ESTs, Weakly similar to
1			1		
1562	10005	1044026	EE NAIN	·	NUCL_RAT Nucleolin (Protein
1563	18205	AI044836	EE, NNN		C23) [R.norvegicus]
			loco		ESTs, Weakly similar to solute
			GGG,		carrier family 25
		İ	ННН,		(carnitine/acylcarnitine
1,504		1,10,45454	General		translocase), member 20 [Rattus
1581	5711	Al045151	Alternate		norvegicus] [R.norvegicus]
			G,		Rattus norvegicus partial mRNA
		110 15000	General		for glycosylphosphatidylinositol
1594	7552	AI045802	Alternate	<u> </u>	phospholipase D (gpld1 gene)
l					ESTs, Highly similar to
	1				HG17_RAT NONHISTONE
					CHROMOSOMAL PROTEIN
1605	10533	AI058430	BBB		HMG-17 [R.norvegicus]
	1	1		ĺ	ESTs, Weakly similar to
1	ļ		A, B,		FIBA_RAT Fibrinogen
			EEE,		alpha/alpha-E chain precursor
1620	8584	AI058911	MMM		[R.norvegicus]
1			FFF,		
	<u> </u>	1	General		
1	1		Core Tox		
1	1		Markers,		ESTs, Weakly similar to
			General		NUCL_RAT Nucleolin (Protein
1667	9067	AI070087	Alternate		C23) [R.norvegicus]
					ESTs, Weakly similar to
					OZF_RAT Zinc finger protein
1689	26184	AI070784	11		OZF (POZF-1) [R.norvegicus]
ł				CCCTC-binding	
				factor (zinc finger	CCCTC-binding factor (zinc finger
1704	7775	Al071481	D	protein)	protein)
					ESTs, Weakly similar to JE0343
1721	3912	AI072035	Z, AA		terf protein - rat [R.norvegicus]

TABL	<b>国</b> 引	ř		A	termay Dockat 44921-5033-01W0 Document No. 1935323.1
	(ID K)o. (GL.GC	Consant Accor Refeed ID	Model Code	Known Cene Name	Unigane Sequence Civeter Title
			A, B, OO, FFF, GGG, HHH, OOO,		ESTs, Weakly similar to
1723	9191	Al072107	General Core Tox Markers		2008147B protein RAKc [Rattus norvegicus] [R.norvegicus]
1727	5021	AI072308	RR		ESTs, Weakly similar to DnaJ (Hsp40) homolog, subfamily A, member 2 [Rattus norvegicus] [R.norvegicus]
1737	1501	AI072634	A, I, W, PP, QQ, VV, FFF, GGG, General Core Tox Markers		Rattus norvegicus cytokeratin-18 mRNA, partial cds
1766	10573	Al101003	м		ESTs, Weakly similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus]
1788	18642	AI102023	s		Rattus norvegicus mRNA for ribosomal protein L35
1803	5967	AI102520	EEE, MMM		ESTs, Weakly similar to GABA(A) receptor-associated protein like 2; ganglioside expression factor 2 [Rattus norvegicus] [R.norvegicus]
1803	5969	Al102520	EEE,		ESTs, Weakly similar to GABA(A) receptor-associated protein like 2; ganglioside expression factor 2 [Rattus norvegicus] [R.norvegicus]
1813	23538	Al102727	A, B, Q, R	solute carrier family 20 (phosphate transporter), member 1	solute carrier family 20 (phosphate transporter), member 1
1815	17850	AI102750	GGG		ESTs, Weakly similar to JQ0866 T-complex protein 1 - rat [R.norvegicus]
1818	4898	Al102879	Q, R		ESTs, Weakly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus] ESTs, Weakly similar to I60486
1819	11655	AI102881	т		gene trg protein - rat (fragment) [R.norvegicus]

TABL	e1:				tomey Docket 44221-5033-01WO Document No. 1985323.1
Scq : 10	ELEC BLCC	(CON: 500); AGG OT REISOG (D)	Model Code	Known Cane Neme	Ünigene Sequence Cluster Title
			U, LL,		Rattus norvegicus mRNA for
			RRR,		carbonyl reductase/NADP-retinol
1830	3279	AI103224	sss, uuu		dehydrogenase, complete cds
1.000	-		N, MM,	-	Rattus norvegicus CDK110
1836	14981	Al103396	TIT		mRNA
			<u> </u>	polypyrimidine tract	polypyrimidine tract binding
1837	3905	Al103403	JJ, KK	binding protein	protein
		1			ESTs, Weakly similar to
				Ì	ZF94_RAT Zinc finger protein 94
	1		DD, EE,		(Zfp-94) (Zinc finger protein Y1)
1839	2961	AI103415	PP, QQ		(RLZF-Y) [R.norvegicus]
				SH2-B PH domain	
				containing signaling	SH2-B PH domain containing
1860	1440	AI104139	ww	mediator 1	signaling mediator 1
					ESTs, Highly similar to
					ACTB_HUMAN Actin,
			_		cytoplasmic 1 (Beta-actin)
1867	18831	AI104357	S, T, W		[R.norvegicus]
1					ESTs, Moderately similar to
					GTM1_RAT Glutathione S-
	1				transferase YB1 (Chain 3) (GST
4004					M1-1) (GST class-Mu 1)
1881	24323	AI104798	DDD, LLL		[R.norvegicus]
					ESTs, Weakly similar to
1002	47770	A1405004			ARF6_HUMAN ADP-ribosylation
1893	17770	Al105294	LL		factor 6 [R.norvegicus]
			\		Rat mRNA for RT1.D beta chain,
					Rattus norvegicus Class II MHC RT1.D(u) beta chain precursor
1901	16718	Al111537	XX, YY		(RT1.D(u)) mRNA, complete cds
1301	107.10	A1111337	^^, ''		(KTT.D(u)) IIIKNA, complete cus
1			V, BB,		ESTs, Weakly similar to
ŀ			EEE, III,		vitronectin [Rattus norvegicus]
1926	4969	Al113008	JJJ, MMM		[R.norvegicus]
			500, 1		Rattus norvegicus mRNA for a
					novel kinesin-related protein,
1940	5559	AI136892	L		KIF1D
					ESTs, Weakly similar to
					GPV_RAT Platelet glycoprotein V
			E, PP,		precursor (GPV) (CD42D)
1952	7122	AI137468	JJJ		[R.norvegicus]
					ESTs, Weakly similar to
					KEAP_RAT Kelch-like ECH-
					associated protein 1 (Cytosolic
				•	inhibitor of Nrf2) (INrf2)
1977	14259	Al145037	PP, QQ		[R.norvegicus]
					ESTs, Weakly similar to S57449
					fusca protein homolog - rat
1981	2917	AI145614	s, uuu		[R.norvegicus]

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Seq :	erec .		Model -		
œ	(F)	RefSeq ID,	Godo	Known Gene Name:	Unicipio Sequence Cluster Title
					ESTs, Weakly similar to
		1			GTO1_RAT Glutathione
				HMm:glutathione	transferase omega 1 (GSTO 1-1)
		İ		transferase zeta 1	(Glutathione-dependent
			PPP,	(maleylacetoacetate	dehydroascorbate reductase)
1996	17812	AI169075	QQQ	isomerase)	[R.norvegicus]
					ESTs, Weakly similar to
		1			PON1_RAT Serum
		i		,	paraoxonase/arylesterase 1
					(PON 1) (Serum
					aryldiakylphosphatase 1) (A-
		}	PPP,		esterase 1) (Aromatic esterase 1)
1998	1335	AI169105	QQQ		[R.norvegicus]
					ESTs, Weakly similar to S70642
					ubiquitin ligase Nedd4 - rat
2015	5716	AI169347	RR		(fragment) [R.norvegicus]
		-			Rattus norvegicus transcription
2043	18671	Al170270	FF		factor IIIA mRNA, partial cds
					ESTs, Weakly similar to A35362
			}		UDPglucoseglycogen
	ļ		İ		glucosyltransferase (EC
			PP, QQ,	HMm:glycogen	2.4.1.11), hepatic - rat
2054	11585	AI170502	YY	synthase 3, brain	[R.norvegicus]
					ESTs, Weakly similar to
					1917150A
				•	collagen:SUBUNIT=alpha1:ISOT
			E, NN,		YPE=VIII [Rattus norvegicus]
2055	13361	AI170516	00		[R.norvegicus]
					ESTs, Weakly similar to
					GABA(A) receptor-associated
					protein like 2; ganglioside
					expression factor 2 [Rattus
2067	5968	AI170692	TT		norvegicus] [R.norvegicus]
					ESTs, Weakly similar to 156246
					lipopolysaccharide binding protein
2097	18837	AI171583	G		- rat [R.norvegicus]
					ESTs, Weakly similar to
			MM, III,		1617160A phenylethanolamine N-
			JJJ, KKK,		methyltransferase [Rattus
2106	5339	AI171727	TTT		norvegicus] [R.norvegicus]
					ESTs, Weakly similar to ubiquitin-
]			1	HMm:ubiquitin-	conjugating enzyme E2D 2
	<u> </u>			conjugating enzyme	[Rattus norvegicus]
2141	21564	Al172301	E	E2L 3	[R.norvegicus]
		·		RNA binding protein	
2144	23390	AI172328	G, GGG	p45AUF1	RNA binding protein p45AUF1
					ESTs, Highly similar to 2008109A
					set gene [Rattus norvegicus]
2145	23325	AI172405	D		[R.norvegicus]

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TABL	31			+ 4 A	iomey Docket 44921-5033-01WO Document No. 1933:23.1
\$69 D	39J9	Consoni Acc or Reiseg ID	Model Codo		Unigene Sequence Cluster Title
2148	23157	Al172489	Q, R		ESTs, Moderately similar to STRN_RAT Striatin [R.norvegicus]
					ESTs, Weakly similar to ROD_RAT Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)
2159	2895	Al175095	W		[R.norvegicus]
2166	4445	Al175466	N		ESTs, Weakly similar to RASH_RAT TRANSFORMING PROTEIN P21/H-RAS-1 (C-H- RAS) [R.norvegicus]
2167	3418	Al175475	MM, TTT, General Core Tox Markers		ESTs, Highly similar to NHPX_RAT NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27) [R.norvegicus]
2178	23519	AI175935	บบ		R.norvegicus myr3 mRNA for myosin I heavy chain
2197	20823	Al176302	XX, YY		ESTs, Highly similar to UBIM_RAT UBIQUITIN-LIKE PROTEIN FUBI [R.norvegicus]
2214	16518	AI176546	н, т, п	HMm:heat shock protein, 86 kDa 1	ESTs, Moderately similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
2216	2532	Al176590	General Core Tox Markers		ESTs, Weakly similar to S68418 protein phosphatase 1M chain M110 isoform - rat (fragment) [R.norvegicus]
			JJ, KK, NN, OO, EEE, HHH,	HMm:adenine phosphoribosyl	ESTs, Highly similar to APT_RAT ADENINE PHOSPHORIBOSYLTRANSFER
2251	14384	AI177096	MMM GG, HH, II, FFF,	transferase NF-E2-related factor	ASE (APRT) [R.norvegicus]
2258	1169	AI177161	KKK J, GG,	2 NF-E2-related factor	NF-E2-related factor 2
2258	1170	AI177161	нн, ккк	2	NF-E2-related factor 2
2285	6189	Al178027	G, CC, NN, OO, QQ, PPP, QQQ	·	ESTs, Weakly similar to GTP_RAT Glutathione S- transferase P (GST 7-7) (Chain 7) (GST class-pi) [R.norvegicus]
2290	18672		H, General Alternate		Rattus norvegicus transcription factor IIIA mRNA, partial cds

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TABL	<b>3</b> 9 "		111-		10 mey Docket 44921-5033-91WO
					👺 🕼 Document No. 1935323.1
Seg . [D	ELEG:	Leised in Signaturia	Model Codo	Known Cono Name	Unigene Sequence Cluster Title
					ESTs, Moderately similar to
					TVRTYP GTP-binding protein
2295	19586	Al178239	LL		Rab1 - rat [R.norvegicus]
					ESTs, Weakly similar to
					ACDV_RAT Acyl-CoA
					dehydrogenase, very-long-chain
					specific, mitochondrial precursor
2315	3968	Al178764	RR, SS		(VLCAD) [R.norvegicus]
0000	4570	A1470000	EEE, JJJ,	eukaryotic translation initiation factor 4E	eukaryotic translation initiation
2320	1572	AI178828	МММ	binding protein 1	factor 4E binding protein 1
					ESTs, Weakly similar to NF-E2-
0000	47000	A1470400			related factor 2 [Rattus
2328	17890	Al179123	AA UU		norvegicus] [R.norvegicus]
2222	14002	A1170150	F, S, HH, SS		Rattus norvegicus CDK110 mRNA
2332	14983	AI179150	55		ESTs, Weakly similar to Gasz
					[Rattus norvegicus]
2355	16656	AI179634	YY		[R.norvegicus]
2333	10030	A1173034	7 1		ESTs, Highly similar to S60038
		•	к, тт,		multicatalytic endopeptidase
			LLL, SSS,		complex (EC 3.4.99.46) alpha
2368	9032	AI179950	UUU		chain RC6-I - rat [R.norvegicus]
2000	3032	A1173300			ESTs, Weakly similar to
2372	6455	Al179984	XX, YY, PPP, QQQ		CPI3_RAT CONTRAPSIN-LIKE PROTEASE INHIBITOR 3 PRECURSOR (CPI-23) (SERINE PROTEASE INHIBITOR 1) (SPI- 1) [R.norvegicus]
					ESTs, Highly similar to
2373	17349	AI179987	AAA		HG17_RAT NONHISTONE CHROMOSOMAL PROTEIN HMG-17 [R.norvegicus]
					ESTs, Moderately similar to
					S21348 probable pol polyprotein-
					related protein 4 - rat
2376	12568	AI180044	RR		[R.norvegicus]
2377	19828	AI180087	F		ESTs, Weakly similar to OZF_RAT Zinc finger protein OZF (POZF-1) [R.norvegicus]
2311	13020	A1100001		small zinc finger-like	OZI (I OZI - I) [IX.HOI VEGICUS]
2386	22835	AI180367	MM, TTT	protein	small zinc finger-like protein
2000	22000	100007		mitogen activated	one zao mgor mo protest
					mitogen activated protein kinase
2387	1455	AI180373	w	kinase 1	kinase kinase 1
					ESTs, Weakly similar to S53358
					ubiquitin-conjugating enzyme
2404	16801	AI227894	тт		E2.17kB - rat [R.norvegicus]
<b>24U4</b>	10001	MIZZ / 094			EZ. 17KD + Tat [N.1101Vegicus]

TABL	≣ብ‹	ar election		A)	torney Docket 44921-5033-01000 Document No. 1935323.1
Seq 10	ELEC	Consant Accor ReiSeg ID	Model	eme Name	Unigene Sequence Cluster Tille
12.23					ESTs, Weakly similar to
					K6A1_RAT Ribosomal protein S6
					kinase alpha 1 (S6K-alpha 1) (90
	]	ļ			kDa ribosomal protein S6 kinase
					1) (p90-RSK 1) (Ribosomal S6
					kinase 1) (RSK-1) (pp90RSK1)
2407	12413	AI227953	D		[R.norvegicus]
					ESTs, Weakly similar to A Chain
					A, Crystal Structure Of S-
		 			Glutathiolated Carbonic
2423	9038	Al228419	T		Anhydrase lii [R.norvegicus]
l		 			ESTs, Weakly similar to
•	l				FIBA_RAT Fibrinogen
	7000	A1000470			alpha/alpha-E chain precursor
2449	7892	Al229172	N		[R.norvegicus] ESTs, Weakly similar to
			General		2209311A coagulation factor X
l			Core Tox		[Rattus norvegicus]
2451	6604	AI229192	Markers		[R.norvegicus]
2451	0004	M1229192	IVIAINCIS		ESTs, Weakly similar to A57514
					RNA helicase HEL117 - rat
2461	23858	Al229450	K, L		[R.norvegicus]
					ESTs, Weakly similar to S21055
ļ	1	<u> </u>			translation elongation factor eEF-
2467	23573	AI229595	D		1 alpha chain - rat [R.norvegicus]
2407	23373	A1229393	<u> </u>		Taipha Chair - Fat [13.16170gicus]
			V, III, JJJ,		ESTs, Weakly similar to
			General		MOT2 RAT Monocarboxylate
			Core Tox		transporter 2 (MCT 2)
2476	12587	AI229979	Markers		[R.norvegicus]
20	12007	/			ESTs, Weakly similar to
	1				KUCR_RAT Kupffer cell receptor
2481	7650	AI230142	O, P		[R.norvegicus]
<u> </u>	<del>                                     </del>				ESTs, Weakly similar to
1					2208374A cis-Golgi/intermediate
					compartment protein [Rattus
2483	18425	Al230208	000		norvegicus] [R.norvegicus]
					ESTs, Weakly similar to coated
	1				vesicle membrane protein (Rattus
2507	11553	Al230765	BB, CC		norvegicus] [R.norvegicus]
					ESTs, Highly similar to R3RT3A
			X, Y, AA,		ribosomal protein L23a, cytosolic
2520	20845	Al231140	TT		[validated] - rat [R.norvegicus]
					ESTs, Highly similar to R3RT3A
	1		N, XX,		ribosomal protein L23a, cytosolic
2520	20846	Al231140	YY		[validated] - rat [R.norvegicus]

TABLI	<b>31</b>		. 4		iomey Docket 44921-5038-01WO 
Seq :	id ko Greć	Acc or	Model Gode	Known Cene Name	Unigene Sequence Cluster Title
					ESTs, Highly similar to
					S611_HUMAN Protein transport
		·			protein Sec61 alpha subunit
					isoform 1 (Sec61 alpha-1)
2523	21816	AI231217	L		[R.norvegicus]
				1.18.4	ESTs, Weakly similar to 3- phosphoglycerate dehydrogenase
				HMm:glyoxylate	, , , , ,
2557	22542	AI232066	QQ, XX, YY	reductase/hydroxypyr uvate reductase	[R.norvegicus]
2557	22342	A1232000	11	uvale reductase	ESTs, Weakly similar to
					GABA(A) receptor-associated
					protein like 2; ganglioside
					expression factor 2 [Rattus
2572	17566	AI232301	М		norvegicus] [R.norvegicus]
2012	.7000	711202001			ggg
					ESTs, Weakly similar to
	,				MTE1 RAT Acyl coenzyme A
				į į	thioester hydrolase, mitochondrial
	į				precursor (Very-long-chain acyl-
			K, U, FF,		CoA thioesterase) (MTE-I)
2589	5602	Al232611	BBB, RRR		[R.norvegicus]
					ESTs, Weakly similar to
ļ				*	ribosomal protein S27a [Rattus
2591	14070	Al232649	FF		norvegicus] [R.norvegicus]
					ESTs, Weakly similar to
					ROD_RAT Heterogeneous
					nuclear ribonucleoprotein D0
					(hnRNP D0) (AU-rich element
					RNA-binding protein 1)
2599	2896	AI232957	VV		[R.norvegicus]
					ESTs, Weakly similar to
0000	40070	A 102000 4			OZF_RAT Zinc finger protein OZF (POZF-1) [R.norvegicus]
2602	12873	Al232984	11		ESTs, Weakly similar to
					ZF37 RAT Zinc finger protein 37
2606	13377	AI233056	ss		(Zfp-37) [R.norvegicus]
2000	10077	A1233030	FFF,		(Zip-07) [renorvegious]
			GGG,		
			ннн,		ESTs, Weakly similar to
			General		HE47 RAT Probable ATP-
			Core Tox		dependent RNA helicase p47
2609	3823	Al233147	Markers		[R.norvegicus]
					ESTs, Weakly similar to
			X, Y, LLL,		ribosomal protein S23 [Rattus
2620	23296	Al233316	บบบ		norvegicus] [R.norvegicus]
			JJ, KKK,		
	3073	Al233494	NNN	Mk1 protein	Mk1 protein
2626	3074	Al233494	JJ	Mk1 protein	Mk1 protein
2626	3075	Al233494	F, JJ	Mk1 protein	Mk1 protein

TABL				A	tomey Docket 44921-5038-01WO Document No. 1935328.1
		(Consonk	1		
Seq	@L@C	Ace or	Model .		2: 3.
	ID No.	Rossog ID	ලිලේල	Known Cone Name	Unigene Sequence Cluster Title
				HMm:fibroblast	
		0 W 6		growth factor	Rattus norvegicus mRNA for
2636	13023	AI233740	lvv	regulated protein	aldose reductase-like protein
				melastatin like 2	
2669	14676	Al234615	E	protein	melastatin like 2 protein
					ESTs, Weakly similar to S25644
				İ	Ig mu chain C region - rat
2675	22609	AI234828	X, Y		(fragment) [R.norvegicus]
					ESTs, Highly similar to RL9_RAT
l					60S RIBOSOMAL PROTEIN L9
2696	18252	AI235497	11		[R.norvegicus]
					ESTs, Weakly similar to
					ZF94_RAT Zinc finger protein 94
					(Zfp-94) (Zinc finger protein Y1)
2697	14740	AI235511	Z, AA		(RLZF-Y) [R.norvegicus]
					ESTs, Weakly similar to T42751
					sulfonylurea receptor 2 - rat
2701	3650	AI235738	S		[R.norvegicus]
			·		ESTs, Weakly similar to
]	1		1		C1TC_RAT C-1-tetrahydrofolate
1	]		1		synthase, cytoplasmic (C1-THF
					synthase) [Includes:
					Methylenetetrahydrofolate
					dehydrogenase;
				·	Methenyltetrahydrofolate
			V V		cyclohydrolase;
2700	7207	AIDDEODE	X, Y,		Formyltetrahydrofolate
2708	7307	AI235935	บบบ		synthetase ] [R.norvegicus] ESTs, Highly similar to
j	1				NIDO RAT NIDOGEN
2709	22717	AI235948	м		(ENTACTIN) [R.norvegicus]
2714	7604	Al236039	00	reticulocalbin	reticulocalbin
2714	7004	A1230039		reticulocalbilit	Rattus norvegicus epidermal
					Langerhans cell protein LCP1
2726	13911	AI236262	Q, R		mRNA, complete cds
	10011	7 11200202	α,		ESTs, Weakly similar to
			i	1	NHPX_RAT NHP2-like protein 1
1	1		ł		(High mobility group-like nuclear
					protein 2 homolog 1) ([U4/U6.U5]
				į	tri-snRNP 15.5 kDa protein)
2730	19298	AI236338	บบบ		(OTK27) [R.norvegicus]
		<u> </u>			Rattus norvegicus mRNA for
2734	17571	Al236484	XX, YY	-	hnRNP protein, partial
					Rattus norvegicus transcription
2735	14777	Al236565	V	<u> </u>	factor IIIA mRNA, partial cds

1	31	(A) 1		A	torney Docket 44921-5033-01WO Document No. 1935321.1
Seq 10	ID KJ& @F@@	Constant Acc or Rowsed (D _{.+1}	Model Codo	emski emoð rkvérki	Unigene Sequence Cluster Title
			1		ESTs, Weakly similar to dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine
2750	16978	AI236777	κ		dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus]
					ESTs, Weakly similar to DHI1_RAT Corticosteroid 11-beta-dehydrogenase, isozyme 1 (11-DH) (11-beta-hydroxysteroid dehydrogenase 1) (11-beta-
2760	21091	AI236972	O, P		HSD1) [R.norvegicus]
					ESTs, Weakly similar to sialyltransferase 3; sialyltransferase (N-acetyllacosaminide alpha 2,3-sialyltransferase) [Rattus
2768	13513	AI237091	<b>J</b> JJ		norvegicus] [R.norvegicus]
					ESTs, Moderately similar to PKL2_RAT PROTEIN KINASE C-LIKE 2 (PROTEIN-KINASE C-RELATED KINASE 2) (PROTEASE-ACTIVATED KINASE 2) (PAK-2)
2773	14827	AI237404	QQ		[R.norvegicus]
2786	21043	AI237813	MM, TTT	HMm:MAP kinase- activated protein kinase 2	ESTs, Weakly similar to A34366 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II delta chain - rat [R.norvegicus] ESTs, Moderately similar to
2788	3467	Al237835	E		MXI1_RAT MAX interacting protein 1 (MXI1 protein) [R.norvegicus]
					ESTs, Weakly similar to ATS4_RAT ADAMTS-4 precursor (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM- TS 4) (ADAM-TS4) (Aggrecanase
2832	8106	AI639534	M, LL		1) [R.norvegicus]
2837	6601	AJ131902	S, Z, AA	growth arrest specific 7 dihydrolipoamide	growth arrest specific 7
2844	5050	D10655	υυ, ww	acetyltransferase	dihydrolipoamide acetyltransferase
2864	959	D38072	DD, EE	protein tyrosine phosphatase, non- receptor type 12	protein tyrosine phosphatase, non receptor type 12

	3 <b>1</b>			A A	torney Docket 44221-5033-01W0 Document No. 1935323.1
	id no Grec	Consent Assorti Raiseg ID	Modal Codo	emieW enconva	Unigene Sequence Cluster Ville
2878	2744	D87991	T, UU, DDD, EEE, MMM		ESTs, Highly similar to JC5026 UDP-galactose transporter related protein 1 - rat [R.norvegicus]
2885	238	E03859	<b>v</b>	RAB11a, member RAS oncogene family	RAB11a, member RAS oncogene family
2886	62	E06822	A, B, P, General Core Tox Markers, General Alternate	20 alpha- hydroxysteroid dehydrogenase	20 alpha-hydroxysteroid dehydrogenase
2887	930	E12159	RR	130kDa-Ins(1,4,5)P3 binding protein	130kDa-Ins(1,4,5)P3 binding protein Rattus norvegicus dynein light
2900	9745	H31847	Q, R		intermediate chain 1 mRNA, complete cds
2903	3815	H31907	FFF, GGG	G protein pathway suppressor 1	G protein pathway suppressor 1
2952	107	L14001	XX, YY,		Rattus norvegicus clone 15 polymeric immunoglobulin receptor mRNA, 3'UTR microsatellite repeats
2953	108	L14002	L, MM, DDD, TTT		Rattus norvegicus clone 15 polymeric immunoglobulin receptor mRNA, 3'UTR microsatellite repeats
2955	109	L14004	M, N, V, SS, TT, DDD		Rattus norvegicus clone 15 polymeric immunoglobulin receptor mRNA, 3'UTR microsatellite repeats
2960	24518	L19927	GG	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
2966	1373	L24907	L	calcium/calmodulin- dependent protein kinase I	calcium/calmodulin-dependent protein kinase I
2971	1791	L28801	RR, 000	general transcription factor III C 1	general transcription factor III C 1
2972	1695	L35921	XX, YY, PPP, QQQ	G-protein gamma 8 subunit	G-protein gamma 8 subunit
2982	17883	M11851	PP, QQ, III, JJJ		Rat heart myosin light chain 2 (MLC2) mRNA, 3' end

TABL		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	\$ 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	A	107719: Docket 44921-5033-01WO 1235323.1 Document No. 1935323.1
599 ID:	id ko:	Contant Accor	Modal Codo		Unigene Sequence Cluster Title
3005	1540	M25073	BB, CC, II, NNN, General Alternate	alanyl (membrane) aminopeptidase	alanyl (membrane) aminopeptidase
3017	17211	M34331	DDD		Rattus norvegicus mRNA for ribosomal protein L35
3017	26030	M34331	F, DDD		Rattus norvegicus mRNA for ribosomal protein L35
3028	24662	M59786	V	Ca channel, voltage- dependent, L type, alpha 1c subunit	Ca channel, voltage-dependent, L type, alpha 1c´subunit
3035	239	M75153	D	RAB11a, member RAS oncogene family	RAB11a, member RAS oncogene family
3035	240	M75153	FF, LL	RAB11a, member RAS oncogene family	RAB11a, member RAS oncogene family
3054	1410	M96548	ww	zinc finger protein 354A	zinc finger protein 354A
3072	20305	NM 012532	N, V	Ceruloplasmin (ferroxidase) (Cp), mRNA. 11/2002 Length = 3700	R.norvegicus mRNA for bilitranslocase
3101	18726	NM 012645	F, M, DDD, LLL, RRR, UUU, General Alternate	RT1 class lb gene (RT1Aw2), mRNA. 11/2002 Length = 1540	Rattus norvegicus MHC class lb RT1.S3 (RT1.S3) mRNA, partial cds
3113	7101	NM_012679	II, TT	clusterin (Clu), mRNA. 10/2002 Length = 1638	Clusterin
				Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length =	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone
3119	18718	NM_012695	X, Y FFF, General	1000 Nucleolin (NcI),	(DHEA) -preferring, member 1
3134	8829	NM_012749	Core Tox Markers	mRNA. 11/2002 Length = 2142	Nucleolin
3138	721	NM_012780	RR	Aryl hydrocarbon receptor nuclear translocator 1 (Arnt1), mRNA. 11/2000 Length = 2431	Aryl hydrocarbon receptor nuclear translocator 1

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TABLE	ี่ ยี	17.			iomay Docket 44921-5033-01W0 Document No. 1935323.1
S09 ⁷ [D:	erec'	Consent Accor Resco ID	Codo Modol	7. G	Unicomo Soquemee Cluster Thile
3183	19108	NM_012963	V	high mobility group box 1 (Hmgb1), mRNA. 10/2002 Length = 1225 high mobility group	High mobility group 1
3183	19109	NM_012963	JJ, KK	box 1 (Hmgb1), mRNA. 10/2002 Length = 1225	High mobility group 1
3183	19110	NM_012963	JJ, KK, PP, QQ, HHH	high mobility group box 1 (Hmgb1), mRNA. 10/2002 Length = 1225 CD81 antigen (target	High mobility group 1
3215	8898	NM_013087	G, H, J	of antiproliferative antibody 1) (Cd81), mRNA. 11/2000 Length = 1303	CD81 antigen (target of antiproliferative antibody 1)
3215	8899	NM_013087	G, H, I, J, S, SSS, UUU	CD81 antigen (target of antiproliferative antibody 1) (Cd81), mRNA. 11/2000 Length = 1303	CD81 antigen (target of antiproliferative antibody 1)
3215	8900	NM_013087	PPP, QQQ	CD81 antigen (target of antiproliferative antibody 1) (Cd81), mRNA. 11/2000 Length = 1303	CD81 antigen (target of antiproliferative antibody 1)
3232	16448	NM 013197	м, т	Aminolevulinate synthase 2, delta (Alas2), mRNA. 11/2000 Length = 1899	Aminolevulinate synthase 2, delta
			G, K, S, X, JJ, KK, NN, DDD, EEE, GGG, HHH,	aflatoxin B1 aldehyde reductase (Afar), mRNA. 11/2002	
3236	20864	NM_013215	MMM Z, AA,	Length = 1272 cofilin 1 (Cfl1), mRNA. 11/2002	aflatoxin B1 aldehyde reductase
3289	18925	NM_017147	HH	Length = 1039 cysteine rich protein 1 (Csrp1), mRNA. 1/2002 Length =	Bone morphogenetic protein 6
3290	13392	NM_017148	Т	1403 rabin 3 (RABIN3), mRNA, 11/2000	cysteine rich protein 1
3337	16182	NM_017313	JJ, KK	Length = 1407	rabin 3

TABL	<b>3</b> 9 .	4 (			torney Docket 44921-5033-01WC Document No. 1986328.1
599. 10:4	@r@c	COMPENI ACCOT ROBEQ ID	Codo: Modal		Unigene Sequence Cluster Title
3346	20848	NM_017343	A, B, P	myosin regulatory light chain (MRLCB), mRNA. 6/2001 Length = 1139	Rat mRNA for myosin regulatory light chain (RLC)
3346	20849	NM_017343	A, TT	myosin regulatory light chain (MRLCB), mRNA. 6/2001 Length = 1139	Rat mRNA for myosin regulatory light chain (RLC)
3390	24883	NM_019293	OO, General Core Tox Markers	carbonic anhydrase 5 (Ca5a), mRNA. 11/2002 Length = 1201	
3393	1099	NM 019303	W, CC, General Core Tox Markers	Cytochrome P450, subfamily IIF, polypeptide 1 (Cyp2f1), mRNA. 11/2000 Length = 1768	Cytochrome P450, subfamily IIF, polypeptide 1
			·	Proprotein convertase subtilisin/kexin type 3 (paired basic amino acid cleaving enzyme, furin, membrane associated receptor protein) (Pcsk3), mRNA. 10/2002	Paired basic amino acid cleaving
3395	16331	NM_019331 NM_019331	S, W	Length = 4259 Proprotein convertase subtilisin/kexin type 3 (paired basic amino acid cleaving enzyme, furin, membrane associated receptor protein) (Pcsk3), mRNA. 10/2002 Length = 4259	enzyme (furin)  Paired basic amino acid cleaving enzyme (furin)
3396	5264		JJ, KK	regulator of G-protein signaling 3 (Rgs3), mRNA. 11/2002 Length = 3722	
	23226	NM_019360		cytochrome oxidase subunit VIc (Cox6c), mRNA. 11/2000 Length = 418	cytochrome oxidase subunit VIc

TABL	<u>ደ</u> ብ	jug.		A	torney Docket 44921-5036-01WO Document No. 1985323.1
509 (D)	id ko Gree	LEESEN LEESEN LEESEN	Cogo :	Knovn Cone Kine	Unigene Sequence Cluster Title
				Ly6-C antigen gene (Ly6c), mRNA. 11/2000 Length =	
3418	18705	NM_020103	D	405	Ly6-C antigen gene
3425	18724	NM_021585	F	surface protein MCA- 32 (Mca32), mRNA. 11/2002 Length = 1659	Rattus norvegicus MHC class Ib RT1.S3 (RT1.S3) mRNA, partial cds
			E, BB,	ERM-binding phosphoprotein (LOC59114), mRNA. 11/2002 Length =	
3427	17340	NM_021594	cc	1492 Chemokine receptor	ERM-binding phosphoprotein
				(LCR1) (Cxcr4), mRNA. 5/2002	01 (1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0
3447	20248	NM_022205	III, JJJ	Length = 1050 Chemokine receptor	Chemokine receptor (LCR1)
			SS, EEE,	(LCR1) (Cxcr4), mRNA. 5/2002	
3447	20249	NM_022205	МММ	Length = 1050	Chemokine receptor (LCR1)
3464	15931	NM_022385	Т	ADP-ribosylation factor-like 1 (Arl1), mRNA. 11/2002 Length = 893	ADP-ribosylation factor-like 1
3467	22413	NM 022392	A, B	growth response protein (CL-6) (LOC64194), mRNA. 12/2000 Length = 2410	growth response protein (CL-6)
		_		mitochondrial processing peptidase beta (Pmpcb), mRNA. 12/2000	mitochondrial processing
3468	23178	NM_022395	D, SS	Length = 1570 2-oxoglutarate carrier	peptidase beta
			W, DD, EE, BBB,	(LOC64201), mRNA. 12/2000 Length =	
3469	23300	NM_022398	ccc	946 acidic ribosomal	2-oxoglutarate carrier
3471	1069	NM_022402	V, CC, LL, DDD	protein P0 (Arbp), mRNA. 12/2000 Length ≈ 1046	acidic ribosomal protein P0
3474	2236	NM_022512	ввв, ссс	short chain acyl- coenzyme A dehydrogenase (Acads), mRNA. 12/2000 Length = 1749	short chain acyl-coenzyme A dehydrogenase

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3 4		Geuraux	Model Code		elli receule concupée chécif ille
3476	162	NM_022516	vv	polypyrimidine tract binding protein (Ptb), mRNA. 11/2002 Length = 2723	malate dehydrogenase mitochondrial
3476	3900	NM_022516	vv	polypyrimidine tract binding protein (Ptb), mRNA. 11/2002 Length = 2723	polypyrimidine tract binding protein
3481	8097	NM_022536	BB, CC	cyclophilin B (Ppib), mRNA. 12/2000 Length = 840	cyclophilin B
3482	8597	NM_022538	BB, CC, NN, OO, QQ, ZZ, AAA	phosphatidate phosphohydrolase type 2a (Ppap2a), mRNA. 5/2002 Length = 871	phosphatidate phosphohýdrolase type 2a
3485	9296	NM_022541	LLL	small zinc finger-like protein DDP2 (Ddp2), mRNA. 12/2000 Length = 494	small zinc finger-like protein DDP2
3486	9541	NM_022542	W, II, QQ	rhoB gene (Arhb), mRNA. 12/2000 Length = 2183	rhoB gene
3488	12192	NM_022545	м, нн	phosphoribosylpyrop hosphate synthetase- associated protein (39 kDa) (Prpsap1), mRNA. 12/2000 Length = 1581	phosphoribosylpyrophosphate synthetase-associated protein (39 kDa)
3488	12193	NM_022545		phosphoribosylpyrop hosphate synthetase- associated protein (39 kDa) (Prpsap1), mRNA. 12/2000 Length = 1581	phosphoribosylpyrophosphate synthetase-associated protein (39 kDa)
3489	12422	NM_022546	H, T, DD, EE, KKK	Death-associated like kinase (Dapkl), mRNA. 12/2000 Length = 1514 Death-associated like	Death-associated like kinase
3489	12423	NM_022546	D, DD, EE, KKK	kinase (Dapkl), mRNA. 12/2000 Length = 1514	Death-associated like kinase

TABL	≣ੀ			A A A	torney Docket 44921-5033-01WO Document No. 1935323.1
		(Censenia	,		
Seq	@L@C		Modej		
		Refeed ID		Known Gene Name	Chit relevis, concupes caegial
			O, P, NN,		
			00, VV,	10-	
			EEE, III,	formyltetrahydrofolat	
			JJJ,	e dehydrogenase (Fthfd), mRNA.	
		•	MMM, General	12/2000 Length =	10-formyltetrahydrofolate
3490	12606	NM 022547	Alternate	3109	dehydrogenase
3490	12000	14141_022547	Alternate	histone 2b (H2b),	ESTs, Highly similar to 0506206A
				mRNA. 1/2001	histone H2B [Rattus norvegicus]
3501	12542	NM_022647	А, В	Length = 378	[R.norvegicus]
1000	12042	11111_0220 11		Matrin F/G (Matr1),	[·····································
			Í	mRNA. 1/2001	
3502	24442	NM_022667	JJ	Length = 2748	Matrin F/G
				GABA(A) receptor-	·
				associated protein	
1	٠.	1		like 2 (Gabarapl2),	
				mRNA. 5/2002	GABA(A) receptor-associated
3514	24458	NM_022706	L, LL	Length = 975	protein like 2
				DnaJ-like protein	
			l	(Hsj2), mRNA.	
			C, Q, R,	11/2002 Length =	
3520	6891	NM_022934	DD, EE	1610	DnaJ-like protein
				clathrin-associated	
l				protein 17 (Ap2s1), mRNA. 1/2001	
2526	20681	NM_022952	G, Н	Length = 797	clathrin-associated protein 17
3526	20001	14101_022932	0, 11	ADP-ribosylation	Clatifiti-associated protein 17
				factor 5 (Arf5),	
				mRNA. 11/2002	
3538	15367	NM 024149	X, Y	Length = 1058	ADP-ribosylation factor 5
<del></del>	† · · · · · · · · · · · · · · · · · · ·		l '	ADP-ribosylation	
				factor 6 (Arf6),	
		1	O, P, Q,	mRNA. 11/2002	
3540	21696	NM_024152	R	Length = 995	ADP-ribosylation factor 6
				RNA binding protein	
				p45AUF1 (Hnrpd),	
[			_	mRNA. 3/2001	
3559	23387	NM_024404	E	Length = 1240	RNA binding protein p45AUF1
	1			RNA binding protein	
				p45AUF1 (Hnrpd),	
2550	22200	NINA 004404		mRNA. 3/2001	RNA binding protein p45AUF1
3559	23388	NM_024404	С	Length = 1240	KNA biliding protein p45AUF1
				RNA binding protein p45AUF1 (Hnrpd),	
				mRNA. 3/2001	
3559	25682	NM_024404	MM TTT	Length = 1240	RNA binding protein p45AUF1
2000	1-0005	1. 111 02 7 7 0 7	1	1	[

TABL	<u> ខ្</u> ត			: A	tomey Docket 44921-5033-01000
	id kaj Grec	Conson: Acc or Refseq ID.	lebom (ceboo)	emen ened awoan	elifi retevid concuped saccin
				N- acetylglucosaminyltra	
				nsferase I (Mgat1),	
3572	15186	NM 030861	DD, EE	mRNA. 4/2001 Length = 2546	N-acetylglucosaminyltransferase I
3372	13700	1410_030001	OD, EL	N-	in acceptiglaces an intylical sterase i
				acetylglucosaminyltra	
			FF, TT,	nsferase I (Mgat1), mRNA. 4/2001	
3572	15187	NM_030861	NNN	Length = 2546	N-acetylglucosaminyltransferase I
				N-	
				acetylglucosaminyltra nsferase I (Mgat1),	
			DD, EE,	mRNA. 4/2001	
3572	15188	NM_030861	GG, 000	Length = 2546 Guanine nucleotide-	N-acetylglucosaminyltransferase I
				binding protein beta 1	
				(Gnb1), mRNA.	
3575	21801	NM 030987	ZZ, AAA	4/2002 Length = 2837	Guanine nucleotide-binding protein beta 1
3373	2 1001	14M_030901	22, 700	Guanine nucleotide-	protein beta 1
				binding protein beta 1	
			O P W	(Gnb1), mRNA. 4/2002 Length =	Guanine nucleotide-binding
3575	21802	NM_030987	AAA	2837	protein beta 1
				p38 mitogen	
				activated protein kinase (Mapk14),	
				mRNA. 10/2002	p38 mitogen activated protein
3583	16561	NM_031020	DD, EE	Length = 3132	kinase
				p38 mitogen activated protein	
				kinase (Mapk14),	·
2502	16563	NIM 031030	E T 00	mRNA. 10/2002	p38 mitogen activated protein
3583	16562	NM_031020	L, 1, DD	Length = 3132 p38 mitogen	kinase
				activated protein	
		<u> </u>		kinase (Mapk14), mRNA. 10/2002	p38 mitogen activated protein
3583	16564	NM 031020	E, W, TT	Length = 3132	kinase
				macrophage	
		:		migration inhibitory factor (Mif), mRNA.	
				11/2002 Length =	macrophage migration inhibitory
3590	15138	NM_031051	G, H, Y	551	factor
				mitochondrial intermediate	
				peptidase (Mipep),	
2521	44000	NA 004050	000	mRNA. 11/2002	mitochondrial intermediate
3591	11899	NM_031052	000	Length = 2337	peptidase

TABL	<b>E</b> 1		,	Att	torney Docket 4/1921-5033-01WO Document No. 1936328.1
Scq [D	ELEC ID No. ;	CONSTANT AGG OT ROSSEG ID	Model - Code -	Known Cene Name	Oliti relevio concupce eneginu
				mismatch repair protein (Msh2), mRNA. 11/2002	
3593	16104	NM_031058	D	Length = 3002	mismatch repair protein
0500	10100			mismatch repair protein (Msh2), mRNA. 11/2002	
3593	16106	NM_031058	Τ	Length = 3002	mismatch repair protein
0500	00.40	NN4 024077		PCTAIRE-1 protein kinase, alternatively spliced (Pctk1), mRNA. 10/2002	PCTAIRE-1 protein kinase,
3596	6348	NM_031077	PP, QQ	Length = 3111 ribosomal protein L37	alternatively spliced
2004	20007	NH 024400	F, T, U,	(Rpl37), mRNA. 11/2002 Length =	aibaaa mada in 127
3604	20807	NM_031106	FFF	366 suppression of	ribosomal protein L37
3612	23569	NM 031122	X, Y, BB, CC, DD, EE, KKK, NNN	tumorigenicity 13 (colon carcinoma)	suppression of tumorigenicity 13 (colon carcinoma) Hsp70- interacting protein
			Q, R, PPP,	tripeptidylpeptidase II (Tpp2), mRNA. 4/2001 Length =	
3616	15487	NM_031137	QQQ	4566	tripeptidylpeptidase II
3616	15489	NM 031137		tripeptidylpeptidase II (Tpp2), mRNA. 4/2001 Length = 4566	tripeptidylpeptidase II
3617	17379	NM_031138	R, DD, EE, MM, WW, TTT, General Alternate	ubiquitin conjugating	ubiquitin conjugating enzyme
3619	21624	NM_031144	vv ·	actin (Actx), mRNA. 4/2001 Length = 1128 cytoplasmic beta-	actin, beta
3619	21625	NM_031144	11	actin (Actx), mRNA. 4/2001 Length = 1128	actin, beta

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TABL	ਭੂੀ : :			<i>BLA</i>	tomay Docket 44921-5053-01WO : Document No. 1985823.1
599; [D	ELEG.	Refsogip.	Model Codo	Knovn Geno Name	Unigaño Sequence Civetor IIIIe
3621	15273	NM_031237	PPP, QQQ	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5) (Ube2d3), mRNA. 4/2001 Length = 1531	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)
3689	16178	NM_031785	T, V, JJ, KK	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1 (Atp6s1), mRNA. 5/2001 Length = 2089	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1
2606	17525	NIA 031916	D	retinoblastoma binding protein 7 (Rbbp7), mRNA. 11/2002 Length = 1947	retinoblastoma binding protein 7
3696	17535	NM_031816	D	1341	realization a stricting protein /
3698	23407	NM_031819	Q, R	FAT tumor suppressor (Drosophila) homolog (Fat), mRNA. 5/2001 Length = 14,746	FAT tumor suppressor (Drosophila) homolog
3705	10267	NM_031838	LL	ribosomal protein S2 (Rps2), mRNA. 11/2002 Length = 817	ribosomal protein S2
3705	10269	NM 031838	cc	ribosomal protein S2 (Rps2), mRNA. 11/2002 Length = 817	ribosomal protein S2
3706	10947	NM 031839		arachidonic acid epoxygenase (Cyp2c23), mRNA. 11/2002 Length = 2153	arachidonic acid epoxygenase
3706	10949	NM 031839	FF, EEE,	arachidonic acid epoxygenase (Cyp2c23), mRNA. 11/2002 Length = 2153	arachidonic acid epoxygenase
3721		NM_031986		syntenin (Sdcbp), mRNA. 5/2001 Length = 2077	syntenin
13141	112100	114141 02 1200	10, IX	Longar = 2011	9311(011111

TABL	E1			A	tomey Docket 44921-5038-011W0 Document No. 1985328.1
599 : ID	(CLGC)	Constall Acc or Roßeg ID	Model Code : #	Known Cono Namo	Unigene Sequence Cluster Title
3738	24419	NM_033539	Υ	eukaryotic translation elongation factor 1 alpha 2 (Eef1a2), mRNA. 11/2002 Length = 1404 RAN, member RAS oncogene family	eukaryotic translation elongation factor 1 alpha 1
3766	14670	NM_053439	บบบ	(Ran), mRNA. 11/2002 Length = 1084	RAN, member RAS oncogene family
3781	18401	NM 053532	K, X, Y, UUU	proteasome (prosome, macropain) subunit, beta type, 7 (Psmb7), mRNA. 11/2001 Length = 993	proteasome (prosome, macropain) subunit, beta type, 7
3796	21445	NM_053587	W, BB	S100 calcium-binding protein A9 (calgranulin B) (S100a9), mRNA. 11/2001 Length = 494	S100 calcium-binding protein A9 (calgranulin B)
3799	20902	NM 053593	С, G, H	cyclin-dependent kinase 4 (Cdk4), mRNA. 11/2001 Length = 1232	cyclin-dependent kinase 4
3820	24728	NM_053753	X, Y, EEE, MMM	Kupffer cell receptor (Kclr), mRNA. 11/2001 Length = 1888	Kupffer cell receptor
				ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (Atp5g3), mRNA. 11/2001 Length =	ATP synthase, H+ transporting, mitochondrial F0 complex,
3821	10909	NM_053756	U	723 Arg/Abl-interacting	subunit c (subunit 9) isoform 3
3826	14016	NM_053770	A	protein ArgBP2 (Argbp2), mRNA. 11/2001 Length = 6331	Arg/Abl-interacting protein ArgBP2
3826	14017	NM_053770		Arg/Abl-interacting protein ArgBP2 (Argbp2), mRNA. 11/2001 Length = 6331	Arg/Abl-interacting protein ArgBP2

TABU	≅¶~;;;		- In eye t	AS	torney Docket 44921-5093-01WO Document No. 1995323.1
509 (D	. 29.19 @L@G	Consont Accor Refseq ID	Model; Code	Known Cene Name	Unigene Sequence Cluster Title
			PP, QQ,	potassium channel, subfamily K, member 6 (TWIK-2) (Kcnk6),	ESTs, Weakly similar to
3830	19827	NM_053806	YY, PPP, QQQ	mRNA. 11/2001 Length = 2243	OZF_RAT Zinc finger protein OZF (POZF-1) [R.norvegicus]
				v-ral simian leukemia viral oncogene homolog B (ras related) (Ralb), mRNA. 11/2001	v-ral simian leukemia viral
3835	20421	NM_053821	O, P, W	Length = 2074	oncogene homolog B (ras related)
				eukaryotic translation initiation factor 4E binding protein 1 (Eif4ebp1), mRNA. 11/2002 Length =	eukaryotic translation initiation
3842	1570	NM_053857	O, P	843	factor 4E binding protein 1
2040	4574	<b>ANA</b> 052057	100	eukaryotic translation initiation factor 4E binding protein 1 (Eif4ebp1), mRNA. 11/2002 Length =	eukaryotic translation initiation
3842	1571	NM_053857	W	843 valosin-containing protein (Vcp), mRNA. 11/2002 Length =	factor 4E binding protein 1
3843	18357	NM_053864	N	2870	valosin-containing protein
3843	18358	NM_053864	LL	valosin-containing protein (Vcp), mRNA. 11/2002 Length = 2870	valosin-containing protein
3847	1453	NM 053887	li	mitogen activated protein kinase kinase kinase 1 (Map3k1), mRNA. 11/2001 Length = 5180	mitogen activated protein kinase kinase kinase 1
3852	4588	NM_053923		phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide (Pik3c2g), mRNA. 11/2001 Length = 5990	
3855	16190	NM_053961	U, FF, BBB	endoplasmic retuclum protein 29 (Erp29), mRNA. 11/2001 Length = 4529	ESTs, Weakly similar to F Chain F, 2-Enoyl-Coa Hydratase, Data Collected At 100 K, Ph 6.5 [R.norvegicus]

TABL			\$ . t	A	tomey Docket 44921-5033-011WC Document No. 1935323.1
Seq. ID:	ELEC SOLO	CONSINX Acc or Roßog ID	Model Codo	Known Cene Name	Unigene Sequence Civeter Title
3857	16546	NM_053965	U, FF, LL, BBB, CCC, RRR, SSS		solute carrier family 25 (carnitine/acylcarnitine translocase), member 20
3857	16547	NM_053965	RRR, SSS	solute carrier family 25 (carnitine/acylcarnitin e translocase), member 20 (Slc25a20), mRNA. 11/2001 Length = 1231	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20
3858	6357	NM 053969	S	G protein pathway suppressor 1 (Gps1), mRNA. 11/2001 Length = 1794	G protein pathway suppressor 1
3861		NM 053979	R	ADP-ribosylation factor-like 5 (Arl5), mRNA. 11/2001 Length = 2717	ADP-ribosylation factor-like 5
3867	17739	NM_053995	General Alternate	3-hydroxybutyrate dehydrogenase (heart, mitochondrial) (Bdh), mRNA. 11/2001 Length = 1420	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)
3869	24655	NM_053998	RR	mel transforming oncogene (derived from cell line NK14)- RAB8 homolog (Mel), mRNA. 11/2001 Length = 840	mel transforming oncogene (derived from cell line NK14)- RAB8 homolog
3876	16043	NM_057100	N, Z, AA, JJ, KK, UUU	growth arrest specific 6 (Gas6), mRNA. 11/2002 Length = 2573	ESTs, Highly similar to growth arrest specific 6 [Rattus norvegicus] [R.norvegicus]
3877	17709	NM_057101	E, J, W, UU, III,	Cytochrome P450, subfamily XXI (steroid 21- hydroxylase) (Cyp21), mRNA. 10/2002 Length = 1964	Tenascin X

TABL	<b>3</b> 1			AG	tomey Docket 4/921-5033-01WO Document No. 1986323.1
S99 ID.		Consent Accor Refsog ID	Model Code	Known Cene Name	Unigene Sequence Cluster Title
3881	23307	NM_057119	ннн	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10 (Sfrs10), mRNA. 11/2001 Length = 1978	splicing factor, arginine/serine- rich (transformer 2 Drosophila homolog) 10
3881	23309	NM 057119	w	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10 (Sfrs10), mRNA. 11/2001 Length =	splicing factor, arginine/serine- rich (transformer 2 Drosophila homolog) 10
3882	921		ккк	peroxisomal biogenesis factor 6 (Pex6), mRNA. 11/2001 Length =	peroxisomal biogenesis factor 6
				fertility protein SP22 (SP22), mRNA. 11/2001 Length =	
3887	15838 15839		Q, R, JJ, KK, NNN	1097 fertility protein SP22 (SP22), mRNA. 11/2001 Length = 1097	fertility protein SP22  fertility protein SP22
3890	17477	NM 057194	w	phospholipid scramblase 1 (Plscr1), mRNA. 11/2002 Length =	phospholipid scramblase 1
3893	14126	NM_057208	w	tropomyosin 3, gamma (Tpm3), mRNA. 11/2001 Length = 1101	R.norvegicus mRNA for tropomyosin isoform 6, tropomyosin 3, gamma
3914	9952	NM_080902	C, General Alternate	hypoxia induced gene 1 (Hig1), mRNA. 1/2002 Length = 355 proteasome	hypoxia induced gene 1
3922	18810	NM_130430	000	(prosome, macropain) 26S subunit, non- ATPase, 9 (Psmd9), mRNA. 1/2002 Length = 1448	mitochondrial H+-ATP synthase alpha subunit

TABL	ደ 1			A	iomey Docket 44921-5033-011WO Document No. 1995323.1
	erec Bro	Kefseq ID	Model Code	Known Gens Nams	ellii retevid concupce cneginu
3928	7863	NM_130823	11	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16 kDa (Atp6l), mRNA. 2/2002 Length = 1082	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16 kDa
3928	7865	NM_130823	000	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16 kDa (Atp6l), mRNA. 2/2002 Length = 1082	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16 kDa
3320	7000	1441_100020		splicing factor YT521- B (YT521), mRNA. 3/2002 Length =	
3942	9571			2968 natural killer cell group 7 sequence (Nkg7), mRNA. 11/2002 Length = 813	splicing factor YT521-B natural killer cell group 7 sequence
3950	745	NM 133567	нн	centaurin, alpha 1 (Centa1), mRNA. 3/2002 Length = 1281	centaurin, alpha 1
3952	1183	NM_133578	Q	MAP-kinase phosphatase (cpg21) (Cpg21), mRNA. 3/2002 Length = 2436	MAP-kinase phosphatase (cpg21)
3953	15029	NM_133583	NN, FFF, General Core Tox Markers	N-myc downstream- regulated gene 2 (Ndrg2), mRNA. 3/2002 Length = 1998	N-myc downstream-regulated gene 2
3953	16993	NM_133583	A, B, H, NN, OO, FFF, III, JJJ, PPP, QQQ, General Core Tox Markers	N-myc downstream- regulated gene 2 (Ndrg2), mRNA. 3/2002 Length = 1998	N-myc downstream-regulated gene 2

TABL	<b>E</b> 1				termay Docket 44921-5033-011W0 Document No. 1985323.1
Seq [D	ID No.	(Continui Ace or (Reference)	Model Code	Known Cene Neme	Unigene Sequence Cluster Title
3954	4312	NM_133586		carboxylesterase 2 (intestine, liver) (Ces2), mRNA. 3/2002 Length = 1902	carboxylesterase 2 (intestine, liver)
3965	23321	NM_134407	C, K, W, BB, CC, NN, OO, GGG, III, JJJ, LLL	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) (Akr7a2), mRNA. 3/2002 Length = 1272	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
3965	23322	NM_134407	L, BB, CC, NN, OO	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) (Akr7a2), mRNA. 3/2002 Length = 1272	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
3974	61	NM_138510	General Alternate	20 alpha- hydroxysteroid dehydrogenase (LOC171516), mRNA. 4/2002 Length = 1215	20 alpha-hydroxysteroid dehydrogenase
3977	21439	NM_138533	S, General Core Tox Markers, General Alternate	F-spondin (LOC171569), mRNA. 4/2002 Length = 2325	F-spondin
3980	16922	NM_138549	S, Z, AA, General Alternate	synaptic glycoprotein SC2 (SC2), mRNA. 4/2002 Length = 1178	synaptic glycoprotein SC2
3980	25479	NM_138549	A, B, S, Z, AA, FF, General Alternate	synaptic glycoprotein SC2 (SC2), mRNA. 4/2002 Length = 1178	synaptic glycoprotein SC2
3985	5719	NM_138871	DD, EE	tudor repeat associator with PCTAIRE 2 (Pctaire2bp), mRNA. 4/2002 Length = 3874	tudor repeat associator with PCTAIRE 2
3990	5656	NM_138885	ccc	golgi-associated protein GCP360 (LOC192243), mRNA. 4/2002 Length = 10,170	golgi-associated protein GCP360

TABL	₹¶.		The second second	A	iomey Dockei 44921-5093-011W0 Document No. 1935323.1
Seq : (D	10 kg.	CONSIDERA ACCOR ROBER	Modal Codo , ,	Known Cene Name	Unigene Sequence Cluster Ville
3991	3015	NM_138895	Т	polyubiquitin (Loc192255), mRNA. 4/2002 Length = 1115	polyubiquitin
3992	7635	NM 138896	K, M, ZZ,	rotein carrying the RING-H2 sequence motif (Neurodap1), mRNA. 4/2002 Length = 4758	rotein carrying the RING-H2 sequence motif
0002	7 000	100000		rotein carrying the RING-H2 sequence motif (Neurodap1), mRNA. 4/2002	rotein carrying the RING-H2
3992	7636	NM_138896	ZZ, AAA	Length = 4758 mitochondrial acyl- CoA thioesterase 1 (Mte1), mRNA.	sequence motif
3994	18083	NM_138907	BBB, RRR, SSS	4/2002 Length = 1711 defender against cell	mitochondrial acyl-CoA thioesterase 1
3995	21915	NM_138910	Z, AA, OO	death 1 (Dad1), mRNA. 11/2002 Length = 342 defender against cell	defender against cell death 1
3995	21916	NM_138910	00	death 1 (Dad1), mRNA. 11/2002 Length = 342	defender against cell death 1
3996	11840	NM 138911	H, Z, AA, DD	stress-induced- phosphoprotein 1 (Hsp70/Hsp90- organizing protein) (Stip1), mRNA. 4/2002 Length = 1632	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)
0000	11040	100317	,	peptidylprolyl isomerase C- associated protein (Ppicap), mRNA. 5/2002 Length =	peptidylprolyl isomerase C-
4001	16444	NM_139096	0, P, 00, VV	2151 CD48 antigen	associated protein
4005	17854	NM_139103	О, Р	(Cd48), mRNA. 5/2002 Length = 1422	CD48 antigen
4007	14463	NM_139110	Z, AA	G protein-coupled hepta-helical receptor lg-Hepta (Ig-Hepta), mRNA. 5/2002 Length = 4951	G protein-coupled hepta-helical receptor Ig-Hepta

TABL	<b>3</b> 1			A	torney Docket 44921-5033-01WO Document No. 1935323.1
Seq (D)	ELEC	Consonk Ace or Roßeg (D	Model	Known Cene Name.	ellii retevid eencupes eneginu
			M, V, FFF, General	ribosomal protein L15	
4008	15239	NM_139114	Core Tox Markers V, UU,	(Rpl15), mRNA. 5/2002 Length = 691 pincher (Ehd4),	ribosomal protein L15 pinocytic chaperone; similar to
4013	19150	NM_139324	General Alternate	mRNA. 11/2002 Length = 3438 Na+/Pi-cotransporter	Homo sapiens EHD4 and mouse Past2
4017	4949	NM_139338	D	type IIc (LOC246234), mRNA. 11/2002 Length = 2075 peptide/histidine	Rattus norvegicus mRNA for Na+/Pi-cotransporter type IIc, complete cds
4018	6735	NM_139341	к	transporter PHT2 (Pht2), mRNA. 11/2002 Length = 1979	Rattus norvegicus mRNA for peptide histidine transporter 1 homolog rPHT2, complete cds
4020	15703	NM_144750	E, FFF, General Alternate	Lysophospholipase (LOC246266), mRNA. 11/2002 Length = 2525	Rattus norvegicus mRNA for Lysophospholipase, complete cds
4021	11494	NM 144755	Q, W	kinase (LOC246273), mRNA. 11/2002 Length = 2004	ESTs, Weakly similar to A53621 AMP-activated protein kinase - rat [R.norvegicus]
4025	16345	NM_145724	RR	zinc finger protein Y1 (RLZF-Y) (RIzfy), mRNA. 11/2002 Length = 2472	Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds
4039	8278	NM_148892	Q, R	factor 1 (Ostf1), mRNA. 11/2002 Length = 835	ESTs, Weakly similar to BRCA1- associated RING domain protein 1 [Rattus norvegicus] [R.norvegicus]
4044	20784	NM_153308	Z, AA, HH, WW	NMDA receptor glutamate-binding chain (Grina), mRNA. 10/2002 Length = 1742	ESTs, Moderately similar to S19586 N-methyl-D-aspartate receptor glutamate-binding chain - rat [R.norvegicus]
4071	18647	S69316	LL		ESTs, Weakly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
4076	1460	S76054	G, H, VV, General Alternate	·	ESTs, Highly similar to K2C8_RAT Keratin, type II cytoskeletal 8 (Cytokeratin 8) (Cytokeratin endo A) [R.norvegicus]

TABL	न द			00	orney Docket 44921-5058-01WO
المركانا	ຸ			649	Document No. 1925323.1
		Gentant.	<u> </u>		
Seq	GLGC :		Model		
D .; .	(ID K)@. :	Re(Seq (D :	Code	Known Cene Name	Unigene Sequence Cluster Title
					Rattus norvegicus clone 15
					polymeric immunoglobulin
1					receptor mRNA, 3'UTR
4085	110	U01145	D, F		microsatellite repeats
				A kinase anchor	
4086	347	U01914	Q, WW	protein 8	A kinase anchor protein 8
					Rattus norvegicus clone 15
1	1				polymeric immunoglobulin
1			MM, SS,		receptor mRNA, 3'UTR
4088	111	U02506	NNN, TTT		microsatellite repeats
		1			Rattus norvegicus Sprague-
			E, S, MM,		Dawley fibrinogen B beta chain
4091	2010	U05675	KKK, TTT		mRNA, complete cds
					ESTs, Highly similar to 2019405A
1		1			upstream regulator element-
			•		binding protein [Rattus
4094	2686	U08214	Q, R		norvegicus] [R.norvegicus]
					Rattus norvegicus clone ubc2e
			Q, R, ZZ,		ubiquitin conjugating enzyme
4100	22039	U13176	AAA		(E217kB) mRNA, complete cds
					Rattus norvegicus lamina
					associated polypeptide 1C
					(LAP1C) mRNA, complete cds,
	•	1			Rattus norvegicus tamina-
					associated polypeptide 1C
4105	1949	U19614	XX, YY		(LAP1C) mRNA, complete cds
	}			solute carrier family	
	<u> </u>			17 vesicular	
ŀ				glutamate	
			GG, JJJ,	transporter), member	solute carrier family 17 vesicular
4114	1558	U28504	NNN	1	glutamate transporter), member 1
1		1		solute carrier family	
1		1		17 vesicular	
		1		glutamate	
				transporter), member	solute carrier family 17 vesicular
4114	1559	U28504	NNN	1	glutamate transporter), member 1
	}	1	M, VV,		
			DDD,		
			GGG,		
1			LLL, UUU,		
			General		
	4.77	110004	Core Tox	D	D
4118	1478	U32314	Markers	Pyruvate carboxylase	Pyruvate carboxylase

TABL	≣1			ĀG	torney Docket 44921-5033-011WO Document No. 1935323.1
S09 :	(D) (Mo.		Model Code	Known Gene Name	Unigeno Sequence Cluster Title
4118	1479	U32314	M, X, VV, DDD, GGG, LLL, UUU, General Core Tox Markers NN, PP,	Pyruvate carboxylase	Pyruvate carboxylase
4120	154	U32681	EEE, MMM	deleted in malignant brain tumors 1	deleted in malignant brain tumors 1
4120	155	U32681	BB, CC, NN, PP, QQ, EEE, MMM	deleted in malignant brain tumors 1	deleted in malignant brain tumors
4127	18038	U39943	CC, NN, OO, BBB, CCC, General Alternate		Rattus norvegicus cytochrome P450 pseudogene (CYP2J3P1) mRNA
4128	18036	U40004	G, H, OO, General Alternate		Rattus norvegicus cytochrome P450 pseudogene (CYP2J3P1) mRNA
4129	1623	U41164	N	Cys2/His2 zinc finger protein (rKr1)	Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) mRNA, complete cds
4132	2685	U47312	Q, R, PP, QQ	CTD-binding SR-like	ESTs, Highly similar to 2019405A upstream regulator element-binding protein [Rattus norvegicus] [R.norvegicus]
4134	734	U49055	N, PP,	protein rA8	CTD-binding SR-like protein rA8
4137	746	U51013	QQ, XX, YY	centaurin, alpha 1 SH2-8 PH domain	centaurin, alpha 1
4146	1439	U57391	ww	containing signaling mediator 1	SH2-B PH domain containing signaling mediator 1
4156	904	U67082	DDD	Kruppel associated box (KRAB) zinc finger 1	Kruppel associated box (KRAB) zinc finger 1
4159	15516	U68544	N		Rattus norvegicus cyclophilin D mRNA, nuclear gene encoding mitochondrial protein, complete cds

TABL	를 <b>1</b>				tomay Docket 44921-5038-01WO
المركية الم	<u> </u>				1000 February 1222 Pebruary 1012 1932 P. (1013 Inserver)
		CONSTANT AGG OT	Model	Manage Const.	
(D)	ID No.:	Roisog ID .		CANOWA CENE REMO	Unigene Sequence Civster Tille
			I, J,	Dratain kinana aAAAD	
1			OOO, General	Protein kinase, cAMP dependent,	Protein kinase, cAMP dependent,
4169	1314	U75932	Alternate	regulatory, type 1	regulatory, type 1
11.00	1011	10,0002		rogalatory, typo i	regulatory, type :
			O, P, GG,		
			PP, QQ,		
4179	9841	U94856	XX, YY	paraoxonase 1	paraoxonase 1
		Í			
l .			A, B, BB, CC, GG,		
			HH, NN,		
ł		-	00, PP,		
1			QQ, BBB,		
1			ccc,	,	
	1		ннн,		<b> </b>
			PPP,		
4179	9842	U94856	QQQ	paraoxonase 1	paraoxonase 1
4184	20818	X02904	G	glutathione S- transferase, pi 2	glutathione S-transferase, pi 2
4104	20010	702904	G	transierase, pr z	ESTs, Highly similar to
1	1				TBB1 RAT TUBULIN BETA
		:			CHAIN (T BETA-15)
					[R.norvegicus], Rat mRNA for
4186	1700	X03369	NN, UU		beta-tubulin T beta15
			00 00		ESTs, Moderately similar to
4196	19584	X13905	QQ, RR, UU		TVRTYP GTP-binding protein
4231	1141	X59601	UU, KKK	plectin	Rab1 - rat [R.norvegicus] plectin
1201			00, 1440	produr	picouri
			II, JJ, KK,		
1			DDD,		
1	-		FFF,		
			GGG,		ESTs, Highly similar to
4238	4441	X62146	General Alternate		RL11_HUMAN 60S ribosomal
4230		AUZ 140	G, H, JJ,		protein L11 [R.norvegicus]
1			KK. UU.		
			GGG,		
1	•		ннн,		ESTs, Highly similar to RL3_RAT
			General		60S RIBOSOMAL PROTEIN L3
4239	13646	X62166	Alternate		(L4) [R.norvegicus]
			Z, AA, OO, JJJ,		ESTs, Highly similar to R3RT25
4241	15387	X62482	00, 333, NNN		ribosomal protein S25, cytosolic [validated] - rat [R.norvegicus]
7271	.0007	702702	141414	· · · · · · · · · · · · · · · · · · ·	ESTs, Highly similar to R3RT3A
			General		ribosomal protein L23a, cytosolic
4248	20844	X65228	Alternate		[validated] - rat [R.norvegicus]
				prolyl 4-hydroxylase	prolyl 4-hydroxylase alpha
4265	23302	X78949	AA, RR	alpha subunit	subunit

TABL	<b>E</b> 1			A A	torney Docket 44921-5033-011WO Document No. 1935326.1
509 (D)	99.19 (U. Ko.	Conson: Accor Ressen ID	Model Code	Known Cene Name	Unigene Sequence Cluster Tille
4270 4278	537 18031	X83231 X94551	D RR	pre-alpha-inhibitor, heavy chain 3 laminin, gamma 1	pre-alpha-inhibitor, heavy chain 3 laminin, gamma 1
4286	3831	Y12635	O, P, Q, II, MM, VV, PPP, TTT	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta 56/58 kDa, isoform 2	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta 56/58 kDa, isoform 2
220	10157	AA819527	XX, YY	HHs:amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	ESTs, Highly similar to S23094 beta-amyloid protein precursor - rat [R.norvegicus]
1018	10155	AA956735	V	HHs:amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	ESTs, Highly similar to S23094 beta-amyloid protein precursor - rat [R.norvegicus]
2503	23013	AI230743	O, VV, HHH	actin-related protein 3	actin-related protein 3
4211	20872	X51707	F, K, II, JJ, KK, VV, EEE, FFF, GGG, MMM, General Alternate	ribosomal protein S19	ESTs, Highly similar to R3RT19 ribosomal protein S19, cytosolic [validated] - rat [R.norvegicus]
32	20843	AA799545	vv		ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) [R.norvegicus]
887	12301	AA944727	EE, PP, QQ, III, JJJ, NNN		ESTs, Weakly similar to A44437 regenerating liver inhibitory factor RL/IF-1 - rat [R.norvegicus]
1375	3693	Al011448	GG		ESTs, Highly similar to A49128 cell-fate determining gene Notch2 protein - rat [R.norvegicus] ESTs, Highly similar to 0506206A
1409	2250	Al012354	Q, R		histone H2B [Rattus norvegicus] [R.norvegicus]
1955	22598	Al137506	U, BB, EEE, MMM		ESTs, Weakly similar to A29035 thyroid hormone-regulated proteinase inhibitor - rat (fragment) [R.norvegicus]

TABL	<b>E</b> 1	S.L.		A	тоттау Docket 44921-5063-01000
S09 (D)		Constant Accor		Known Cene Name	Document No. 1985323.1 Unigene Sequence Cluster Tille
w :		၂၀၀၈ ဇေဍ (၁၁ ၄.	0003		ESTs, Weakly similar to S44204 procollagen-proline dioxygenase (EC 1.14.11.2) alpha chain - rat
2165	6678	AI175454	Q, R		[R.norvegicus] ESTs, Weakly similar to
					CAG7_RAT ÁLPHA-N- ACETYLGALACTOSAMINIDE ALPHA-2,6- SIALYLTRANSFERASE
2256	16175	AI177145	XX, YY		(ST6GALNACIII) (STY) [R.norvegicus]
2506	20055	Al230762	V, EEE, MMM		ESTs, Weakly similar to A53742 calponin, acidic - rat [R.norvegicus]
			A, B, H, S, GGG,		ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA)
2635	13294	Al233731	ннн		[R.norvegicus]
3409	18141	NM_019383	Y, JJ	ATP synthase subunit d (Atp5jd), mRNA. 11/2000 Length = 581 ATP synthase subunit d (Atp5jd), mRNA. 11/2000	ATP synthase subunit d, ESTs, Moderately similar to T46317 hypothetical protein DKFZp434A0612.1 - human [H.sapiens]
3409	22727	NM 019383	GG	Length = 581	ATP synthase subunit d
3511	19375	NM_022699	AA	ribosomal protein L30 (Rpl30), mRNA. 11/2002 Length = 392	EST, Moderately similar to R6RT30 ribosomal protein L30, cytosolic [validated] - rat [R.norvegicus]
3608	19161	NM 031111	ww	ribosomal protein S21 (Rps21), mRNA. 11/2002 Length = 359	ribosomal protein S21
3608	19162	NM_031111	ccc	ribosomal protein S21 (Rps21), mRNA. 11/2002 Length = 359 ribosomal protein	ribosomal protein S21
3862	15468	NM_053982	F	S15a (Rps15a), mRNA. 11/2001	ribosomal protein S15a EST, Moderately similar to
3862	19544	NM_053982	KK	S15a (Rps15a), mRNA. 11/2001 Length = 449	JC2234 ribosomal protein S15a, cytosolic [validated] - rat [R.norvegicus]

TABL	E1		· · · · · · · · · · · · · · · · · · ·	A9 	torney Docket 44921-5068-01WO 
500 [D	ELEC	Refeed ID Resor	Moddi Codo	Known Cene Name	Unigene Sequence Cluster Title
				monokine induced by gamma interferon (Mig), mRNA.	ESTs, Weakly similar to JN0572 neutrophil chemo-attractant Gro
4023 147	9845 2830	NM_145672 AA818025	EEE, MMM XX, YY	11/2002 Length = 386 CD59 antigen	protein precursor - rat [R.norvegicus] CD59 antigen
14/	2030	7440 10023	/// 11 ·	CD39 artiger	CD39 antigen
147	2831	AA818025	L, XX, YY	CD59 antigen signal peptidase	CD59 antigen
1611	3550	AI058606	I, J	complex (18kD)  Cytochrome c	signal peptidase complex (18kD)
1872	23574	Al104520	LL	oxidase subunit VIa (liver)	Cytochrome c oxidase subunit Vla (liver)
2558	573·	Al232087	A, B, M, OOO, UUU, General Core Tox Markers F, PP,	hydroxyacid oxidase 3 (medium-chain) Glutathione-S-	hydroxyacid oxidase 3 (medium- chain)
2905	21011	H32189	QQ, TT, DDD	transferase, mu type 2 (Yb2)	Glutathione-S-transferase, mu type 2 (Yb2)
2922	21012	J02592	GG, NN, OO, EEE, LLL, MMM	Glutathione-S- transferase, mu type 2 (Yb2)	Glutathione-S-transferase, mu type 2 (Yb2)
2925	17284	J02827	vv, xx,	Branched chain alpha-ketoacid dehydrogenase subunit E1 alpha	Branched chain alpha-ketoacid dehydrogenase subunit E1 alpha
2926	21014	J03914	N, BB, CC, NN	Glutathione-S- transferase, mu type 2 (Yb2)	Glutathione-S-transferase, mu type 2 (Yb2)
2949	3548	L11319	MMM	signal peptidase complex (18kD)	signal peptidase complex (18kD)
2949	3549	L11319	O, HH, XX, YY, PPP, QQQ	signal peptidase complex (18kD)	signal peptidase complex (18kD)
3121	15616	NM_012699	Q	dnaJ homolog, subfamily b, member 9 (Dnajb9), mRNA. 11/2002 Length = 1936	DnaJ (Hsp40) homolog, subfamily B, member 9
3251	21013	NM_017014	F, N, DD, EE, TT, DDD	Glutathione-S- transferase, mu type 2 (Yb2) (Gstm2), mRNA. 11/2000 Length = 1055	Glutathione-S-transferase, mu type 2 (Yb2)

TABL	<b>3</b> 1		1 (1) (2) 1 (2) (3) (4)	A	Normsy Docket 44921-5033-01W0 Document No. 1935323.1
Seq:		Recessor ID Accor Comeanix	Model Code		Unigano Sequence Cluster Title
3251	21015	NM_017014	F, K, N, TT, DDD	Glutathione-S- transferase, mu type 2 (Yb2) (Gstm2), mRNA. 11/2000 Length = 1055	Glutathione-S-transferase, mu type 2 (Yb2)
3293	21975	NM 017154	E, FF, LLL, RRR, SSS, UUU, General Alternate	xanthine dehydrogenase (Xdh), mRNA. 11/2002 Length = 4198	xanthine dehydrogenase.
				vitronectin (Vtn),	·
3361	24362	NM 019156	M, N, SS	mRNA. 11/2002 Length = 1588	vitronectin
·				complement component 1, q subcomponent, beta polypeptide (C1qb), mRNA. 11/2002	complement component 1, q
3383	21443	NM_019262	NN	Length = 1136	subcomponent, beta polypeptide
3420	20816	NM_021261	O, P, NN, OO	thymosin, beta 10 (Tmsb10), mRNA. 1/2002 Length = 539	thymosin, beta 10
3430	17976	NM_021739	Z, AA	Ca++/calmodulin- dependent protein kinase II, beta subunit (Camk2b), mRNA. 11/2002 Length = 1840	Ca++/calmodulin-dependent protein kinase II, beta subunit
3681	18074	NM 031738	RR, UU	solute carrier family 29, member 2 (Slc29a2), mRNA. 11/2002 Length = 1678	solute carrier family 29 (nucleoside transporters), member 2
3709	16535	 NM_031853	Q, R, U, YY	diazepam binding inhibitor (Dbi), mRNA. 11/2002 Length = 512	Diazepam binding inhibitor (GABA receptor modulator, acyl- Coenxyme A binding protein)
3819	18174	NM_053752	ввв, ссс	succinate-CoA ligase, GDP-forming, alpha subunit (Suclg1), mRNA. 11/2001 Length = 1684	succinate-CoA ligase, GDP- forming, alpha subunit

TABL	E 1		.i.s.	A	tornay Docket 4X221-5033-01WO Document No. 1985323.1
Seq.,		Consent Accor Resseq ID	Model Codo ;	Known Cone Name	Unigene Sequence Cluster Title
3819	18175	NM_053752	L, U, BBB, CCC, RRR	succinate-CoA ligase, GDP-forming, alpha subunit (Suclg1), mRNA. 11/2001 Length = 1684	succinate-CoA ligase, GDP- forming, alpha subunit
3998	15134	NM_139081	E, K	Ornithine decarboxylase antizyme (Oaz), mRNA. 10/2002 Length = 1046	ESTs, Highly similar to OAZ_RAT Ornithine decarboxylase antizyme (ODC-Az) [R.norvegicus]
4257	23576	X72757	HH, LL	Cytochrome c oxidase subunit VIa (liver)	Cytochrome c oxidase subunit Vla (liver)
43	18333	AA799614	V		ESTs, Moderately similar to sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae) [Rattus norvegicus] [R.norvegicus]
242	22820	AA848315	GGG, General Alternate		ESTs, Weakly similar to guanosine monophosphate reductase [Rattus norvegicus] [R.norvegicus]
422	309	AA866460	BB, CC, OO, EEE, MMM		ESTs, Weakly similar to T42737 gp330 protein precursor - rat [R.norvegicus]
747	15577	AA924557	C, FF		ESTs, Highly similar to vesicle- associated calmodulin-binding protein [Rattus norvegicus] [R.norvegicus]
776	5110	AA925274	E, BB, UU, General Alternate		ESTs, Highly similar to OKRT2R protein kinase (EC 2.7.1.37), cAMP-dependent, type II-alpha regulatory chain - rat (fragment) [R.norvegicus]
992	5111	AA955729	CC, LL, UU		EST, ESTs, Highly similar to OKRT2R protein kinase (EC 2.7.1.37), cAMP-dependent, type II-alpha regulatory chain - rat (fragment) [R.norvegicus]
1038	1095	AA957676	D	thyroid hormone receptor interactor 10	thyroid hormone receptor interactor 10
1159	23502		General Alternate	·	ESTs, Weakly similar to A60716 somatotropin intron-related protein RDE.25 - rat (fragment) [R.norvegicus]

TABL	<b>E</b> 1			A	tomey Docket 44921-5088-01000 Document No. 1995:23.1
Seq ; ID ::	id kar gege	Conson: Acc or RefSeq ID	Model Code	Known Cone Name	Unigene Sequence Cluster Title
1284	18125	Al008787	FF, BBB		ESTs, Highly similar to S16788 probable reverse transcriptase - rat [R.norvegicus]
1326	6832	AI009685	N		ESTs, Weakly similar to S19597 transcription factor SOX4 - rat [R.norvegicus]
1491	7502	Al029647	xx		ESTs, Weakly similar to ACBP_RAT ACYL-COA- BINDING PROTEIN (ACBP) (DIAZEPAM BINDING INHIBITOR) (DBI) (ENDOZEPINE) (EP) [R.norvegicus]
2092	18126	Al171369	RRR		ESTs, Highly similar to S16788 probable reverse transcriptase - rat [R.norvegicus]
2131	15673	AI172107	G, LLL, SSS, UUU	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)
2340	22258	Al179357	нн		ESTs, Weakly similar to A53798 58K membrane-associated protein - rat [R.norvegicus]
2683	14923	Al235223	SS		ESTs, Weakly similar to A60716 somatotropin intron-related protein RDE.25 - rat (fragment) [R.norvegicus]
2927 2927	1869 1870	J03959 J03959	M, GG, WW M	urate oxidase	urate oxidase
				urate oxidase glycogen synthase kinase 3 alpha (Gsk3a), mRNA. 11/2002 Length =	urate oxidase
3347	17782 24535	NM_017344 NM_022399		2155 calreticulin (Calr), mRNA. 11/2002 Length = 1882	glycogen synthase kinase 3 alpha calreticulin
	24537		M, FF	calreticulin (Calr), mRNA. 11/2002 Length = 1882	calreticulin
3690	22828	NM_031787	YY	homeodomain- interacting protein kinase 3 (Hipk3), mRNA. 5/2001 Length = 4120	homeodomain-interacting protein kinase 3

TABL	31	· ·		A	formey Docket 44921-5088-91W0
	,	(7 o ) =			Document No. 1935323.1
Seq (D	ELEC BLCC	Keiseg (D	Modol :: Codo :::::		Unigene Sequence Cluster Title
3824	1868	NM_053768	м	urate oxidase (Uox), mRNA. 4/2002 Length = 1361	urate oxidase
3853	19942	NM_053946	K, DD, EE, PP, QQ	implantation- associated protein (IAG2), mRNA. 11/2001 Length = 1219	implantation-associated protein
4289	1426	Z48225	К	eukaryotic translation initiation factor 2B	eukaryotic translation initiation factor 2B
835	6691	AA943028	บบบ		ESTs, Highly similar to KFMS_RAT Macrophage colony stimulating factor I receptor precursor (CSF-1-R) (Fms proto- oncogene) (c-fms) [R.norvegicus]
1428	19591	Al012747	BBB		ESTs, Highly similar to BLMH_RAT Bleomycin hydrolase (BLM hydrolase) (BMH) (BH) [R.norvegicus]
1858	16915	Al104104	QQ, YY		ESTs, Highly similar to QYRTGP phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32), cytosolic - rat [R.norvegicus]
2876	19590	D87336	BBB, CCC, RRR	DT4 along the same	ESTs, Highly similar to BLMH_RAT Bleomycin hydrolase (BLM hydrolase) (BMH) (BH) [R.norvegicus]
3004	18638 18618	H33922 M24026	XX, YY Z, AA, EEE, MMM	RT1 class lb gene	RT1 class lb gene RT1 class lb gene
3101	18636	NM_012645		RT1 class lb gene (RT1Aw2), mRNA. 11/2002 Length =	RT1 class to gene
3830	18628	NM_053806	RR, XX, YY	potassium channel, subfamily K, member 6 (TWIK-2) (Kcnk6), mRNA. 11/2001 Length = 2243 CCAAT binding factor of CBF-C/NFY-	RT1 class lb gene  CCAAT binding factor of CBF-
438 484	4339 18489	AA891669	RR_	C RAB11B, member RAS oncogene family	C/NFY-C ESTs

TABL	<b>国</b> 1	×		A	tomay Docket 44921-5033-01WO :- Document No. 1985323.1
S00	(ID K)o. (GLGC	Ace or Refseq ID	Model Code	Known Cene Newe	Unigene Sequence Civeter Tible
ه در کیا	Jus 1008.	ાઉલ્લહ્સ્યું હ	0000 7,	Group-specific	
	1			component (vitamin	Group-specific component
894	17471	AA944965	LL	D-binding protein)	(vitamin D-binding protein)
				stem cell growth	
1207	25149	AB009246	GG	factor	
1			Q, MM,	multiple inositol	
	}	Ţ,	TTT, General	polyphosphate histidine	multiple inositol polyphosphate
1220	15292	AF012714	Alternate	phosphatase 1	histidine phosphatase 1
1220	13232	AI 0121 14	Atemate	tip associating	mstaire phosphatase i
1247	18731	AF093139	R	protein	tip associating protein
				Malic enzyme 1,	<u> </u>
1265	17353	AI008020	ввв, ссс	soluble	Malic enzyme 1, soluble
				serine (or cysteine)	
				proteinase inhibitor,	
				clade A (alpha-1	serine (or cysteine) proteinase
		ļ		antiproteinase, antitrypsin), member	inhibitor, clade A (alpha-1
1357	4213	AI010453	F, S, EE, SS, NNN	januurypsin), member Ia	antiproteinase, antitrypsin), member 1
1337	4213	AI010433	33, 141414	SH3/ankyrin domain	member i
1763	19647	AI100867	JJ, KK	gene 3	SH3/ankyrin domain gene 3
•	<u> </u>			Drosophila polarity	
ļ	1			gene (frizzled)	
				homologue, beta-	
				carotene 15, 15'-	beta-carotene 15, 15'-
1790	19373	Al102044	LL, NNN	dioxygenase	dioxygenase
			0.00	multiple inositol	
	1		Q, SS, General	polyphosphate histidine	multiple inositol polyphosphate
1898	15291	Al111401	Alternate	phosphatase 1	histidine phosphatase 1
-555			BB, CC,	F30P0.000 1	pop.ididoo (
			DD, EE,		
			LL, SS,		·
			DDD, III,		
			JJJ, LLL,		
0003	6470	A14.00000	NNN,	Fibrinogen, gamma	
2027	6479	Al169690	UUU	polypeptide SAC1 (supressor of	Fibrinogen, gamma polypeptide
				actin mutations 1,	SAC1 (supressor of actin
				homolog)-like (S.	mutations 1, homolog)-like (S.
2083	8240	AI171267	11	cerevisiae)	cerevisiae)
1				gamma-aminobutyric	
				acid (GABA) B	gamma-aminobutyric acid
2400	2052	Al227854	RR	receptor, 1	(GABA) B receptor, 1
				Superoxide	Superpuide dismutes 2
2703	21414	Al235842	W, NN	dismutase 2, mitochondrial	Superoxide dismutase 2, mitochondrial
2834	25233	AJ000556	T T	Janus kinase 1	micononai
	1-0-00	500000	·	odilas kinase I	

	<u> </u>				
TABL	<b>13</b> .9			AX	tomey Docket 4/42/1-5053-01WO
4.5	. · 2.	Conson!	<del></del>	<u> </u>	Document No. 1935323.1
Seq	GLGC:		Model :	Burney Barrer	The second of the second of the second
(D)	(D) (No. )	Rassag ID	Cocco	Known Cone Name	Unigene Sequence Cluster Title
			D, G, H,	Insulin-like growth	
2839	21051	D00698		factor I	Insulin-like growth factor I
				proteasome	
1	l			(prosome,	-
				macropain) subunit,	
2860	25281	D30804		alpha type 7	
			G, H, K,		·
0007	0404	D45047	BB, CC,	proteasome beta	
2867	9134	D45247	GGG	type subunit 5	
			i, L, WW,		
1			000,		
			General	P450 (cytochrome)	P450 (cytochrome)
2883	1921	E01524	Alternate	oxidoreductase	oxidoreductase
	1.02.			ATPase, H+,K+-	
				transporting, alpha /	
				(gastric H,K-ATPase	
2923	1577	J02649	D	catalytic subunit)	
				6-Phosphofructo-2-	6-Phosphofructo-2-
				kinase/fructose-2,6-	kinase/fructose-2,6-
			JJ, KK,	bisphosphatase 1	bisphosphatase 1 (liver and
2928	174	J04197	SS	(liver and muscle)	muscle)
ł			c cc		
2937	1264	K01933	S, SS,	Haptoglobin	Haptoglobin
2937	1204	K01933	VV VV , 141414	Haptoglobin	Haptoglobiii
2956	1228	L14684	ввв. ссс	G elongation factor	G elongation factor
2961	854	L20823	RR	Epimorphin	Epimorphin
				Matrix	
ł				metalloproteinase 7	Matrix metalloproteinase 7
2965	395	L24374	SS	(matrilysin)	(matrilysin)
				Group-specific	
			M, S,	component (vitamin	Group-specific component
2984	4254	M12450	NNN	D-binding protein)	(vitamin D-binding protein)
			H, S,	9	·
			GGG,		
			PPP,		
			QQQ, General	Inculin like arouth	
2993	21052	M15481	Alternate	Insulin-like growth factor I	Insulin-like growth factor I
	-1002	10401	G, H,	idotoi i	misumi-ince grown ractor r
			PPP,	Insulin-like growth	
2993	21053	M15481	aaa	factor I	Insulin-like growth factor I
				Coagulation factor IX	
				(plasma .	
				thromboplastic	
				component,	
2000	05.466		N, WW,	Christmas disease,	
3006	25430	M26247	UUU	hemophilia B)	

				255	
TABL	<b>E</b> 1			AG	tomey Docket 44921-5033-01W0 Document No. 1985323.1
S00 [D -	ID No. GLGG	CONSINI AGG OT REFEREN	Code Model	Knovin Cene Name	Unigene Sequence Cluster Title
3019	20699	M35601	E, KKK	Fibrinogen, A alpha polypeptide	Fibrinogen, A alpha polypeptide
3019	20700	M35601	E, L, S, X, Y, NNN	Fibrinogen, A alpha polypeptide	Fibrinogen, A alpha polypeptide
3030	64	M60655	C, I, L, W, XX, YY, LLL, OOO, General Alternate	Adrenergic, alpha 1B- , receptor Retinoic acid	Adrenergic, alpha 1B-, receptor
3043	25060	M81766	D	receptor, beta	
3049	13488	M91599	v	Fibroblast growth factor receptor 4	
3049	13489	M91599	บบบ	Fibroblast growth factor receptor 4	ESTs, Highly similar to JC1450 fibroblast growth factor receptor 4 - rat [R.norvegicus]
				creatine kinase, brain (Ckb), mRNA. 11/2002 Length =	·
3070	4467	NM_012529	ZZ, AAA	1146 Fibrinogen, gamma	Creatine kinase, brain
3080	6477	NM_012559	E, N, LL, MM, KKK, NNN, TTT	polypeptide (Fgg), mRNA. 11/2000 Length = 1358	Fibrinogen, gamma polypeptide
3080	6478	NM_012559	E, J, S, X, Y, DD, EE, KKK, NNN	Fibrinogen, gamma polypeptide (Fgg), mRNA. 11/2000 Length = 1358	Fibrinogen, gamma polypeptide
3081	17237	NM_012562	XX, YY	Fucosidase, alpha-L- 1, tissue (Fuca), mRNA. 11/2002 Length = 1478	Fucosidase, alpha-L-1, tissue
		_	C, I, J, X, EE, MM, UU, WW,	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase,	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase,
3083	20744	NM_012571	Alternate	Length = 1937 Malic enzyme 1, soluble (Me1), mRNA. 11/2000	cytosolic) see also D1Mgh12
3093	18746	NM_012600	BBB	Length = 1761	Malic enzyme 1, soluble

TABL	<b>፪</b> 1	-		, AS	tomey Docket 44921-5038-01WO Document No. 1985323.1
S99 ID ≠:	ELEC;	Centant Acc or Refseg ID :	Model : . Code : :	Known Cong Name	Unigene Sequence Cluster Tille
3093	18747	NM_012600	BBB, LLL, RRR,	Malic enzyme 1, soluble (Me1), mRNA. 11/2000 Length = 1761	Malic enzyme 1, soluble
3093	18749	NM_012600	BBB, LLL, RRR,	Malic enzyme 1, soluble (Me1), mRNA. 11/2000 Length = 1761	Malic enzyme 1, sołuble
3099	172	NM 012621	JJ, KK, WW, YY	6-phosphofructo-2- kinase/fructose-2,6- bisphosphatase 1 (Pfkfb1), mRNA. 11/2002 Length = 1898	6-Phosphofructo-2- kinase/fructose-2,6- bisphosphatase 1 (liver and muscle)
3108	16198	NM 012663	BB, CC	vesicle-associated membrane protein 2 (Vamp2), mRNA. 10/2002 Length = 2071	Vesicle-associated membrane protein (synaptobrevin 2)
3108	16199	NM_012663		vesicle-associated membrane protein 2 (Vamp2), mRNA. 10/2002 Length = 2071	Vesicle-associated membrane protein (synaptobrevin 2)
3124	24545	NM_012713	D	Protein kinase C beta (Prkcb1), mRNA. 11/2000 Length = 2599 Apolipoprotein A-IV	Protein kinase C beta
3132	5317	NM_012737	ввв, ссс	(Apoa4), mRNA. 5/2002 Length = 1423 Inhibitor of DNA	Apolipoprotein A-IV
3144	10247	NM_012797	V	binding 1, helix-loop- helix protein (splice variation) (Id1), mRNA. 10/2002 Length = 1124	Inhibitor of DNA binding 1, helix- loop-helix protein (splice variation)
3144	10248	NM_012797	DD, EE, JJJ, General Core Tox Markers	Inhibitor of DNA binding 1, helix-loop- helix protein (splice variation) (Id1), mRNA. 10/2002 Length = 1124	Inhibitor of DNA binding 1, helix- loop-helix protein (splice variation)

TABU	ड १.			A	tomey Docket 44921-5033-01W0 Document No. 1935323.1
509 : ID	erec	indensity Accor Refseq ID	Model : Code . :	Known Cene Neme	Unigene Sequence Civeter Title
3154	11137	NM_012839	D, MM, FFF, TTT	cytochrome c, somatic (Cycs), mRNA. 11/2002 Length = 318	Cytochrome C, expressed in somatic tissues
3154	11138	NM_012839		cytochrome c, somatic (Cycs), mRNA. 11/2002 Length = 318	Cytochrome C, expressed in somatic tissues
3164	23651	NM 012881	EEE, MMM	secreted phosphoprotein 1 (Spp1), mRNA. 11/2002 Length = 1457	Sialoprotein (osteopontin)
5104		012001		Protein disulfide isomerase (Prolyl 4- hydroxylase, beta polypeptide) (P4hb),	Protein disulfide isomerase
3191	19391	NM_012998	U, FF, RRR	mRNA. 11/2000 Length = 2460 Protein disulfide	(Prolyl 4-hydroxylase, beta polypeptide)
3191	19392	NM_012998	D, BB	isomerase (Prolyl 4- hydroxylase, beta polypeptide) (P4hb), mRNA. 11/2000 Length = 2460	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide)
3191				Protein disulfide isomerase (Prolyl 4- hydroxylase, beta polypeptide) (P4hb), mRNA. 11/2000	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta
3191	19393 23543		FF V, UU	Length = 2460 Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator) (Psap), mRNA. 11/2000 Length = 2175	polypeptide)  Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator)
			·	Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator) (Psap), mRNA. 11/2000 Length =	Prosaposin (sulfated glycoprotein,
-	23544 2667	•	MM, TTT F, T, LL, RR, EEE, MMM, General Alternate	2175 Tocopherol transfer protein alpha (Ttpa), mRNA. 11/2000 Length = 2182	sphingolipid hydrolase activator)

TABL	<b>E</b> 1	• • • • • • • • • • • • • • • • • • • •		A	tomay Docket 44921-5133-01000 Document No. 1935323.1
509 10 f	(EL&C	Consoni Asc or Roßog ID	Model : Code : : :	Known Gene Name	Unigene Sequence Cluster Tille
3209	16472	NM_013062	JJJ	FLK1 kinase insert domain receptor (VEGF receptor 2) (Kdr), mRNA. 11/2000 Length = 5892 Phosphodiesterase	FLK1 kinase insert domain receptor (VEGF receptor 2)
3219	24	NM_013101	Z, AA, RRR, SSS		Phosphodiesterase 4A
3235	397	NM_013214	I, J, U, FF, BBB	acyl-CoA hydrolase (RBACH), mRNA. 11/2000 Length = 1523 acyl-CoA hydrolase	brain acyl-CoA hydrolase
3235	20851	NM_013214	BBB, CCC, RRR, SSS	(RBACH), mRNA. 11/2000 Length = 1523 B-cell	brain acyl-CoA hydrolase
3245	24897	NM_016993	QQ	leukemia/lymphoma 2 (Bcl2), mRNA. 11/2002 Length = 1179	B cell lymphoma 2 associated oncogene
3250	18988	NM_017013	V, NN, · OO	glutathione-S- transferase, alpha type2 (Gsta2), mRNA. 11/2002 Length = 831	Glutathione-S-transferase, alpha type (Ya)
3262	682	NM_017051	EEE, MMM	Superoxide dismutase 2, mitochondrial (Sod2), mRNA. 11/2002 Length = 1492	Superoxide dismutase 2, mitochondrial
3268	11150	NM_017073	II, RR, TT, DDD	Glutamine synthetase (glutamate-ammonia ligase) (Glul), mRNA. 11/2000 Length = 2793	Glutamine synthetase (glutamate- ammonia ligase)
3268	11151	NM_017073		Glutamine synthetase (glutamate-ammonia ligase) (Glul), mRNA. 11/2000 Length = 2793	Glutamine synthetase (glutamate- ammonia ligase)

TABL	图1			A	iomey Doctet 44921-5033-01WC Document No. 1935323.1
Seq.,	ID Kor Grec	Consonk Acc or Refseg ID	Model Code	Known Cene Name	Unigene Sequence Cluster Tille
3268	11152	NM_017073	UU, DDD,	Glutamine synthetase (glutamate-ammonia ligase) (Glul), mRNA. 11/2000 Length = 2793	Glutamine synthetase (glutamate- ammonia ligase)
3268	11153	NM_017073		Glutamine synthetase (glutamate-ammonia ligase) (Glul), mRNA. 11/2000 Length = 2793	Glutamine synthetase (glutamate- ammonia ligase)
3288	20859	NM_017144	D, U, BBB, CCC, RRR, SSS		Troponin I
3331	12350	NM_017290	PP, QQ	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (Atp2a2), mRNA. 11/2002 Length = 5648	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
3339	20789	NM_017319	M, U, LL	glucose regulated protein, 58 kDa (Grp58), mRNA. 11/2002 Length = 1874	glucose regulated protein, 58 kDa
3397	889	NM_019346		solute carrier family 14, member 1 (Slc14a1), mRNA. 11/2002 Length = 1412	solute carrier family 14, member 1
3406	20298	NM_019374		prodynorphin (Pdyn), mRNA. 11/2002 Length = 747 tyrosine 3-	prodynorphin
3407	15680		Q, R, PPP, QQQ	monooxgenase/trypto phan 5- monooxgenase activation protein, gamma polypeptide (Ywhag), mRNA. 11/2002 Length = 3410	14-3-3 protein gamma-subtype
3413	15911	NM_019907	ZZ, AAA	postsynaptic protein Cript (Cript), mRNA. 11/2002 Length = 1435	postsynaptic protein Cript

TABL	ਵ <b>ੀ</b> :			A	tomey Dockst 44921-5033-011WO Document No. 1935323.1
S99 ID. :	@L@C ID No.	CONSONIA AGG OT ROSSONID :	Model Code	Known Cene Name	Unigene Sequence Cluster Title
3421	15335	NM_021264	GGG	ribosomal protein L35a (Rpl35a), mRNA. 11/2002 Length = 348	ribosomal protein L35a
3444	24321	NM 022177	G, J, S, WW, OOO, PPP, QQQ, General Core Tox Markers	Stromal cell-derived factor 1 (Sdf1), mRNA. 11/2002 Length = 1830	Stromal cell-derived factor 1
			м, нн,	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (Serpina1), mRNA. 4/2002 Length =	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin),
3477	4212		SS.	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (Serpina1), mRNA. 4/2002 Length =	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin),
3477	25681	NM_022519	SS	mitochondrial ribosomal protein L23 (Mrpl23), mRNA.	mitochondrial ribosomal protein
3479	5666	NM_022529	C, U, X, DD, EE, DDD, LLL,	1/2002 Length = 540 aquaporin 9 (Aqp9), mRNA. 11/2002	neutral solute channel aquaporin
3528	15755	NM_022960	SSS, UUU	Length = 1495 drebrin-like (DbnI),	9
3631	19096	NM_031352	L	mRNA. 11/2002 Length = 1750 Interleukin 1 beta	drebrin-like
3636	24710	NM_031512	w	(II1b), mRNA. 11/2002 Length = 1329	Interleukin 1 beta

				501	
TABL	물 <b>1</b>			<b>3</b> 0A	tomey Docket 44921-5033-01WO Document No. 1995323.1
S09 ID :	D Kof	(COLEGE) (C) (C) (C) (C) (C) (C) (C) (C) (C) (C	Model :: Code	Kinown Gene Name	Unigene Sequence Cluster Title
3643	4010	NM_031543	EE, MM, TTT	Cytochrome P450, subfamily 2e1 (ethanol-inducible) (Cyp2e1), mRNA. 11/2002 Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-inducible)
3643	4011	NM_031543	K, O, P, FF, II, NN, OO, QQ, EEE, MMM	Cytochrome P450, subfamily 2e1 (ethanol-inducible) (Cyp2e1), mRNA. 11/2002 Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-inducible)
3643	4012	NM_031543	T, EE, FF, MM, EEE, MMM, TTT	Cytochrome P450, subfamily 2e1 (ethanol-inducible) (Cyp2e1), mRNA. 11/2002 Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-inducible)
3651	1919	NM_031576	I, L, WW	P450 (cytochrome) oxidoreductase (Por), mRNA. 11/2002 Length = 2441	P450 (cytochrome) oxidoreductase
3651	1920	NM 031576	C, I, L, MM, WW, OOO, TTT, General Alternate	P450 (cytochrome) oxidoreductase (Por), mRNA. 11/2002 Length = 2441	P450 (cytochrome) oxidoreductase
3665	9428	NM 031656	RR	syntaxin 8 (Stx8), mRNA. 11/2002 Length = 859	syntaxin-like protein 3l35
		_	C, PPP, QQQ, General	MYB binding protein 1a (Mybbp1a), mRNA. 11/2002	
3731	17933	NM_031668 NM_032615	U, BBB, CCC, RRR, SSS	Length = 3834 membrane interacting protein of RGS16 (Mir16), mRNA. 11/2002 Length = 1203	MYB binding protein (P160) 1a  membrane interacting protein of RGS16
3731	17934	NM_032615	U, V, BBB, CCC	membrane interacting protein of RGS16 (Mir16), mRNA. 11/2002 Length = 1203	membrane interacting protein of RGS16

WO 03/064624 PCT/US03/03194

TABU				* A9	tomey Docket 44921-5063-91W0 :: Document No. 1935323.1
Seq :	@L@C_	(Gaisan): Acc or Raiseg (D	Model Code	Known Gene Nema.	Unigano Sequence Cluster Tille
3731	17935	NM_032615	RRR, SSS	membrane interacting protein of RGS16 (Mir16), mRNA. 11/2002 Length = 1203	membrane interacting protein of RGS16
3746	13164	NM_053318	E, S, PP, QQ, WW	hemopexin (Hpx), mRNA 11/2002 Length = 1484	hemopexin
3773	16394	NM_053485	O, P	calcium binding protein A6 (calcyclin) (S100a6), mRNA. 11/2001 Length = 291	calcium binding protein A6 (calcyclin)
3782	14380	NM_053536	w	Kruppel-like factor 15 (Klf15), mRNA. 11/2002 Length = 2458	Kruppel-like factor 15 (kidney)
3806	13005	NM 053623	LL, BBB, CCC, RRR	fatty acid Coenzyme A ligase, long chain 4 (Facl4), mRNA. 11/2002 Length = 4862	fatty acid-Coenzyme A ligase, long chain 4
3833	16311	- NM_053818	G, H	glycine transporter 1 (Glyt1), mRNA. 11/2001 Length = 2558	glycine transporter 1
3838	20868	NM_053843	O, P, NN, OO, VV	Fc receptor, IgG, low affinity III (Fcgr3), mRNA. 11/2002 Length = 1318	Fc receptor, IgG, low affinity III
3838	20869	NM_053843	O, P, V,	Fc receptor, IgG, low affinity III (Fcgr3), mRNA. 11/2002 Length = 1318	Fc receptor, IgG, low affinity III
3932	17560	NM_133283	N	mitogen activated protein kinase kinase 2 (Map2k2), mRNA. 11/2002 Length = 1376	mitogen activated protein kinase kinase 2
3932	17564		I, J, DD, EE	mitogen activated protein kinase kinase 2 (Map2k2), mRNA. 11/2002 Length = 1376	mitogen activated protein kinase kinase 2

TABL	31			AG	torney Docket 44921-5988-91WO Document No. 1985823.1
809 ID. :	@L@& ID Ko.	CONSON ACCO ROBSOND		\	Unigene Sequence Cluster IIIIe
3932	21848	NM_133283	I, J, RRR, UUU	mitogen activated protein kinase kinase 2 (Map2k2), mRNA. 11/2002 Length = 1376 mitogen activated	mitogen activated protein kinase kinase 2
3932	21849	NM_133283	U, RRR	protein kinase kinase 2 (Map2k2), mRNA. 11/2002 Length = 1376	mitogen activated protein kinase kinase 2
3944	15542	NM_133539	G, H	mitochondrial ribosomal protein L17 (Mrpl17), mRNA. 5/2002 Length = 1102	mitochondrial ribosomal protein L17
3944	15543	NM_133539	G, H	mitochondrial ribosomal protein L17 (Mrpl17), mRNA. 5/2002 Length = 1102	mitochondrial ribosomal protein L17
3962	15017	NM 134349	M, S, DD, EE, NNN	microsomal glutathione S- transferase 1 (Mgst1), mRNA. 11/2002 Length = 883	microsomal glutathione S- transferase 1
3998	25250	NM_139081	LL	Ornithine decarboxylase antizyme (Oaz), mRNA. 10/2002 Length = 1046	
4052	1937	R46934	HH	amelogenin	amelogenin
1002	1,00,	1.10004		Asparagine	
4093	1583	U07201	JJJ	synthetase	Asparagine synthetase
4095	58	U09870	W, General Alternate	major vault protein	major vault protein
4106	202	U20181	N	iron-regulatory protein 2	iron-regulatory protein 2
4123	433	U37142	RR	Brevican	Brevican
				brain acyl-CoA	
4136	396	U49694	NNN	hydrolase	brain acyl-CoA hydrolase
4145	1286	U55938	F, UU	Sialyltransferase 8 (GT3 alpha 2,8- sialyltransferase) C	Sialyltransferase 8 (GT3 alpha 2,8-sialyltransferase) C
4149	912	U59184	QQ, UU, General Core Tox Markers	Bcl2-associated X protein	Bcl2-associated X protein

TABL	<b>E</b> 1			Α.	tomey Doctet 44921-5033-01000 Document No. 1936323.1
Soq 10:::	ELEC DEC	IMB±MII Aœ or Aœ or (1) postosi	Model Code	A STREET STREET STREETS	Unigene Sequence Cluster Title
				amine oxidase,	Jeangene declarate dicast vidas
	25083	U72632	RR	copper containing 3	
4174	906	U83112	X	forkhead box M1	forkhead box M1
4190	21054	X06107	G, H, M, S, GGG	Insulin-like growth factor I	Insulin-like growth factor I
4198	15652	X14210	BB, CC, EEE, III, JJJ, MMM	ribosomal protein S4, X-linked	
	1			6-Phosphofructo-2-	6-Phosphofructo-2-
]				kinase/fructose-2,6-	kinase/fructose-2,6-
	l ·		JJ, KK,	bisphosphatase 1	bisphosphatase 1 (liver and
4204	173	X15580	ww	(liver and muscle)	muscle)
4208	25686	X51536	G, H, JJ, KK, GGG, HHH	ribosomal protein S3	
		,	H, EEE,		
			ммм,		
1010	05007		General		
4210	25687	X51706	Alternate	ribosomal protein L9	
4226	5667	X58200	G, H, EEE, MMM, General Core Tox Markers, General Alternate	ribosomal protein L23	
		7.00200	G, H, JJ,	noodinal protein E20	
4237	25718	X62145	ннн	ribosomal protein L8	
4244	25089	X63594	I, J	Inhibitor of nuclear factor of kappa light chain gene enhancer in B-cells, alpha	
4244	25090	X63594	J	Inhibitor of nuclear factor of kappa light chain gene enhancer in B-cells, alpha	·
4251	580	X68812		solute carrier family 8 (sodium/calcium exchanger), member 1	solute carrier family 8 (sodium/calcium exchanger), member 1
	1620	X97374		Prepronociceptin (neuropeptide nociceptin) (N23K)	Prepronociceptin (neuropeptide nociceptin) (N23K)

TABL	31			A	lomey Docket 44921-5033-01WO
	V				Document No. 1935323.1
	~ ~	Consant			
Seq	@L@G		Model	00	00-0
שָׁיַיּיִי, שָׁנוֹ	(ID) (Xio.	RefSeq ID	Codo		Unigene Sequence Cluster Title
				Pyruvate	
				dehydrogenase	
4287	20426	Z12158	SS, WW	(lipoamide) alpha 1	
		1		kynurenine	
4291	1541	Z50144	F	aminotransferase II	kynurenine aminotransferase II
			<u> </u>	kynurenine	
4291	1542	Z50144		aminotransferase II	kynurenine aminotransferase II
1	25098	AA108277	Q		
2	4433	AA684641	R		ESTs
4	4438	AA684919	D, V, UU		ESTs
ŀ					ESTs, Moderately similar to
					ribosome binding protein 1
l			BB, CC,		isoform mRRp61 [Mus musculus]
5	4439	AA685175	NN, OO		[M.musculus]
		Í			
l_			RRR,		
6	16704	AA686132	SSS, UUU		
11	18289	AA686704	SS		
		·			ESTs, Highly similar to
			ĺ.		mitochondrial carrier homolog 2
12	19222	AA799279	L		[Mus musculus] [M.musculus]
					ESTs, Weakly similar to T47122
	ł				cell division protein pelota
					[imported] - fruit fly (Drosophila
13	18396	AA799330	Q, R, W		melanogaster) [D.melanogaster]
15	15083	AA799396	R		ESTs
40	00040	4.4700400	T 1/ 1/1/1/		COT-
16	20042	AA799420	T, V, KKK		ESTs
4.7	10450	44700440			FOT-
17 17	18159 18160	AA799448	D, III, JJJ		ESTs ESTs
17	10100	AA799448	X, Y		
					ESTs, Highly similar to
	1	1			CY1_HUMAN Cytochrome c1, heme protein, mitochondrial
10	4206	AA700474	_		
19 21	18290	AA799474 AA799497	F WW		precursor [H.sapiens] ESTs
<u> </u>	10290	7×1 33431	ZZ, AAA,		LUIS
			PPP,		ESTs, Weakly similar to M18.3.p
			-		
20	17687	AA799531	General Alternate		[Caenorhabditis elegans] [C.elegans]
28	1/00/	W41 9929.1			[C.elegalis]
			A, B, ZZ,		
			AAA, HHH,		
		·	PPP,		
			QQQ,		
'					ESTs, Weakly similar to M18.3.p
			General Core Tox		[Caenorhabditis elegans]
29	17690	AA700524			[Caenornabolitis elegans]
28	17688	AA799531	Markers		ESTs
29 31	18327	AA799537	L, QQ		
٦ I	24628	AA799542	KK		ESTs

TABL	<b>E</b> 1			· A	tomey Docket 44921-5038-011W0 Document No. 1935328.1
500 (D. 4	(ID KJO.)	CONSONIA ACCO ROISON ID	Model Code	Known Cene Name	Unigene Sequence Cluster Tille
	S Marie Marie Marie (1977)		V, Z, AA,	1	
34	17577	AA799566	RR	incisor protein	incisor protein
35	11353	AA799569	II, XX, YY		ESTs
					ESTs, Highly similar to T46259 hypothetical protein
l					DKFZp761E0323.1 - human
38	20971	AA799576	D		(fragment) [H.sapiens]
40	20975	AA799599	DDD		ESTs
41	16696	AA799607	DDD		ESTs
48	22909	AA799654	NNN		ESTs
			DD, EE,		
			NNN,		
48	22910	AA799654	000		ESTs
			C, MM,		
l.,			WW, ZZ,		
49	11314	AA799656	AAA, TTT		ESTs
50 51	16383 17062	AA799671 AA799680	Z, AA HH, UU		ESTs
31	17002	AA799000	Inn, 00		ESTs, Highly similar to
					SPS2 MOUSE Selenide, water
1					dikinase 2 (Selenophosphate
l				HMm:selenophospha	synthetase 2) (Selenium donor
53	2040	AA799700	MM, TTT	te synthetase 2	protein 2) [M.musculus]
					ESTs, Highly similar to
					RPB9_HUMAN DNA-directed
					RNA polymerase II 14.5 kDa
			_		polypeptide (RPB9) (RPB14.5)
54	20994	AA799717	F		[H.sapiens]
55	18346	AA799718	N, SS		ESTs
56	8768	AA799726	W, PP, QQ		ESTs
30	0700	AA199120	QQ		ESTs, Weakly similar to ATP-
					dependent RNA helicase
					[Caenorhabditis elegans]
59	8977	AA799741	Y		[C.elegans]
	<del>                                     </del>		W,		
1			General		
60	18349	AA799744	Alternate		ESTs
61	17494	AA799751	W		ESTs
			L, BB,		
			CC, FF,		
			000, Caparal		
			General Core Tox		
	1		Markers,		
			General		
62	4133	AA799762	Alternate		ESTs
64	6425	AA799784	DDD		ESTs

TABL	E1			Ä	ionney Doctor 4X221-5033-01W0 
<b>S</b> OQ .	Grec.	Constant Accor	Model .		
(D)	ID Ko.	Re(Seq (D. ;		Known Cene Name	Unigeno Sequence Cluster Title
			W, BB,		
			NN, XX,		
68	14504	AA799804	YY		ESTs
			1		ESTs, Moderately similar to
1	Ì	1			PTN3_HUMAN Protein tyrosine
		1			phosphatase, non-receptor type 3
			00, PP,		(Protein-tyrosine phosphatase
69	11423	AA799812	1111		H1) (PTP-H1) [H.sapiens]
			L, TT,		
72	12060	AA799890	DDD		ESTs
73	18180	AA799891	КК, ННН		ESTs
			l, J,		ESTs, Moderately similar to
		}	General		hypothetical protein FLJ10986 ·
76	23202	AA799971	Alternate		[Homo sapiens] [H.sapiens]
			JJ, KK,		
			XX, YY,		ESTs, Moderately similar to
ĺ	ł		General		hypothetical protein FLJ10986
76	23203	AA799971	Alternate		[Homo sapiens] [H.sapiens]
77	18400	AA799991	CC, ZZ, AAA, DDD, LLL	•	ESTs
<del>  ' '                                 </del>	10700	771733331	DOD, LLL		15015
					ESTs, Weakly similar to Yeast ABD1 protein like [Caenorhabditis
81	23343	AA800016	Q, R	•	elegans] [C.elegans]
83	23344	AA800034	U, 00		ESTs
84	19177	AA800062	O, P		ESTs
85	13568	AA800169	1		ESTs
88	16420	AA800191	XX		ESTs
89	18430	AA800197	F		ESTs
91	3692	AA800210	DDD		ESTs
					ESTs, Weakly similar to
	1		MM, ZZ,		C27H6.4.p [Caenorhabditis
92	7947	AA800224	AAA, TTT		elegans] [C.elegans]
97	24228	AA800318	E, BB, EEE, GGG, MMM, PPP, QQQ		ESTs, Moderately similar to IC1_MOUSE Plasma protease C1 inhibitor precursor (C1 Inh) (C1Inh) [M.musculus]
			TT, General Core Tox	·	
98	12064	AA800429	Markers		ESTs
99	14545	AA800456	LLL		ESTs
101	12069	AA800572	V		ESTs
102	19073	AA800576	Α		ESTs
103	2070	AA800597	Z, AA		ESTs

				-300-	
TABU	<b>3</b> 1			A	torney Docket 44921-5133-01WC Document No. 1995323.1
Soq (D: 1	10 Kp.	(CONSINI AGG OF RGSCO (D	(Model) (Code	Known Cene Name	Unigene Sequence Cluster Title
			M, W,		
		1	GG, MM,		
104	13930	AA800613	777		EST
105	21368	AA800626	DD, EE W, OOO,		ESTs
			General		
106	4843	AA800651	Alternate		ESTs
	10.0	1 1 100000			ESTs, Highly similar to KIAA0164
					gene product [Homo sapiens]
108	5257	AA800673	บบ		[H.sapiens]
109	23368	AA800678	E, DD, EE, KKK, OOO		ESTS
110	3604	AA800712	вв, сс		ESTs Wooldy similar to
			1		ESTs, Weakly similar to VIL1 MOUSE Villin 1
111	17649	AA800735	Z, AA		[M.musculus]
	17043	70.0007.50	Q, HHH,		ESTs, Weakly similar to
			General		KT12_YEAST KTI12 PROTEIN
112	21380	AA800739	Alternate		[S.cerevisiae]
113	21389	AA800772	DDD		ESTs
114	12797	AA800790	O, P, NN, OO		ESTs
115	19103	AA800797	C, FFF, III, JJJ, OOO, General Core Tox Markers		ESTs
			_		ESTs, Weakly similar to YNP5_CAEEL HYPOTHETICAL 28.3 KDA PROTEIN T05G5.5 IN
116	11662 8207	AA800803 AA800850	F N. Z. AA		CHROMOSOME III [C.elegans] ESTs
119	10201	MA000000	C, EE,		LUIS
121	21407	AA800912	ZZ, AAA	·	ESTs
<u> </u>	1		BB, CC,		
123	14600	AA801076	NN, OO		ESTs
125	15027	AA801212	PP, QQ		ESTs
127	16889	AA817692	RR		
129	11633	AA817715	FF		ESTs, Weakly similar to T32897 hypothetical protein C42C1.10 - Caenorhabditis elegans [C.elegans]
			A, BB,		
130	24237	AA817726	NN, OO		ESTs ·
131	6304	AA817729	SS		ESTs
132	15094	AA817753	E		ESTs
134	1690	AA817829	CC	i	ESTs

WO 03/064624

TABL	E 1			A	torney Doctat 44921-5033-01W0 Document No. 1995323.1
3		GOVE SUNT			100
Seq	@L@C	Accor ;	Model		000.00
(D):::	ID Ko.	karead in 3		Known Cana Kame	Unigene Sequence Cluster Tille
			W, DDD,		
135	1802	AA817841	บบบ		ESTs
			FFF,		
	10.10		General		SOT.
137	1846	AA817844	Alternate		ESTs ESTs
138	1900 2781	AA817849 AA817925	Z, II		ESTs
140 141	6308	AA817951	o ss	<u> </u>	ESTs
141	10300	AA617951	K, PPP,		12315
142	2485	AA817954	QQQ		ESTs
142	2400	77011334	N, FF, II,	Sulfotransferase	1013
1	1		QQ, YY,	hydroxysteroid gene	Sulfotransferase hydroxysteroid
144	10623	AA817987	บบบ	2	gene 2
146	6698	AA818020	ww		ESTs
			R, EE,		
l			000,		
			General		
149	2897	AA818039	Alternate		ESTs
150	19926	AA818062	PP, QQ		ESTs
			F, N, II,		
151	5996	AA818065	บบบ		ESTs
154	6001	AA818090	YY		EST
					ESTs, Weakly similar to
					hypothetical protein LOC57019
155	3233	AA818105	L		[Homo sapiens] [H.sapiens]
156	6003	AA818107	SS		ESTs
ļ		ŀ	GGG,		ESTs, Weakly similar to T13616
	•		General		hypothetical protein 8D8.8 - fruit
157	6007	AA818123	Core Tox Markers		fly (Drosophila melanogaster)
1137	10007	AA010123	iviarkers		[D.melanogaster] ESTs, Weakly similar to
	1				F13B9.8.p [Caenorhabditis
158	3476	AA818142	YY		elegans] [C.elegans]
100	10470	741010142	A, B, JJ,		[Cicgana] [Cicagana]
			FFF,		*
			GGG,		
	1		ннн,		
	ł		General `		
			Core Tox		
159	6015	AA818158	Markers		ESTs
	1		ннн,		
			PPP,		
162	3757	AA818202	QQQ		ESTs
164	6030	AA818252	T		ESTs
165	4017	AA818287	D, KKK 、		ESTs
			F, M,		·
			General	·	
400	5000	1 4 4 4 4 4 4 4 4 4	Core Tox		
166	5923	AA818355	Markers		ESTs
167	7714	AA818394	LL		ESTs

TABL	<b>3</b> 1		٠.	A	torney Docket 44921-5033-011WO Document No. 1935323.1
		Consant	00-0-0		PACA .
809 (D	id no Grec	Acc or RefSeq ID	Modol Codo	Marina Rossa Maria	Unigene Sequence Cluster Tille
נשו :	וה וגיפי	ાજસાહેસાલી લાહોં.		Known Cone Name	Antibiatra gadramas Arrega, uma
100	10160	AA949449	O, P, X,	cytochrome P450,	- Asabasas D450 0540
168 169	12160 7806	AA818412	TT, DDD	2b19	cytochrome P450, 2b19
170	6222	AA818421 AA818474	Q HH		ESTS
170	0222	IAA616474	DD, EE,		15015
171	8237	AA818512	NNN	ł	ESTs
172	6226	AA818521	PP, QQ		ESTs
11/2	0220	AA010321	rr, aa		E313
					ESTs, Highly similar to COP9
1					(constitutive photomorphogenic)
			1		homolog, subunit 7a (Arabidopsis
l	1		1		thaliana); DNA segment, Chr 6,
		]	1		ERATO Doi 35, expressed; COP9
					complex S7a; COP9 (constitutive
					photomorphogenic), subunit 7a
					(Arabidopsis) [Mus musculus]
173	8360	AA818534	บบ		[M.musculus]
174	17434	AA818574	100		ESTs
175	6231	AA818595	QQ		ESTs
			MM, TIT,		
			General		
177	8728	AA818615	Alternate	*	ESTs
179	6056	AA818664	E		ESTs
181	4250	AA818700	LLL		ESTs
	1		UU,		
			General		
			Core Tox		·
182	6060	AA818702	Markers		ESTs
183	11864	AA818717	RR		ESTs
			I, LLL,		
184	4291	AA818741	SSS		ESTs
					ESTs, Weakly similar to
		İ			ACF7_MOUSE Actin cross-
					linking family protein 7
					(Microtubule actin crosslinking
185	6619	AA818743	HH		factor) (MACF) [M.musculus]
		İ	B, H, JJJ,		
			000,		
			General		
100	4000		Core Tox		507-
186	4330	AA818747	Markers		ESTs
188	6066	AA818781	LL T		ESTs
190	6073	AA818818	T		EST
192	4921	AA818900	K		ESTs
193	4952	AA818907	Q		ESTs

TABL	EI			A	torney Docket 44921-5038-011W0 Document No. 1985328.1
Seq (D ₃₅ )	ELEC.	Genient Acc or Refseq ID :		Known Cene Kame	Unigane Sequence Cluster Tide
			III, JJJ, NNN, General		
194	19729	AA818910	Core Tox Markers		ESTs
195	17408	AA818971	N, PPP, QQQ General		ESTs
196 198	10985 16958	AA818998 AA819021	Alternate		ESTs EST
199	5608	AA819041	General Alternate		ESTs
					ESTs, Weakly similar to G35070 apolipoprotein H-related protein
200 201	6132 6135	AA819055 AA819065	N, PPP MM, TTT		13G1 - mouse [M.musculus] ESTs
202	5863	AA819111	KK		ESTs
205	11988	AA819193	TT		ESTs
207	15147	AA819268	W General		ESTs
208	6438	AA819269	Alternate		ESTs
213	6252	AA819381	EE		ESTs
214	9402	AA819383	JJ, HHH, LLL		ESTs
215	6267	AA819438	D		EST
216	19438	AA819450	LL		EST
217	6275	AA819459	PP, QQ DD, EE,	·	ESTs ESTs, Moderately similar to JC5821 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) CI-B14
221	18723	AA819547	III, JJJ		chain - human [H.sapiens]
223	10988	AA819640	E, RR		ESTs
225	6723	AA819653	Q, R, PP, QQ	·	ESTs, Weakly similar to S44652 f42h10.6 protein - Caenorhabditis elegans [C.elegans]
226	6176	AA819657	T		EST
227	6295	AA819672	DD, MM, WW, TTT		ESTs
228	10695	AA819679	E, II		ESTs
229	6296	AA819680	BB, CC		EST\$
230	6297	A A 9 1 0 6 9 1	ww	·	ESTs, Highly similar to RIKEN cDNA 1200014P03 [Mus
232	11021	AA819681 AA819767	W, AA, DD, General Core Tox Markers	-	musculus] [M.musculus] ESTs

TABL	<b>E</b> 1			A	tomey Docket 44921-5033-01W0 Document No. 1965323.1
(D)	(D) (100	Consent Ace or RefSeq ID	Model   Code : 7 :	Knowniens Kams	Unigene Sequence Cluster Title
234	6190	AA819812	FFF, General Core Tox Markers		ESTs
				·	ESTs, Highly similar to TNFC_MOUSE Lymphotoxin-beta (LT-beta) (Tumor necrosis
235	6200	AA819853	NN		factor C) (TNF-C) [M.musculus]
238	9815	AA848218	Q, R		ESTs
239	24629	AA848238	PPP, QQQ		ESTs
241	17315	AA848309	D		ESTs
243	15030	AA848378	LL		ESTs
			OO, EEE,		ESTs, Weakly similar to Iron- containing alcohol dehydrogenases [Caenorhabditis
244	6614	AA848389	MMM		elegans] [C.elegans]
245	23521	AA848407	A, B, HH		ESTs
246	21125	AA848437	III, JJJ, KKK, General Core Tox Markers		ESTs
240	21125	AA040431	Ivial keis		ESTs, Moderately similar to
247	23505	AA848496	Q, R		IF4B_HUMAN Eukaryotic translation initiation factor 4B (eIF-4B) [H.sapiens]
		,			ESTs, Weakly similar to T19253 hypothetical protein C14A4.11 - Caenorhabditis elegans
248	2324	AA848545	ZZ, AAA		[C.elegans]
249	12088	AA848597	DD, EE		ESTs
250	21135	AA848646	B		EST
251	18244	AA848776	EEE, MMM		ESTs
252	21150	AA848826	Z, AA, III, JJJ		ESTs
253	14604	AA848828	F		ESTs CAROLINA CAROLINA
054	40400				ESTs, Weakly similar to S12207 hypothetical protein (B2 element) -
254	12102	AA848902	UU	· · · · · · · · · · · · · · · · · · ·	mouse [M.musculus]
255	14207	AA848904	General Alternate		ESTs
		•			ESTs, Weakly similar to F18H3.1.p [Caenorhabditis
256	2924	AA848948	C ·		elegans] [C.elegans] ESTs, Moderately similar to
257	12108	AA848963	CC, KKK		S70630 xeroderma pigmentosum group C - mouse [M.musculus]

TABL	<b>E</b> 1		14.0	A	terney Docket 44921-5033-911WO Document No. 1935323.1
Seq [D ::	ELEC	Lace or Respective	Model Code	දැකුවේ දැකුව බැහුකොට	Unigene Sequence Cluster Title
			000,	000000000000000000000000000000000000000	
	1		General		
1			Core Tox		
1			Markers,		
1			General		
259	21173	AA848990	Alternate		ESTs
261	22631	AA849030	UUU		ESTs
262	2056	AA849210	YY		ESTs
	<b> </b>				ESTs, Moderately similar to cell
l			C, MM,	-	cycle progression 2 protein
264	12119	AA849354	TTT		[Homo sapiens] [H.sapiens]
265	12120	AA849365	<b>J</b> J		ESTs
	1		Conormi		ESTs, Weakly similar to
1	1		General Core Tox		YLC4_CAEEL Hypothetical 81.0
266	18908	AA849426	Markers		kDa protein C35D10.4 in chromosome III [C.elegans]
200	10900	AA049420	iviarkers		ESTs, Weakly similar to
	1		General		YLC4_CAEEL Hypothetical 81.0
Ì			Core Tox		kDa protein C35D10.4 in
266	18909	AA849426	Markers		chromosome III [C.elegans]
200	10000	7 4 10 4 20 4 2 0	FF, 000,		chromosome in [c.elegans]
ł			General		
			Core Tox		
267	17339	AA849497	Markers		ESTs
			C, I, J,		
268	11726	AA849518	KKK		ESTs
			I, J, KKK,		
268	11727	AA849518	NNN		ESTs
269	18743	AA849531	K		ESTs
					ESTs, Weakly similar to
					guanosine-3',5'-bis(diphosphate)-
					pyrophosphohydrolase like
					[Caenorhabditis elegans]
271	6862		BB, CC		[C.elegans]
272 273	12989 21275		D		ESTs .
1213	21213		F, II NN, EEE,		ESTs
276	21285		MMM		EST
					ESTs, Moderately similar to NB8M HUMAN NADH-
]					ubiquinone oxidoreductase B18
			[		subunit (Complex I-B18) (CI-B18)
					(Cell adhesion protein SQM1)
280	21327	AA850130	F		[H.sapiens]
281	21333		K		ESTs
	,				
[			U, FF,		į
			UU, BBB,	I	
282	21341	AA850195	RRR, SSS		ESTs

TABL	31			AG	torney Docket 4/1921-5033-011/10 Document No. 1935323.1
Seq	CLCC.	Consens Acc or	Model	Maryan Cana Nama	Unigene Sequence Cluster Title
بنز الا	(D) (No. :)	RefSeq (D .	ලිමෙම	Known Gene Name	Antigene sedaeves chare 11116
			E,		·
	04050		General	1	FOT
283	21353	AA850247	Alternate		ESTs
286	19502	AA850601	OO FFF,		ESTs
1			General		
288	6471	AA850706	Alternate		ESTs
290	5754	AA850738	Z		ESTs
291	3400	AA850771	<del>V</del>	<del>                                     </del>	ESTs
	-	7 4 10 00 7 7 1	<u> </u>	<del></del>	ESTs, Weakly similar to
1		1			F22F7.1.p [Caenorhabditis
293	19575	AA850814	JJJ, KKK		elegans] [C.elegans]
295	21762	AA850886	L		ESTs
297	21773	AA850951	XX		ESTs
298	9514	AA850978	L, Z, AA	<del></del>	ESTs
			G, K, X,		
			тт, ннн,		
300	8872	AA851050	บบบ	glutathione reductase	glutathione reductase
301	22518	AA851065	ZZ, AAA		ESTs
					ESTs, Weakly similar to T33304
					hypothetical protein R01B10.5 -
			RRR,		Caenorhabditis elegans
304	4163	AA851210	SSS, UUU		[C.elegans]
					ESTs, Highly similar to RIKEN
	.=				cDNA 4930548G07 [Mus
305	17699	AA851233	JJ	66	musculus] [M.musculus]
				fasting-inducible	faction in ducible internal
306	18961	AA851238		integral membrane protein TM6P1	fasting-inducible integral
300	10901	AA031236	C General	protein twoP1	membrane protein TM6P1
			Core Tox		
			Markers;		*
			General		
307	4134	AA851240	Alternate		ESTs
308	21694	AA851248	Y		ESTs .
					ESTs, Weakly similar to retinoic
					acid receptor responder
			ĺ		(tazarotene induced) 2 [Homo
309	21466	AA851273	EE, HHH		sapiens] [H.sapiens]
			TT, LLL,		
310	17766	AA851299	บบบ		ESTs
					ESTs, Moderately similar to
İ					hypothetical protein MGC2749
313	22979	AA851372	TT		[Homo sapiens] [H.sapiens]
314	21482	AA851407	CCC		ESTs
316	21510	AA851620	T		ESTs
319	21529	AA851748	F, W, HH		ESTs
200	00040	4 4 0 5 4 5 5 5	L, 00,		
322	23243	AA851803	ΤΤ, UU		ESTs

TABL	<b>E</b> 1 .		•,	: Ag	tomey Doctat 44921-5033-01W0 Document No. 1935328.1
		CON-SANI			(K)
Seq.	(id) kyo-4 (gr@c	Accor	Model		
D.	(ID Ko.:+	Refseq ID	©0000	Known Cone Name:	Unioeno Soquenco Ciuster Title
					ESTs, Moderately similar to
		İ			RIKEN cDNA 2310040G17;
					expressed sequence AI425883
324	18243	AA851920	F		[Mus musculus] [M.musculus]
		Ĭ	BB, NN,		
	İ		EEE,		
327	18580	AA851963	MMM		ESTs
329	21572	AA852011	A, B		ESTs
330	21574	AA852038	W, DD		ESTs
331	1904	AA852046	DD, EE		Rat VL30 element mRNA
			NN, 00,	•	
332	15207	AA858448	PP		ESTs
333	15211	AA858449	N		ESTs
335	15283	AA858548	RR		ESTs
336	21856	AA858550	ww		ESTs
339	23069	AA858572	TT		ESTs
1	1		C, I, J,		
1	1		w, ww,		
1		]	000,		
1		·\	General	•	
341	24161	AA858588	Alternate		ESTs
			I, J, NN,		
343	17382	AA858607	OO, DDD		ESTs
İ					ESTs, Highly similar to mini
	1				chromosome maintenance
	1.004		General		deficient 7 (S. cerevisiae) [Mus
344	1801	AA858636	Alternate		musculus] [M.musculus]
1	-				ESTs, Weakly similar to
0.40	0044	4 4 0 5 0 0 4 0	_		F17C11.8.p [Caenorhabditis
346	6344 6345	AA858649	F		elegans] [C.elegans]
347 352	13229	AA858657	XX, YY		ESTs
352	13229	AA858760	JJ General		ESTs
1			Core Tox		•
1			1		
			Markers,		
353	6389	AA858815	General Alternate		TOTA
333	0309	AA030013	Allemate		ESTs Moderately similar to
					T46271 hypothetical protein
ŀ	1		1		DKFZp564P1263.1 - human
354	11161	AA858817	O, P		[H.sapiens]
355	6390	AA858821	GGG		ESTs ESTs
357	6409	AA858910	FF		ESTs
<del>  -</del>	15-05	, 4,000310	M, XX,		LU13
358	14191	AA858924	000		ESTs
359	14234	AA858928	UUU		ESTs
360	6413	AA858954	RR		EST
361	14210	AA858955	Ľ.		EST
	1		<u> </u>		CV 1

TABL	<b>E</b> 1		. 6	A	iomay Dockei 44921-5093-01WC Document No. 1935323.1
		CONSONX			· it is
Seq	@r@c	Acc or	Model		
ld i	(ID.K)@.	RefSeq ID	ලිලල්ල 🕴 👵	Known Cone Name .	Unigene Sequence Cluster Title
					ESTs, Weakly similar to G35070
	ľ		YY, PPP,		apolipoprotein H-related protein
362	18765	AA859019	QQQ		13G1 - mouse [M.musculus]
					ESTs, Weakly similar to G35070
			PPP,	-	apolipoprotein H-related protein
362	18766	AA859019	QQQ		13G1 - mouse [M.musculus]
			UUU,		
ŀ		1	General		
ļ	İ		Core Tox		-
l		1	Markers,		
			General		
363	4591	AA859029	Alternate		ESTs
1			W, X, BB,		
			CC, LL,		
364	6431	AA859085	NN		ESTs ·
365	17361	AA859114	С		ESTs
373	15157	AA859343	PP, QQ		ESTs
			PP, QQ,		
378	11827	AA859468	LLL, SSS		ESTs
380	18862	AA859520	CCC		ESTs
204	4470		EEE,		
381	4178	AA859536	MMM		ESTs
382	15150	AA859562	SSS		ESTs
200	4.5		EEE,		
383	15	AA859577	MMM	,	ESTs
			C, KK,		
	'		QQ, General		
			Core Tox		
384	14353	AA859585	Markers		ESTs
385	11852	AA859593	W		ESTs
363	111002	AAOJ9J9J	1VV		ESTs, Weakly similar to FYVE
					zinc finger [Caenorhabditis
387	4809	AA859616	LLL		elegans] [C.elegans]
388	11608	AA859633	A, Q, R		ESTs
1500	11000	7, 2,003000	000,		EU 19
1			General		
391	19067	AA859663	Alternate		ESTs
392	19726	AA859665	RR		EST
~~_	1.5.25	1. 5 1000000	1		-01

TABL	E1			A	tomey Docket 44921-5093-01WC Document No. 1935623.1
		reensant	1 1 1 1		
Seq	@F@@	Acc or	Model		3
ID.	ID No.	RefSeq ID	ලා මෙම	Known Cone Name	Unigene Sequence Civeter Title
			C, E, R,		
			вв, сс,		
			DD, MM,		
			QQ, WW,		
	1		III, JJJ,		
	ļ		KKK,		
1			NNN,		
l	1		TTT,		
1	İ	1	General		
1			Core Tox		
394	21707	AA859722	Markers		ESTs
					ESTs, Weakly similar to S61982
ļ		1			probable membrane protein
	1				YOL002c - yeast
1					(Saccharomyces cerevisiae)
395	20034	AA859796	ввв, ссс		[S.cerevisiae]
			Y, UU,		
397	22396	AA859806	ZZ, AAA		ESTs
398	11079	AA859829 .	l, J		ESTs
399	22739	AA859877	ZZ, AAA		ESTs
400	22773	AA859885	X, Y	<u></u>	ESTs
401	22813	AA859897	LL		ESTs
					·
			F, K, LLL,		
			UUU, General	•	
402	16320	AA859899	Alternate		ESTs
403	15165	AA859919	TT		ESTs
403	15166	AA859919	TT		ESTs
1700	10100	70000010	UU, PPP,		2015
		1	QQQ,	;	
			General		
404	22927	AA859920	Alternate		ESTs
405	26034	AA859921	TT		
					ESTs, Moderately similar to
				.v.	hypothetical protein MGC2749
406	22978	AA859931	D	***	[Homo sapiens] [H.sapiens]
413	16322	AA866240	D		EST
413	16323	AA866240	BBB		EST
417	15927	AA866321	PP, QQ		ESTs
418	21690	AA866362	N, V		ESTs
			I, T, DD,		
	1		EE, XX,		
419	15980	AA866426	YY, LLL		ESTs
			L, N, X,	-	
		1	DDD,		İ
420	15987	AA866435	บบบ		EST
421	16854	AA866454	M		ESTs

TABU	<b>E</b> 1			A	ttomey Docket 44921-5033-01W0 Document No. 1995323.1
899 W	(ID Klo.	CONSENIA   Acc or   Reseal D	Modoj. Codo	Emay ens Mems	Unigene Sequence Cluster Illic
					ESTs, Moderately similar to COXM_MOUSE Cytochrome c oxidase polypeptide VIIb, mitochondrial precursor
423	9391	AA866477	Z, AA		[M.musculus]
425	16118	AA874924	O, P		ESTs
429	7040	AA874978	K, T		ESTs
432	16242	AA875019	X, Y		ESTs, Highly similar to ZAP3_MOUSE Nuclear protein ZAP3 [M.musculus]
433	15573	AA875023	Z, AA		ESTs
436	16416	AA875098	FF, NN, OO, EEE, HHH, MMM		ESTs, Highly similar to RIKEN cDNA 1110002023 [Mus musculus] [M.musculus] ESTs, Moderately similar to JE0379 NADH dehydrogenase
437	16495	AA875107	R, RR		(ubiquinone) (EC 1.6.5.3) chain NDUFA3 - human [H.sapiens]
439	15313	AA875126	Q, MM, JJJ, TTT		ESTs
440	15713	AA875143	Z, AA, ZZ, AAA		ESTs
				HMm:ubiquitin conjugating enzyme	ESTs, Highly similar to ubiquitin conjugating enzyme 6; Ubc6p homolog [Mus musculus]
441	10936	AA875146	ZZ, AAA	6	[M.musculus]
443	14285	AA875194	SS		ESTs
446 449	15384	AA875217	K		ESTs
	15401	AA875257	I, J		ESTs ESTs, Highly similar to prostate tumor over expressed gene 1
451	15421	AA875286	SS		[Homo sapiens] [H.sapiens]
452	15509	AA875425	CCC		ESTs
453 · 454	7936 19381	·	L, Z, AA		ESTs ESTs, Weakly similar to 0806162N protein URFA6L [Mus
<del>104</del>	19001		V		musculus] [M.musculus] ESTs, Highly similar to SFR2_MOUSE Splicing factor, arginine/serine-rich 2 (Splicing factor SC35) (SC-35) (Splicing
456	15558		QQ, UU		component, 35 kDa) (PR264 protein) [M.musculus]
457			Q		ESTs
458	15629		RR		ESTs
459	15630	AA875630	EE		ESTs
460 466			K, XX, YY		ESTs
700	11340	W031100	Α		ESTs

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CLGG   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorption   Assorptio	TABL	31 ·		1	# AC	
Seg   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subset   Subs			ിരുത്തം ത്രത്യ	·	\$ d	Document No. 1935223.1
	800	ଜ୍ୟ ଜନ	Acceptance of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the con	Workey		
A67   21909   AA891161   RRR   ESTs	ൈദി	100 CAS:	Poggos III	Coco	Mooma Good Notice	Michael Communic Charles Tittle
AB91161   RRR	TE: 13.	יים ועופיי.	Managad (m. '.		reginación resina ristinta	Tombana sadraitaa cunaan urta
BBB, CCC	107	04000				
N48M_HUMAN NADH-   Ubiquinone oxidoreductase subunit B14.5b) (Cl-B14.5b) [H.sapiens]	467	21909	AA891161	KKK		
A68   15833   AA891171   BBB, CCC   B14.5b) (CI-B14.5b) [H.saplens]	1					
A68	1	l	}			. –
A68		<b>!</b> .				
Head	1,00	45000	4 4 9 9 4 4 7 4		•	
AA891207	468	15833	AA8911/1			B14.5b) (CI-B14.5b) [H.sapiens]
A89						
E, W, DD, EE, SS, LLL, SSS, UUU ESTS  470 21917 AA891220 UUU ESTS  474 1209 AA891222 Z, AA ESTS  474 15152 AA891314 T ESTS  BB, CC, NNN, ESTS  475 16446 AA891423 OOO ESTS  478 19238 AA891542 Z, AA ESTS  479 21905 AA891546 ZZ, AAA ESTS  481 11949 AA891580 ZZ, AAA ESTS  484 18490 AA891689 G, H ESTS  486 17052 AA891689 X, Y ESTS  488 18584 AA891694 Q, R ESTS  488 18584 AA891694 Q, R ESTS  489 1133 AA891717 N, DDD ESTS  489 17039 AA891727 E, NNN ESTS  491 17255 AA891734 O, P, VV  492 11959 AA891735 III, JJJ  493 17693 AA891737 OO, KKK  ESTS  494 17256 AA891739 W, XX elegans] [C.elegans]  495 18287 AA891742 N  MM, SS,	1.00	40500				
EE, SS, LLL, SSS, UUU	469	18582	AA891207	ннн		ESTS
EE, SS, LLL, SSS, UUU			:	- W		
AR891220						
470						·
471         209         AA891222         Z, AA         ESTS           474         15152         AA891314         T         ESTS           475         16446         AA891423         OOO         ESTS           478         19238         AA891542         Z, AA         ESTS           479         21905         AA891560         ZZ, AAA         ESTS           481         11949         AA891680         ZZ, AAA         ESTS           484         18490         AA891699         G, H         ESTS           486         17052         AA891699         X, Y         ESTs           488         18584         AA891694         Q, R         ESTs, Highly similar to USF1_MOUSE Upstream stimulatory factor 1 (Major late transcription factor 1)           490         17039         AA891737         E, NNN         ESTs           491         17255         AA891734         O, P, VV         ESTs           492         11959         AA891735         III, JJJ         ESTs           493         17693         AA891737         OO, KKK         ESTs           494         17256         AA891739         W, XX         ESTs           495         18287         AA891	170					
474						
BB, CC, NNN,   ST						
NNN,	4/4	15152	AA891314	<u> </u>		ESTS
475       16446       AA891423       OOO       ESTs         478       19238       AA891542       Z, AAA       ESTs         479       21905       AA891546       ZZ, AAA       ESTs         481       11949       AA891580       ZZ, AAA       ESTs         484       18490       AA891669       G, H       ESTs         488       18584       AA891694       Q, R       ESTs         489       1133       AA891694       Q, R       ESTs, Highly similar to USF1_MOUSE Upstream stimulatory factor 1 (Major late transcription factor 1)         490       17039       AA891727       E, NNN       ESTs         491       17255       AA891734       O, P, VV       ESTs         492       11959       AA891735       III, JJJ       ESTs         493       17693       AA891737       OO, KKK       ESTs         494       17256       AA891739       W, XX       ESTs         495       18287       AA891742       N       ESTs	1					
478       19238       AA891542       Z, AA       ESTs         479       21905       AA891546       ZZ, AAA       ESTs         481       11949       AA891580       ZZ, AAA       ESTs         484       18490       AA891669       G, H       ESTs         488       18584       AA891694       Q, R       ESTs         489       1133       AA891694       Q, R       ESTs, Highly similar to USF1_MOUSE Upstream stimulatory factor 1 (Major late transcription factor 1)         490       17039       AA891727       E, NNN       ESTs         491       17255       AA891734       O, P, VV       ESTs         492       11959       AA891735       III, JJJ       ESTs         493       17693       AA891737       OO, KKK       ESTs         494       17256       AA891739       W, XX       ESTs         495       18287       AA891742       N       ESTs	175	40440	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4			
479       21905       AA891546       ZZ, AAA       ESTs         481       11949       AA891580       ZZ, AAA       ESTs         484       18490       AA891669       G, H       ESTs         486       17052       AA891689       X, Y       ESTs         488       18584       AA891694       Q, R       ESTs         ESTs, Highly similar to USF1_MOUSE Upstream stimulatory factor 1 (Major late transcription factor 1) [M.musculus]       [M.musculus]         490       17039       AA891727       E, NNN       ESTs         491       17255       AA891734       O, P, VV       ESTs         492       11959       AA891735       III, JJJ       ESTs         493       17693       AA891737       OO, KKK       ESTs         ESTs, Weakly similar to F52H3.5.p [Caenorhabditis elegans] [C.elegans]       ESTs         494       17256       AA891739       W, XX       ESTs         495       18287       AA891742       N       ESTs						L
481         11949         AA891580         ZZ, AAA         ESTs           484         18490         AA891669         G, H         ESTs           486         17052         AA891689         X, Y         ESTs           488         18584         AA891694         Q, R         ESTs, Highly similar to USF1_MOUSE Upstream stimulatory factor 1 (Major late transcription factor 1) [M.musculus]           489         1133         AA891717         N, DDD         ESTs           490         17039         AA891727         E, NNN         ESTs           491         17255         AA891734         O, P, VV         ESTs           492         11959         AA891735         III, JJJ         ESTs           493         17693         AA891737         OO, KKK         ESTs           494         17256         AA891739         W, XX         ESTs           495         18287         AA891742         N         ESTs           495         18287         AA891742         N         ESTs						
484       18490       AA891669       G, H       ESTs         486       17052       AA891689       X, Y       ESTs         488       18584       AA891694       Q, R       ESTs, Highly similar to USF1_MOUSE Upstream stimulatory factor 1 (Major late transcription factor 1)         489       1133       AA891717       N, DDD       [M.musculus]         490       17039       AA891727       E, NNN       ESTs         491       17255       AA891734       O, P, VV       ESTs         492       11959       AA891735       III, JJJ       ESTs         493       17693       AA891737       OO, KKK       ESTs         494       17256       AA891739       W, XX       ESTs         495       18287       AA891742       N       ESTs						
486       17052       AA891689       X, Y       ESTs         488       18584       AA891694       Q, R       ESTs, Highly similar to USF1_MOUSE Upstream stimulatory factor 1 (Major late transcription factor 1) [M.musculus]         489       1133       AA891717       N, DDD       [M.musculus]         490       17039       AA891727       E, NNN       ESTs         491       17255       AA891734       O, P, VV       ESTs         BB, CC, BB, CC, ST, NN, OO, KKK       ESTs       ESTs         493       17693       AA891737       OO, KKK       ESTs         494       17256       AA891739       W, XX       ESTs         495       18287       AA891742       N       ESTs	L					I
488 18584 AA891694 Q, R  ESTs  ESTs, Highly similar to USF1_MOUSE Upstream stimulatory factor 1 (Major late transcription factor 1) [M.musculus]  490 17039 AA891727 E, NNN ESTs  491 17255 AA891734 Q, P, VV ESTs  BB, CC, HII, JJJ ESTs  S, T, NN, 493 17693 AA891737 OO, KKK ESTs  ESTs, Weakly similar to F52H3.5.p [Caenorhabditis elegans] [C.elegans] 494 17256 AA891742 N ESTs  MM, SS,						
### ESTs, Highly similar to USF1_MOUSE Upstream stimulatory factor 1 (Major late transcription factor 1)  ###################################						
USF1_MOUSE Upstream   stimulatory factor 1 (Major late transcription factor 1)   [M.musculus]	488	18584	AA891694	Q, R		
489       1133       AA891717       N, DDD       Image: English of the stranscription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcription factor of transcripti						
transcription factor 1) [M.musculus] 490 17039 AA891727 E, NNN ESTs 491 17255 AA891734 O, P, VV ESTs  BB, CC, 492 11959 AA891735 III, JJJ ESTs  S, T, NN, 493 17693 AA891737 OO, KKK ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS  ESTS						
489       1133       AA891717       N, DDD       [M.musculus]         490       17039       AA891727       E, NNN       ESTs         491       17255       AA891734       O, P, VV       ESTs         BB, CC,       BB, CC,       ESTs         492       11959       AA891735       III, JJJ       ESTs         493       17693       AA891737       OO, KKK       ESTs         ESTs, Weakly similar to F52H3.5.p [Caenorhabditis elegans] [C.elegans]       F52H3.5.p [Caenorhabditis elegans] [C.elegans]         494       17256       AA891739       W, XX       ESTs         495       18287       AA891742       N       ESTs						
490 17039 AA891727 E, NNN ESTS  491 17255 AA891734 O, P, VV ESTS  BB, CC,  492 11959 AA891735 III, JJJ ESTS  S, T, NN,  493 17693 AA891737 OO, KKK ESTS  ESTS, Weakly similar to F52H3.5.p [Caenorhabditis elegans] [C.elegans]  494 17256 AA891739 W, XX elegans] [C.elegans]  495 18287 AA891742 N ESTS	400	4400				
491 17255 AA891734 O, P, VV ESTs  492 11959 AA891735 III, JJJ ESTs  493 17693 AA891737 OO, KKK ESTs  494 17256 AA891739 W, XX elegans] [C.elegans]  495 18287 AA891742 N ESTs						
492 11959 AA891735 III, JJJ ESTS  493 17693 AA891737 OO, KKK ESTS  494 17256 AA891739 W, XX elegans] [C.elegans]  495 18287 AA891742 N ESTS						L
492 11959 AA891735 III, JJJ ESTs  493 17693 AA891737 OO, KKK ESTs  494 17256 AA891739 W, XX elegans] [C.elegans]  495 18287 AA891742 N ESTs	491	1/255	AA891734			ESIS
493 17693 AA891737 OO, KKK  ESTs  ESTs, Weakly similar to F52H3.5.p [Caenorhabditis elegans] [C.elegans] 494 17256 AA891739 W, XX  495 18287 AA891742 N  ESTs  MM, SS,	,,,	44050	4 4 90 4 7 6 7			
493 17693 AA891737 OO, KKK ESTs  ESTs, Weakly similar to F52H3.5.p [Caenorhabditis elegans] [C.elegans] 494 17256 AA891739 W, XX elegans] [C.elegans] 495 18287 AA891742 N  ESTs	492	11959				ESIS
## ESTs, Weakly similar to F52H3.5.p [Caenorhabditis elegans] [C.elegans] ## ESTs ### ESTs ### ESTs ### ESTs ### ESTs #### ESTs #### ESTs ####################################	400	47000				
F52H3.5.p [Caenorhabditis   F52H3.5.p [Caenorhabditis   elegans] [C.elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.5.p [Caenorhabditis   elegans]   F52H3.p [Caenorhabditis   elegans]   F52H3.p [Caenorhabditis   elegans]   F52H3.p [Caenorhabditis   elegans]   F52H3.p [Caenorhabdit	493	17693	AA891737	00, KKK		
494       17256       AA891739       W, XX       elegans] [C.elegans]         495       18287       AA891742       N       ESTs         MM, SS,       MM, SS,						
495 18287 AA891742 N ESTs MM, SS,		47050	44004===			
MM, SS,						
	495	18287				ESTs
406 113686 LAAQA4740 IMAM TTT 1   ICCT.						
490   13000   AA091749   WW, 111   ESTS	496	13686	AA891749	ww, TTT		ESTs

TABL	<b>3</b> 1	-4"		A	torney Docket 44921-5093-01W0
Seq [D] =	erec	RefSeq ID RefSeq ID		Known Cene Name.	Unigere Sequence Cluster Title
			E, F, G, L, O, P, V, W, FF, EEE, III, JJJ, MMM, General Core Tox		-
498	9905	AA891774	Markers		ESTs Mackly similar to A54756
499	17289	AA891785	X, Y, XX		ESTs, Weakly similar to A54756 isocitrate dehydrogenase (NADP+) (EC 1.1.1.42), cytosolic rat [R.norvegicus]
499	17290	AA891785	II, XX, YY		ESTs, Weakly similar to A54756 isocitrate dehydrogenase (NADP+) (EC 1.1.1.42), cytosolic rat [R.norvegicus]
500	22124	AA891790	Q		ESTs
503	17311	AA891818	R		ESTs
506	14289	AA891838	s		ESTs, Weakly similar to F10E7.5.p [Caenorhabditis elegans] [C.elegans]
	20523		O, P, W, NN, EEE, III, JJJ,		ESTs
507 508	20616	AA891842 AA891851	MMM D		ESTs
511	22314	AA891877	MM, UU,		ESTs
512	17321	AA891881	Р		ESTs
514	17308	AA891902	O, P		ESTs
516	17811	AA891922	LL		ESTs
517	19319	AA891937	π		ESTs, Highly similar to S66254 dolichyl-diphosphooligosaccharide-protein glycotransferase (EC 2.4.1.119) 50K chain - human [H.sapiens]
					ESTs, Moderately similar to 149635 mouse Dhm1 protein -
518 520	23107 17437	AA891938	V		mouse [M.musculus]
		AA891943	C, I, WW, OOO, General		ESTs
521	22862	AA891944	Alternate		ESTs
522	1159	AA891949	E, L, Y		ESTs
523	9826	AA891950	III, JJJ, KKK		ESTs

TABL	31		•	A	torney Docket 44921-5033-01WO Document No. 1935323.1
Sco D	(10 Kg.	Genlenk Ass or Refsog ID	Model Code	Known Cene Name	Unigene Sequence Cluster Title
524	4473	AA891965	U		ESTs, Highly similar to fructosamine 3 kinase [Mus musculus] [M.musculus]
525	4474	AA891969	D		ESTs
526	17374	AA891978	к, т		ESTs
528	2106	AA892006	ss	HMm:ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1	ESTs, Highly similar to VAA1_MOUSE Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (V-ATPase A subunit 1) (Vacuolar proton pump alpha subunit 1) (V-ATPase 69 kDa subunit 1) [M.musculus]
528	2106	AA692006		HMm:ATPase, H+ transporting, lysosomal 70kD, V1	ESTs, Highly similar to VAA1_MOUSE Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (V-ATPase A subunit 1) (Vacuolar proton pump alpha subunit 1) (V-ATPase 69
528	2107	AA892006	AAA	subunit A, isoform 1	kDa subunit 1) [M.musculus]
529	15087	AA892010	PPP, QQQ, RRR		ESTs, Weakly similar to T22242 hypothetical protein F45G2.10 - Caenorhabditis elegans [C.elegans]
530	23047	AA892027	Z, AA, II	· · · · · · · · · · · · · · · · · ·	ESTs
531 532	3847 13420	AA892036 AA892042	ZZ, AAA LL, UU		ESTs, Highly similar to T13964 probable histone deacetylase (EC 3.5.1) HDA2 - mouse [M.musculus] ESTs
533	22865	AA892083	Q, R		ESTs
536	14595	AA892128	U, FF, WW, BBB, RRR		ESTs
538	12010 14330	AA892137	DD, EE, KKK, NNN NN		ESTs, Highly similar to open reading frame 12 [Mus musculus] [M.musculus] ESTs
539 540	11384	AA892146 AA892149	ZZ, AAA	<del></del>	ESTs
542	20917	AA892238	Q, R		ESTS
544	15666	AA892248	u, k		2013
544	15667	AA892248	11		
546	11981	AA892257	Y Y		ESTs
547	18165	AA892259	O, P, VV		ESTs, Highly similar to ICSB_MOUSE INTERFERON CONSENSUS SEQUENCE BINDING PROTEIN (ICSBP) [M.musculus]

TABIL	E1			Ą	tornay Docket 44921-5033-911W0 Document No. 1935323,1
Seq.	SOLO OLO OLO OLO OLO OLO OLO OLO OLO OLO	CONSIDERATION . AGE OF ROSSON ID	Model Code: .:		Unigene Sequence Cluster Title
٠٠,٠٠			U, ZZ,	, saissass 2000 cann.ş.	(Language 20 4 20 20 20 20 20 20 20 20 20 20 20 20 20
549	11982	AA892284	AAA		ESTs
	1		T, III, JJJ,		
551	4244	AA892300	KKK		ESTs
557	15492	AA892376	F, L		ESTs
558	3474	AA892378	ISS		ESTs, Weakly similar to F13B9.8.p [Caenorhabditis elegans] [C.elegans]
				Solute carrier family 11 member 2 (natural resistance- associated macrophage protein	Solute carrier family 11 member 2 (natural resistance-associated
560	2013	AA892390	NN	2)	macrophage protein 2)
563	4495	AA892399	ZZ, AAA		ESTs
565	17439	AA892446	Z, AA		ESTs
568	11991	AA892483	V		ESTs
571	23888	AA892520	O, GG		ESTs
571	23889	AA892520	BB		ESTs
574	16507	AA892547	GGG, HHH		ESTs, Highly similar to hypothetical protein CL25022 [Homo sapiens] [H.sapiens]
575	4507	AA892551	K		EST
576	11202	AA892554	III, JJJ, KKK		ESTs
576	11203	AA892554	BB, CC, OO, QQ, III, JJJ M, S,		ESTs
577 577	13574 13575	AA892557 AA892557	DDD, PPP, QQQ, General Alternate		ESTs
<del>                                    </del>	133/3	r4092001	D, M, S F, X,		ESTs
578 579	18906 7906	AA892561 AA892570	F, A, GGG PP, QQ		ESTs ESTs
581	19085	AA892598	C, M, MM, KKK, OOO, TTT, General Core Tox Markers		ESTs, Weakly similar to putative nucleotide binding protein, estradiol-induced [Homo sapiens] [H.sapiens]

TABL	E1			A	tomey Docket 44921-5033-01WO Document No. 1995323.1
Scq :	id ko Grec	Contoni Accor Refseq ID	Modol Codo	Known Cene Name	Unigene Sequence Cluster Title
		,	C, MM,		
			FFF, TTT,		ESTs, Weakly similar to putative
	.]	1	General		nucleotide binding protein,
	İ		Core Tox		estradiol-induced [Homo sapiens]
581	19086	AA892598	Markers		[H.sapiens]
582	16825	AA892602	Z, AA		ESTs
583	2119	AA892607	GG		ESTs
584	20088	AA892666	E, L		ESTs
585	4523	AA892754	UU		ESTs
			W, III,	7	
	1		JJJ,		
1	İ		General		
1	ì		Core Tox		
l			Markers,		
	1	}	General		
586	23783	AA892773	Alternate		ESTs
			R, PP,		
587	4527	AA892774	QQ, LLL		ESTs
589	4590	AA892778	SS, III, JJJ, NNN, PPP, QQQ, General Core Tox Markers, General Alternate		ESTs
303	14330	74032110	Alternate		2313
590	17421	AA892789	ввв, ссс		ESTs
591	19251	AA892796	GG		ESTs
				HMm:3'-	ESTs, Highly similar to 2204316A
		1			ATP sulfurylase-adenosine
			K, ZZ,	phosphosulfate	phosphosulfate kinase [Mus
595	17332	AA892829	AAA	synthase 1	musculus] [M.musculus]
<b>506</b>	10442	A A 9 0 2 9 2 2	M, GG, HH, III, JJJ, General		ECT-
596	19443	AA892832	Alternate		ESTs
600	17589	AA892851	E, W, PP, QQ, FFF, III, JJJ		ESTs
600	17590	AA892851	A, E, W, KK, UU, ZZ, AAA, III, JJJ, General Alternate		ESTs

TABL	31			A	torney Docket 44221-5033-01W0 Document No. 1935323.1
829 D	@L@@ @L@@	Cenifini Accor Refer ID	Model Code	Known Cene Name	Unigene Sequence Civeter Title
601	18887	AA892860	K, DDD		ESTs
602	9053	AA892861	III, JJJ, KKK, OOO, General Core Tox Markers		ESTs
602	9000	AA692661	ivialkers		2018
603	7756	AA892864	RRR, SSS		ESTs
604	4531	AA892868	PP, QQ		EST
605	16366	AA892888	BB, CC, GG, HH, NN, EEE, LLL, MMM		EST
605	16367	AA892888	V, BB, CC, GG, HH, NN, DDD, EEE, MMM		EST
606	12848	AA892916	E, BB, CC		ESTs, Weakly similar to JC7260 strictosidine synthase (EC 4.3.3.2) homolog 2 - fruit fly (Drosophila melanogaster) [D.melanogaster]
607	2727	AA892918	C, I		ESTs
	·				ESTs, Moderately similar to A Chain A, Crystal Structure Of The Accessory Subunit Of Murine Mitochondrial Polymerase
610	14465	AA892950	MM, TTT I, J, HH, LLL, OOO, SSS, UUU, General		Gamma [M.musculus]
611	8438	AA892986	Alternate		ESTs
613	3853	AA892999	A, B		ESTs
615	3131		E, G, H, I, J, III, JJJ, KKK, OOO, General Core Tox Markers		ESTs
616	12020	AA893035	M	HP33	HP33

TAEL	EI				tomay Docket 44221-5033-01WO Document No. 1935323.1
Seq	id ko Grec	. Resident Acc or Resident	Model ©ode	Known Cone Name	Unigeno Soquenco Chestor The
			E, NN, OO, PP, III, KKK, OOO, General Core Tox Markers, General		
618	13332	AA893080	Alternate		ESTs
619	21305	AA893082	F, NNN	<del></del>	ESTs
620	17691	AA893088	RR		ESTs
621	19745	AA893199	VV, BBB, CCC, General Alternate		ESTs, Highly similar to RIKEN cDNA 1500004D14 [Mus musculus] [M.musculus]
622	2356	AA893202	Z, AA		ESTs
623 625	548	AA893217 AA893235	O, P A, B, E, DD, EE		ESTs ESTs, Highly similar to G0S2_MOUSE Putative lymphocyte G0/G1 switch protein 2 (G0S2-like protein) [M.musculus]
627	10538	AA893239	Т	2-hydroxyphytanoyl- CoA lyase	2-hydroxyphytanoyl-CoA lyase
629 632	17752 3783	AA893244 AA893320	U, X, Y, II, VV, LLL, SSS, UUU, General Alternate Z, AA		ESTs ESTs
635	17800	AA893436	DD		ESTs
			E, H, S, KK, GGG, III, JJJ, OOO, General Core Tox		
636	12312	AA893453	Markers		ESTs
637	21980		E, I, L, JJ, KK, LL, UU, HHH, OOO		ESTs
			C, XX,	• 1	
638	2480		YY, DDD		ESTs

TABL	<b>E</b> 1		3.	$\boxtimes$	tomey Docket 44921-5033-01WO Document No. 1936328.1
Seq.: [D	ELEC	CONSING ACCO RESECTIO	Cogo Mogaj	Known Cene Name	Unigene Sequence Cheter Title
					ESTs, Highly similar to RIKEN cDNA 4930548G07 [Mus
641	17698	AA893596	JJ, KK		musculus] [M.musculus]
642	4540	AA893603	ZZ, AAA		ESTs
643	22150	AA893607	ZZ, AAA, UUU		ESTs
					ESTs, Highly similar to synembryn [Mus musculus]
645	17838	AA893641	ZZ, AAA		[M.musculus]
646	14495	AA893658	GG, EEE, MMM		ESTs
647	4544	AA893664	ZZ, AAA	TEMO	TEMO
649	12028	AA893670	ZZ, AAA		ESTs
653	3035	AA893821	ZZ, AAA		ESTs
654	17891	AA893885	F		ESTs
655	17896	AA893905	UU, General Alternate		ESTs
655	17897	AA893905	G, H, I, J, General Alternate		ESTs
656	23240	AA893939	FFF		ESTs, Highly similar to DSS1_HUMAN Deleted in split hand/split foot protein 1 (Split hand/foot deleted protein 1) [M.musculus]
657	23731	AA894004	O, P, VV, UUU		ESTs, Highly similar to CAPG_MOUSE Macrophage capping protein (Myc basic motif homolog-1) (Actin-capping protein GCAP39) [M.musculus]
	<u> </u>		General	<del></del>	
658	22584	AA894009	Alternate	-	ESTs
659	10540	AA894027	II, JJ, FFF		
660	3895	AA894029	O, P, V, VV		ESTs
663	17953	AA894090	JJ, KK, ZZ, AAA		ESTs
664	2979	AA894099	N		ESTs, Highly similar to vacuolar protein sorting protein 4a; RIKEN cDNA 4930589C15 gene [Mus musculus] [M.musculus]

TABL	E1			. AV	liomey Dockel 44921-5033-011WO Document No. 1935:23.1
S09 10	GLGC	CONSIDE ACCOT ROSSES	Model Code	Known Cone Name	
	III KISPÉ	kransed in	Roce.	emen ende myenn	Unigene Sequence Ciuster Titile ESTs, Moderately similar to PNAD_MOUSE PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2- TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA)
665	3216	AA894101	NNN		[M.musculus]
					ESTs, Moderately similar to PNAD_MOUSE PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA)
665	3217	AA894101	L		[M.musculus]
668	21989	AA894188	Q, R		ESTs
671 671	3928 3929	AA894233 AA894233	Z, AA, RR JJ		ESTs ESTs
07.4	00054				
674 675	26051 19120	AA894316 AA894318	BBB, CCC ZZ, AAA		ESTs ESTs
676	23332	AA894321	D		ESTs, Weakly similar to I49759 hepatocyte growth factor- regulated tyrosine kinase substrate Hrs [imported] - mouse [M.musculus]
677	1578	AA894338	III, JJJ		ESTs, Weakly similar to T24832 hypothetical protein T11F9.11 - Caenorhabditis elegans
678	17788	AA899045	x		[C.elegans] ESTs, Moderately similar to ESTD_HUMAN Esterase D [H.sapiens]
679	21230	AA899057	O, P, Q, R		ESTs
680	4107	AA899109	RR		ESTs
681	18477	AA899120	D, E		
682	12195	AA899121	RR		ESTs, Highly similar to hypothetical protein FLJ20602 [Homo sapiens] [H.sapiens]
683	4607	AA899152	W, SS		ESTs

TAB				A	tomey Docket 44921-5093-01000 Document No. 1935323.1
Seq.,	. GLGC	AGE OF AGE OF OI POSION	Modgi (Codg	emeń eneo myony	Unigene Sequence Cluster Title
					ESTs, Moderately similar to IF4G_HUMAN Eukaryotic translation initiation factor 4
684	12203	AA899256	z		gamma (elF-4-gamma) (elF-4G) (elF4G) (P220) [H.sapiens]
685	4196	AA899304	FF, XX, BBB, CCC		ESTs
			F, RRR,		ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans
688	22051	AA899498	บบบ		[C.elegans]
688	22052	A A 800 400		·	ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans
689	22308	AA899498 AA899535	K C, 000		[C.elegans] ESTs
	22000	7.0.00000	0, 000		ESTs, Highly similar to 2020285A BRG1 protein [Mus musculus]
690	18588	AA899635	TT, DDD		[M.musculus]
691	12094	AA899681	U, LL, CCC, DDD		ESTs, Weakly similar to C16C10.11.p [Caenorhabditis elegans] [C.elegans]
692	21354	AA899721	U, FF, LL, BBB, RRR, SSS, UUU		ESTs
693	4663	AA899723	Q, R		EST
695	20038	AA899797	BBB, RRR		EST
696	4095	AA899814	O, P, VV		ESTs
697	2559	AA899828	C, UU		ESTs
698	4674	AA899847	JJ, WW,		ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse (fragment) [M.musculus]
700	22060	AA899898	General Alternate		ESTs
701	4689	AA899899	DDD U, NN, BBB, RRR,	:	ESTs
702	18890	AA899964	บบบ		ESTs
703	8988	AA900148	S		ESTs
707	4730	AA900326	G, H		ESTs
708 709	15992	AA900422	FF ·		ESTs
109	4746	AA900452	NNN		EST

Social Color	TABL	EI		1	₹Aŭ	tomey Doctet 44921-5033-011WO Document No. 1935323.1
17368	600 : E00 :	10 Kg			EMIELA EMES MXXXMX	Unigene Sequence Cluster Title
Trace						
17368	1					
Test	710	17200	A A D D D E 4 D			
12210	112	11/300	AA900546			[C.elegans]
Title	713	12210	AA900593			ESTe
ESTs, Highly similar to S78418   ribosomal protein RL32, mitochondrial [validated] - rat (tentative sequence) (fragment)   [R.norvegicus]						
Ribosomal protein RL32, mitochondrial [validated] - rat (tentative sequence) (fragment)	<del>                                     </del>	10200	7 0 000010	-		
Title	i					
Tit	İ	1				
717         16067         AA900976         UUU         [R.norvegicus]           718         4801         AA900981         C         EST           719         4822         AA901041         W         ESTs           721         11467         AA901069         D         ESTs           722         22897         AA901107         V, NN         ESTs           722         22898         AA901107         V, NN         ESTs           724         4866         AA901350         Alternate         ESTs           725         4879         AA923852         MM, TTT         ESTs           726         3963         AA923955         LLL, SSS         ESTs           728         4894         AA923998         Q, R         ESTs           729         17644         AA924036         ZZ         ESTs           730         16370         AA924059         A, B         ESTs           731         14297         AA924092         K         [C.elegans]           734         4171         AA924144         R         elegans] [C.elegans]           735         22969         AA924151         KK         ESTs           736	1			LLL. SSS.		
T19	717	16067	AA900976			
T21	718	4801	AA900981	С		
722         22897         AA901107         V, NN         ESTs           722         22898         AA901107         V         ESTs           724         4866         AA901350         Alternate         ESTs           725         4879         AA923852         MM, TTT         ESTs           726         3963         AA923955         LLL, SSS         ESTs           728         4894         AA923998         Q, R         ESTs           729         17644         AA924036         ZZ         ESTs           730         16370         AA924059         A, B         ESTs           8         ESTs, Weakly similar to T29507         hypothetical protein W05H7.3 - Caenorhabditis elegans         C.elegans]           731         14297         AA924092         K         [C.elegans]           8         ESTs, Weakly similar to T29507         hypothetical protein W05H7.3 - Caenorhabditis elegans           731         14297         AA924192         K         ESTs           8         ESTs, Weakly similar to T29H10.2 p. [Caenorhabditis elegans]         C.elegans]           735         22969         AA924151         KK         ESTs           8         ESTs         ESTs	719	4822	AA901041	W		ESTs
T22			AA901069	1		
T24	1	22897				
Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Canaral   Cana	722	22898	AA901107			ESTs
724         4866         AA901350         Alternate         ESTs           725         4879         AA923852         MM, TTT         ESTs           726         3963         AA923955         LLL, SSS         ESTs           728         4894         AA923998         Q, R         ESTs           729         17644         AA924036         ZZ         ESTs           730         16370         AA924059         A, B         ESTs           FSTs, Weakly similar to T29507         hypothetical protein W05H7.3 - Caenorhabditis elegans         [C.elegans]           731         14297         AA924092         K         ESTs, Weakly similar to T28H10.2.p. [Caenorhabditis elegans]           734         4171         AA924144         R         elegans] [C.elegans]           735         22969         AA924151         KK         ESTs           ESTs, Weakly similar to guanyltransferase [Caenorhabditis elegans]         [C.elegans]           736         22235         AA924152         Z           737         20771         AA924169         VV         ESTs           739         4933         AA924301         NN         ESTs           741         22914         AA924335         O, P         <				1 '		·
Restance	724	4866	AA901350	Alternate		ESTs
T26	725	4879	AA923852	MM, TTT		ESTs
728         4894         AA923998         Q, R         ESTs           729         17644         AA924036         ZZ         ESTs           730         16370         AA924059         A, B         ESTs           8         ESTs, Weakly similar to T29507 hypothetical protein W05H7.3 - Caenorhabditis elegans         Caenorhabditis elegans           731         14297         AA924092         K         ESTs, Weakly similar to T28H10.2.p [Caenorhabditis elegans]           734         4171         AA924144         R         ESTs           735         22969         AA924151         KK         ESTs           8         ESTs, Weakly similar to guanyltransferase [Caenorhabditis elegans]         ESTs, Weakly similar to guanyltransferase [Caenorhabditis elegans]           736         22235         AA924152         Z         [C.elegans]           737         20771         AA924169         VV         ESTs           739         4933         AA924301         NN         ESTs           741         22914         AA924335         O, P         ESTs           8         General         H         ESTs, Moderately similar to hypothetical protein MNCb-0169 [Mus musculus] [M.musculus]           746         4954         AA924444         RR						
729         17644         AA924036         ZZ         ESTS           730         16370         AA924059         A, B         ESTs           8         ESTs, Weakly similar to T29507 hypothetical protein W05H7.3 - Caenorhabditis elegans         Caenorhabditis elegans           731         14297         AA924092         K         ESTs, Weakly similar to T28H10.2.p [Caenorhabditis elegans]           734         4171         AA924144         R         elegans] [C.elegans]           735         22969         AA924151         KK         ESTs           8         ESTs, Weakly similar to guanyltransferase [Caenorhabditis elegans]         ESTs, Weakly similar to guanyltransferase [Caenorhabditis elegans]           736         22235         AA924152         Z         [C.elegans]           737         20771         AA924169         VV         ESTs           739         4933         AA924301         NN         ESTs           741         22914         AA924335         O, P         ESTs           8         General         Hypothetical protein MNCb-0169 [Mus musculus] [M.musculus]           745         18434         AA924443         Alternate         ESTs           746         4954         AA924444         RR         ESTs     <						
Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Tabl						
ESTs, Weakly similar to T29507 hypothetical protein W05H7.3 - Caenorhabditis elegans [C.elegans]  ESTs, Weakly similar to T28H10.2.p [Caenorhabditis elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.elegans] [C.e			1			
hypothetical protein W05H7.3 - Caenorhabditis elegans   C.elegans	730	16370	AA924059	A, B		
Caenorhabditis elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   ESTs, Weakly similar to   T28H10.2.p [Caenorhabditis   elegans ] [C.elegans]   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   ESTs   ESTs, Weakly similar to   Guanyltransferase   Caenorhabditis   elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans						
Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Tabl						
ESTs, Weakly similar to   T28H10.2.p [Caenorhabditis   elegans] [C.elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10.2.p [Caenorhabditis   elegans]   T38H10	704	44007				
T28H10.2.p [Caenorhabditis elegans] [C.elegans]  734 4171 AA924144 R elegans] [C.elegans]  735 22969 AA924151 KK ESTs, Weakly similar to guanyltransferase [Caenorhabditis elegans]  736 22235 AA924152 Z [C.elegans]  737 20771 AA924169 VV ESTs  739 4933 AA924301 NN ESTs  741 22914 AA924335 O, P ESTs  742 CESTS	/31	14297	AA924092	K		
734         4171         AA924144         R         elegans] [C.elegans]           735         22969         AA924151         KK         ESTs           736         22235         AA924152         Z         [C.elegans]           737         20771         AA924169         VV         ESTs           739         4933         AA924301         NN         ESTs           741         22914         AA924335         O, P         ESTs           G, H, General         General         hypothetical protein MNCb-0169           745         18434         AA924413         Alternate         [Mus musculus] [M.musculus]           746         4954         AA924444         RR         ESTs           748         24310         AA924578         M         ESTs						
735       22969       AA924151       KK       ESTs         736       22235       AA924152       Z       [Caenorhabditis elegans]         737       20771       AA924169       VV       ESTs         739       4933       AA924301       NN       ESTs         741       22914       AA924335       O, P       ESTs         G, H, General       General       hypothetical protein MNCb-0169         745       18434       AA924413       Alternate       [Mus musculus] [M.musculus]         746       4954       AA924444       RR       ESTs         748       24310       AA924578       M       ESTs	724	1171	A A O 2 A 1 A A	n		
ESTs, Weakly similar to guanyltransferase [Caenorhabditis elegans]  736 22235 AA924152 Z [C.elegans]  737 20771 AA924169 VV ESTs  739 4933 AA924301 NN ESTs  741 22914 AA924335 O, P ESTs  G, H, General hypothetical protein MNCb-0169  745 18434 AA924413 Alternate [Mus musculus] [M.musculus]  746 4954 AA924444 RR ESTs  748 24310 AA924578 M ESTs					<del></del>	
guanyltransferase   [Caenorhabditis elegans]	1,33	22303	77324131			
Caenorhabditis elegans   [Caenorhabditis elegans]	l	}	}			
736         22235         AA924152         Z         [C.elegans]           737         20771         AA924169         VV         ESTs           739         4933         AA924301         NN         ESTs           741         22914         AA924335         O, P         ESTs           G, H, General         Hypothetical protein MNCb-0169         hypothetical protein MNCb-0169           745         18434         AA924413         Alternate         [Mus musculus] [M.musculus]           746         4954         AA924444         RR         ESTs           748         24310         AA924578         M         ESTs	1					
737 20771 AA924169 VV ESTs  739 4933 AA924301 NN ESTs  741 22914 AA924335 O, P ESTs  G, H, General hypothetical protein MNCb-0169  745 18434 AA924413 Alternate [Mus musculus] [M.musculus]  746 4954 AA924444 RR ESTs  748 24310 AA924578 M ESTs	736	22235	AA924152	7		
739         4933         AA924301         NN         ESTs           741         22914         AA924335         O, P         ESTs           G, H, General         General         hypothetical protein MNCb-0169           745         18434         AA924413         Alternate         [Mus musculus] [M.musculus]           746         4954         AA924444         RR         ESTs           748         24310         AA924578         M         ESTs				$\overline{\nabla}$		
741         22914         AA924335         O, P         ESTs           G, H, General         General         hypothetical protein MNCb-0169           745         18434         AA924413         Alternate         [Mus musculus] [M.musculus]           746         4954         AA924444         RR         ESTs           748         24310         AA924578         M         ESTs						
G, H,   ESTs, Moderately similar to hypothetical protein MNCb-0169   [Mus musculus] [M.musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus musculus]   [Mus mu						
General   hypothetical protein MNCb-0169		<b>†</b>				
745       18434       AA924413       Alternate       [Mus musculus] [M.musculus]         746       4954       AA924444       RR       ESTs         748       24310       AA924578       M       ESTs						
746     4954     AA924444     RR     ESTs       748     24310     AA924578     M     ESTs	745	18434	AA924413			
748 24310 AA924578 M ESTs						
749   18780   AA924586   XX   ESTs	748	24310	AA924578	М		ESTs
	749	18780	AA924586	XX		ESTs

TABL	EI			<i>X</i> : A0	iomey Docket 44921-5033-011WO Document No. 1935323.1
809 (D	ELEC	Lesses Lesses Reservant	Model Codo	Known Gene Name	Unigene Sequence Cluster Title
			U, OO, BBB, RRR,		
750	18891	AA924598	บบบ		ESTs
751	2683	AA924604	LL		ESTs
752	4997	AA924673	D		ESTs
756	5011	AA924751	ZZ, AAA		ESTs
757	23030	AA924763	I, J, NNN		ESTs
			LLL, General Core Tox Markers, General		
758	5026	AA924783	Alternate		EST
759	21735	AA924787	DDD		ESTs
760	12372	AA924803	V		ESTs
761	4067	AA924813	ww		ESTs
763	2888	AA924902	U, DDD		ESTs
764	19444	AA924993	NN		ESTs
765	12379	AA925004	D		ESTs
766	22534				
767		AA925045	L, HH FFF		ESTs
/6/	21458	AA925049	FFF		ESTs
769	5073	AA925061	AA		ESTs, Moderately similar to S20710 hypothetical protein, 16K mouse [M.musculus]
770	20063	AA925063	z, PP, QQ		ESTs, Weakly similar to T33571 hypothetical protein Y59C2A.2 - Caenorhabditis elegans [C.elegans]
771	23147	AA925137	S		ESTs, Weakly similar to RCA1_YEAST MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 (TAT-BINDING HOMOLOG 12) [S.cerevisiae]
772	23448	AA925167	C, L, HH, GGG	-	ESTs
773	4904	AA925186	E		ESTs
779	5131	AA925341	UU		ESTs
780	23978	AA925352	III, JJJ		ESTs
					Rat mRNA for acetyl-coenzyme A carboxylase (EC 6.4.1.2.) 3'
782	5141	AA925393	J		untranslated region
783	5150	AA925432	S		ESTs
786	20805	AA925478	AAA		ESTs

TABL	를 이				Antenna Manalisat (1409) Bassa (240)
0 CANEY	35 V			ES	forney Docket 44921-5063-01W0 Document No. 1935323.1
Seq [D :	(ELGC	(CON-SAN) AGG OT RE(SEQ (D)	Model Codo :	Known Cene Name	Unigene Sequence Cluster Title
787	24225	AA925490	III, JJJ, General Core Tox Markers, General Alternate		ESTs
788	3993	AA925540	Y	<u> </u>	ESTs
790	8092	AA925542	W		ESTs
792	17156	AA925556	O, P		ESTs, Highly similar to B46132 c- Jun leucine zipper interactive (cDNA JZA-20) - mouse (fragment) [M.musculus]
793	4271	AA925603	U, FF, YY, BBB, RRR, SSS		ESTs
795	5213	AA925767	FF		ESTs
796	10588	AA925826	JJ, KK		ESTs
797	18441	AA925849	E		EST
798	3791	AA925854	AA, General Core Tox Markers, General Alternate		ESTs
799	3794	AA925868	ННН		ESTs
800	22224	AA925869	BBB		ESTs
801	23464	AA925876	UU		ESTs
802 803	12196 5241	AA925983 AA925986	X, Y Y		ESTs, Highly similar to hypothetical protein FLJ20602 [Homo sapiens] [H.sapiens]
804	5242	AA925994	S		ESTs ESTs
805	23068	AA926036	FFF		ESTs
806	5251	AA926037	SS		ESTs
807	4007	AA926066	GG		ESTs
808	23468	AA926067	JJ, KK		ESTs
809	22967	AA926080	DDD		ESTs
810	5256	AA926088	L		ESTs
811	5258	AA926089	DDD KKK, OOO,		ESTs, Highly similar to KIAA0164 gene product [Homo sapiens] [H.sapiens]
813 814	17496 17157	AA926109 AA926129	General Core Tox Markers E, O, VV		ESTs ESTs

TABI	<u> </u>			:: A	tomay Doctat 44921-5033-91WO Document No. 1985323.1
Seq.	@L@C		Model		
(D,	ID Ko.	RefSeq (D,	ලිලල්ල :	Known Cone Name:	Unigene Sequence Cluster Title
			FFF,		
			GGG,		
			General		ESTs, Moderately similar to
			Core Tox		S29993 P311 protein - mouse
816	22928	AA926262	Markers		[M.musculus]
819	12401	AA926354	P		ESTs
			000,		
1	i		General		
1			Core Tox		
			Markers,		
			General		
820	22870	AA926360	Alternate		ESTs
			1		ESTs, Highly similar to
					SKIW_HUMAN Helicase SKI2W
			M, DD,		(Helicase-like protein) (HLP)
822	21827	AA933158	EE	·	[H.sapiens]
823	22008	AA942670	UUU		ESTs
					ESTs, Highly similar to
	1				hematological and neurological
					expressed sequence 1 [Mus
825	6039	AA942716	VV		musculus] [M.musculus]
			EE, NN,		
			RR, EEE,		
827	23005	AA942770	MMM		ESTs
828	21318	AA942774	A, B		ESTs
j					ESTs, Weakly similar to Iron-
ļ					containing alcohol
	0045		OO, EEE,		dehydrogenases [Caenorhabditis
830	6615	AA942889	MMM		elegans] [C.elegans]
•	}		General		·
l			Core Tox		•
1			Markers,		
024	22055	14040000	General		COT-
831	23055	AA942929	Alternate		ESTs
1	1	İ			ESTs, Highly similar to S57500
832	22121	AA942961	l.		signal recognition particle - mouse [M.musculus]
833	11168	AA943009	V T		
834	22130	AA943009 AA943020	ZZ, AAA		ESTs ESTs
837	21987	AA943110	KK		ESTs
840	22187	AA943229	MM, TTT		EST
843	24140	AA943501	D		ESTs
844	22242	AA943506	W		ESTs
F			1		ESTs, Weakly similar to
1	1				Y53C10A.5.p [Caenorhabditis
846	10394	AA943564	ZZ		elegans] [C.elegans]
		1			ESTs, Highly similar to cDNA
			]		sequence AB012808; organic
		1	General		cation transporter BOCT [Mus
847	21962	AA943588	Alternate		musculus] [M.musculus]
				L	

				-333-	
TABL	E 9 ·			ASS	torney Docket 44921-5093-011VO Document No. 1935323.1
509 ID	(ELGC)	Conson: Acc or Rowson ID	Model 	Known Cene Neme	Unigene Sequence Cluster Title
					ESTs, Weakly similar to T13C5.6.p [Caenorhabditis
849	22092	AA943734	Z, AA		elegans] [C.elegans]
851	19220	AA943740	777		ESTs
	<del>                                     </del>		NN, III,		
852	12277	AA943800	111		ESTs
853	13027	AA943835	SS		ESTs
856	9549	AA943891	KK		ESTs
858	19129	AA943990	GG		ESTs
860	23527	AA944061	ss		ESTs, Weakly similar to T28052 hypothetical protein ZK858.7 - Caenorhabditis elegans [C.elegans]
861	11255	AA944079	AA		ESTs
862	2658	AA944155	V		ESTs
863	22368	AA944157	OOO, General Core Tox Markers		ESTs
864	22370	AA944158	H, U, BBB, FFF, General Core Tox Markers, General Alternate		ESTs
867	22378	AA944212	1, J		ESTs
868	8321	AA944233	ZZ, AAA		ESTs
			BBB,		
869	13507	AA944244	CCC		ESTs
871	18855	AA944347	D		ESTs
872	4511	AA944348	GG		ESTs
873	16910	AA944352	Z, AA		ESTs, Moderately similar to SUR2_MOUSE Surfeit locus protein 2 (Surf-2) [M.musculus]
874	17901	AA944355	V ===		ESTs
875	22416	AA944380	U, FF, BBB, RRR, SSS		ESTs, Weakly similar to T26648 hypothetical protein Y38A8.1 - Caenorhabditis elegans [C.elegans]
877	15606	AA944401	V, DD, III, NNN		ESTs, Moderately similar to B Chain B, Vhs Domain Of Tom1 Protein From H. Sapiens [H.sapiens]
878	22681	AA944413	B, W, II	,	ESTs
879	19229	AA944419	R		ESTs
883	5138		WW		ESTs
888	12140	AA944752	KKK		ESTs

Seq   SUGG   Ass or   Model   Constant   Model   Constant   Model   Constant   Model   Constant   Model   Constant   Model   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Constant   Const	-01W0 5323.1
C, F, DD, GG, MM, SS, UU, KKK, TTT	
B91	edit re
B91	
B91	
B91	
B92   22519	
B93   23029   AA944935   I, J, KKK, NNN   ESTs	
B93   23029   AA944935   NNN   ESTS   ESTS, Weakly similar to A3   complement factor H-relate protein 3A4/5G4 - mouse (fragment) [M.musculus]   ESTS	
B93   23029   AA944935   NNN   ESTS   ESTS, Weakly similar to A3   complement factor H-relate protein 3A4/5G4 - mouse (fragment) [M.musculus]   ESTS	
BSTs, Weakly similar to A3 complement factor H-relate protein 3A4/5G4 - mouse (fragment) [M.musculus]	
Complement factor H-relate protein 3A4/5G4 - mouse (fragment) [M.musculus]	5000
B95   23985   AA944998   H	
895         23985         AA944998         H         (fragment) [M.musculus]           896         22548         AA945031         Z         ESTs           897         2813         AA945052         RRR         lyase         3-hydroxy-3-methylglutaryl lyase           898         2254         AA945076         Markers         ESTs           899         13557         AA945090         DD         ESTs           900         22558         AA945123         Markers         EST           906         12309         AA945193         W         ESTs           907         22574         AA945268         Alternate         ESTs           900         6592         AA945325         JJ, KK         ESTs	ď
B96   22548   AA945031   Z	
3-hydroxy-3-methylglutaryl CoA   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-methylglutaryl lyase   3-hydroxy-3-meth	
Methylglutaryl CoA   3-hydroxy-3-methylglutaryl lyase   1989   22554   AA945076   Markers   ESTs	
897         2813         AA945052         RRR         Iyase         Iyase           898         22554         AA945076         Markers         ESTs           899         13557         AA945090         DD         ESTs           900         22558         AA945123         Markers         EST           906         12309         AA945193         W         ESTs           907         22574         AA945268         Alternate         ESTs           910         6592         AA945325         JJ, KK         ESTs	
G, FFF, HHH, General Core Tox	CoA
HHH,   General   Core Tox	
Seneral   Core Tox   Markers   ESTs	
Core Tox   B98   22554   AA945076   Markers   ESTs	
898         22554         AA945076         Markers         ESTs           899         13557         AA945090         DD         ESTs           GGG, General Core Tox         General Core Tox         EST           900         22558         AA945123         Markers         EST           906         12309         AA945193         W         ESTs, Weakly similar to C5 complement C5 precursor mouse [M.musculus]           907         22574         AA945268         Alternate         ESTs           910         6592         AA945325         JJ, KK         ESTs	
899 13557 AA945090 DD ESTS  GGG, General Core Tox 900 22558 AA945123 Markers EST  ESTS, Weakly similar to C5 complement C5 precursor mouse [M.musculus]  General 907 22574 AA945268 Alternate ESTs  910 6592 AA945325 JJ, KK ESTs	
GGG,   General   Core Tox	
General   Core Tox	
900 22558 AA945123 Markers EST  906 12309 AA945193 W ESTs  907 22574 AA945268 Alternate ESTs  910 6592 AA945325 JJ, KK ESTs	
900 22558 AA945123 Markers EST  906 12309 AA945193 W mouse [M.musculus]  907 22574 AA945268 Alternate ESTs  910 6592 AA945325 JJ, KK ESTs	
ESTs, Weakly similar to C5   complement C5 precursor   mouse [M.musculus]	
Complement C5 precursor	MC
906   12309   AA945193   W   mouse [M.musculus]	
General	
907         22574         AA945268         Alternate         ESTs           910         6592         AA945325         JJ, KK         ESTs	
910 6592 AA945325 JJ, KK ESTs	
(MILL 100M) 100M(DS/D 1KK ) INC.	
913 22601 AA945574 S ESTs	
Q, R, X,	
918 22266 AA945601 NNN ESTs	İ
918 22267 AA945601 X, Y ESTs	
RRR,	
919 22050 AA945604 SSS ESTs	
925 22625 AA945704 Q ESTs	
Y, DDD,	
926 21382 AA945708 LLL, OOO ESTs	İ
F, VV,	
General	•
927 23035 AA945712 Alternate ESTs	
928 18661 AA945751 C, UUU ESTs	
929 18993 AA945763 DDD ESTs	

TABL	€1			All All	Torney Docket 44921-5033-01W0 Document No. 1935323.1
800	GLGC .	CONSTRUCT.	Mostoli :		
509 . ID .	(ID) Ko	RefSeq ID	Modal ;	දියකුතු ලෙනුනු වනුනු	Unigeno Sequence Cluster Title
	,,			ejouda a consea municonan	
930	22645	AA945765	Р		ESTs
932	16489	AA945784	C		ESTs
933	14419	AA945792	Z, AA		ESTs
934	2671	AA945826	XX, YY		ESTs
	ł		EE, UU,		
			III, JJJ,		
935	6720	AA945828	ккк		ESTs
					ESTs, Weakly similar to S12207
					hypothetical protein (B2 element)
936	18939	AA945875	ITT		mouse [M.musculus]
937	11256	AA945898	AAA		ESTs
938	22713	AA945904	GG		ESTs
	1		II, General		
939	8860	AA945915	Alternate		ESTs
940	13482	AA945938	VV		ESTs
	\ <u> </u>				ESTs, Weakly similar to RIKEN
					cDNA 4933419D20 [Mus
941	22690	AA945970	NN, 00	•	musculus] [M.musculus]
942	12318	AA946031	D		ESTs
943	12585	AA946034	ЈЈ, ННН		ESTs
945	18337	AA946046	Z, AA		ESTs
	1			liver regeneration p-	liver regeneration p-53 related
946	22715	AA946120	F	53 related protein	protein
	<del> </del>			•	
			UU, DDD,		
947	22729	AA946167	บบบ		ESTs
948	8639	AA946221	W		ESTs
949	22755	AA946323	НН		ESTs
950	22069	AA946349	J		ESTs
953	22770	AA946428	PP, QQ		ESTs
1000		70.010.20	M, Z, AA,		
954	21968	AA946434	KKK		ESTs
955	22772	AA946444	RR		ESTs
956	21878	AA946448	DDD		ESTs
330	21070	777340440	1000		ESTs, Moderately similar to CGI-
			1		105 protein [Homo sapiens]
957	21947	AA946451	NN, 00		[H.sapiens]
937	21941	AA940431	W, NN,		[n.sapiens]
050	17400	4 4 0 4 6 4 6 7			FOTo
958	17499	AA946467	00		ESTs
050	00040		EEE,		SOT-
959	22042	AA946476	MMM	,	ESTs
960	12963	AA946486	Р		ESTs
l					ESTs, Highly similar to JC6524
1	1	1	1		26S proteasome regulatory
					complex chain p44.5 - human
962	22953	AA946509	K		[H.sapiens]
963	23750	AA946530	ww		ESTs
964	19143	AA946531	ww		ESTs

TABU	夏1			A	torney Docket 44921-5033-011WC Document No. 1985328.1
<b>S</b> 99	@L@c	Acc or	Model		
(D)	(D) (No	RefSeq ID	Codo	Known Cone Name	Unigene Sequence Cluster Title
					ESTs, Highly similar to
10				W1	FOL2_MOUSE Folate receptor
					beta precursor (FR-beta) (Folate
					receptor 2) (Folate-binding
965	23578	AA955042	lv		protein 2) [M.musculus]
967	23360	AA955104	D		ESTs
968	23471	AA955162	J		ESTs
			GG, KK,		
969	23320	AA955164	ccc		ESTs
970	23478	AA955181	ww		ESTs
971	23492	AA955211	D		ESTs
					ESTs, Highly similar to
	j		1		HSPC025; eIEF associated
					protein HSPC021 [Homo sapiens]
972	11231	AA955240	ннн		[H.sapiens]
973	23512	AA955282	EE		ESTs
974	16509	AA955287	Z, AA		ESTs
975	23520	AA955305	GG		ESTs
976	15383	AA955358	FF		ESTs
977	16823	AA955369	11		ESTs
979	23555	AA955443	C, BB		ESTs
	<u> </u>	-			ESTs, Highly similar to Werner
	Ì				helicase interacting protein,
				,	isoform 1; putative helicase
					RUVBL [Homo sapiens]
980	23557	AA955447	ZZ, AAA		[H.sapiens]
983	23268	AA955506	ww		ESTs
984	23369	AA955523	DD, EE		ESTs
					ESTs, Weakly similar to
	1				ELL MOUSE RNA
					POLYMERASE II ELONGATION
i I			1		FACTOR ELL (ELEVEN-
			1		NINETEEN LYSINE-RICH
					LEUKEMIA PROTEIN)
985	9984	AA955536	V		[M.musculus]
			B, DD,		
			General		
986	23626	AA955540	Alternate		ESTs
	23629	AA955552	I, J		ESTs
			•		ESTs, Weakly similar to T21697
					hypothetical protein F40E10.6 -
					Caenorhabditis elegans
988	12928	AA955564	w, qq		[C.elegans]
			PPP,		<u> </u>
989	23657	AA955630	QQQ	•	ESTs
	23673	AA955684	HH		ESTs
991	23674	AA955691	SS		ESTs

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TABL	E 1 ·		· ·	A	tornay Docket 44221-5033-01000 • Document No. 1935323.1
Seq	@rec	Constant Accor	Model		
(D)	(D) (Xo.	- OI posier	ලිමේම .	Known Cene Kame	Unigene Sequence Ciuster Title
			H, GGG,		
		ł	General		
996	14510	AA955871	Alternate		ESTs
			C, MM,		
997	24251	AA955887	TTT		ESTs
1					ESTs, Highly similar to
1			1		CDK9_HUMAN Cell division
					protein kinase 9 (Serine/threonine
				ļ	protein kinase PITALRE) (C-2K)
999	4191	AA955926	BB, CC		[H.sapiens]
			C, WW,		
			General		
			Core Tox		
1000	17844	AA955927	Markers		ESTs
			General		
1001	24277	AA955962	Alternate		ESTs
1002	23285	AA955976	FFF		ESTs .
1003	19938	AA955980	L		ESTs
1007	497	AA956278	O, P		ESTs
1011	23766	AA956456	DDD		ESTs
1012	23773	AA956476	Р		ESTs
1013	23792	AA956502	D		EST
					ESTs, Highly similar to
					hypothetical protein ET [Homo
L	23799	AA956530	GG		sapiens] [H.sapiens]
1015	22899	AA956555	T		ESTs
	23835	AA956668	S		ESTs
1019	12447	AA956769	K, DDD		ESTs
1020	24152	AA956785	UU		ESTs
1024	23928	AA957010	II, UUU		ESTs
1026	23936	AA957044	D		ESTs
1027	23971	AA957160	T		ESTs
1029	24012	AA957335	JJ, HHH		ESTs
1032	24051	AA957452	Z		ESTs
	24069	AA957500	F		ESTs
	22476	AA957585	AA, II		ESTs
	24091	AA957612	D		EST
1037	2230	AA957643	JJ, KK		ESTs
1040	26094	AA957818	RR		
1041	8725	AA957935	DD, EE		ESTs
	0700		General		ror-
1041	8726	AA957935	Alternate		ESTs
	20333	AA958005	DDD	<u> </u>	ESTs
	18653	AA962998	K		ESTs
	2725	AA963000	F		ESTs
	12513	AA963257	T		ESTs
1050	2049	AA963369	Q		ESTs
1051	2677	AA963443	J		ESTs
1052	2158	AA963505	K		ESTs
1053	2163	AA963560	EE	l	EST

				A	tomay Docket 44921-5033-01000
		CONSINCTION IN THE STREET		19 m 20 m 20 m 20 m 20 m 20 m 20 m 20 m 2	
800 T	GLGC.	Accor	Model		Unigene Sequence Cluster Tille
		RefSeq ID		known ceue nawe	
	2170	AA963590	T		EST
1055	23031	AA963661	KKK	•	ESTs
1056	2481	AA963664	F		ESTs
					ESTs, Highly similar to
					P2G4_MOUSE Proliferation-
ł					associated protein 2G4
ļ					(Proliferation-associated protein
ŀ					1) (Protein p38-2G4)
	24246	AA963703	G		[M.musculus]
1059	18138	AA963815	FF		ESTs
1061	24322	AA964068	KK		ESTs
1063	15474	AA964114	CCC		ESTs
1065	2304	AA964212	E		EST
1066	5936	AA964214	บบ		ESTs
1			A, B,		
1			General		·
	2319	AA964259	Alternate		ESTs
	2320	AA964263	NN, OO		ESTs
	2335	AA964302	T		ESTs
1	2342	AA964336	MM, TTT		ESTs
1071	2095	AA964362	DDD		ESTs
				•	ESTs, Highly similar to G01932
					queuine tRNA-ribosyltransferase
			H, PPP,		(EC 2.4.2.29) - human
	2350	AA964368	QQQ		[H.sapiens]
	2649	AA964377	V		ESTs
	2373	AA964455	JJ		ESTs
1076	19452	AA964500	Y, CCC		EST .
	2383	AA964514	00		ESTs
	11274	AA964535	11		ESTs
1079	2393	AA964544	П		ESTs
					ESTs, Moderately similar to SH3-
		•			domain GRB2-like B1
					(endophilin) [Mus musculus]
	23714	AA964563	HHH		[M.musculus]
	19145	AA964613	KKK		ESTs
1082	2424	AA964617	K, L	-	ESTs
			PP, QQ,		
1085	2430	AA964641	III, JJJ		ESTs
	0.455		D, L, Q,		
1086	2433	AA964653	R, S		ESTs
			PP, QQ,		
			General		
1087	2444	AA964692	Alternate		ESTs
			U, FF,		
			BBB,		
	2457	AA964752	RRR		ESTs
1089	2459	AA964755	A, B, VV		ESTs

TABL	E1			A	torney Docket 4X921-5033-91W0 Document No. 1935323.1
Seq :	@r@c	CENLINI AGE OT	Model		
(D): 454	. ON OI	Roßog ID	Code: :::	Known Cene Name	Unigene Sequence Cluster Title
			General		
			Core Tox		
			Markers,		ESTs, Weakly similar to
			General	\	K05C4.2.p [Caenorhabditis
1091	2468	AA964807	Alternate		elegans] [C.elegans]
			F, Y,		
			General		
1092	11324	AA964832	Alternate		ESTs
	1		S, MM,		
			TT, WW,	٦	
			General		
1094	2486	AA964871	Alternate		ESTs
1004	12400	74304071	JJ,		1013
l			General	·	
		1	Core Tox		
1		1	Markers,		
			General		
1096	12361	AA965031	Alternate.		ESTs
			General		
1098	2691	AA965075	Alternate		ESTs
1099	2566	AA965118	SS		ESTs
			1		ESTs, Weakly similar to S48963
	'				hypothetical protein YHR121w - yeast (Saccharomyces
1100	2568	AA965120	UU	,	cerevisiae) [S.cerevisiae]
1.00	2000	77.303120	-		cerevisiae) [O.cerevisiae]
			A, K, KK,		
			uu, ww,		·
			ZZ, FFF,		
			GGG,		
			ннн,		
			000,		ESTs, Weakly similar to T24832
			General		hypothetical protein T11F9.11 -
4404	0500		Core Tox		Caenorhabditis elegans
1101	2569	AA965122	Markers		[C.elegans]
	ł	1			ESTs, Weakly similar to 164799 sepiapterin reductase (EC
		1			1.1.1.153) - rat (fragment)
1102	2581	AA965162	GG		[R.norvegicus]
1103	2584	AA965168	X, Y		EST
1104	16680	AA965190	KKK		ESTs
1106	2620	AA965278	RR		EST
1107	2794	AA996412	N		ESTs
			General		
1108	15907	AA996422	Alternate		ESTs
1109	8527	AA996461	K, FF		ESTs
4445	070-		General		
1110	6783	AA996463	Alternate		ESTs
1113	2860	AA996581	Z, AA		ESTs

TABU	<b>E</b> 1				tomay Docket 44921-5033-01W0
		(censank	7	T	Document No. 1935323.1
Seq	@r@c		March 1	***	, <del>1</del>
		ReiSeg ID.	Model Code	Known Cene Name	Unigene Sequence Ciuster Tille
				Minewi Gene Ketina	·
1114	2874	AA996640	S	· · · · · · · · · · · · · · · · · · ·	EST
1115		AA996688	Q, R		ESTs
1116	2898	AA996697	ZZ, AAA		ESTs
j	1	ļ	C, I, J, KKK,		
		1	General		
			Core Tox		
1117	2905	AA996727	Markers		ESTs
1118	2918	AA996797	S, SS		ESTs
1119	2922	AA996816	GG		ESTs
1120	12589	AA996864	K		ESTs
1122	2940	AA996886	D		ESTs
1123	16496	AA996955	L		ESTs
					ESTs, Highly similar to 1802387B
i	1	1			transcription factor
	į	1			IIE:SUBUNIT=small 34kD [Homo
1124	2978	AA996974	T		sapiens] [H.sapiens]
			PPP,		
		į.	QQQ,		
1			General		
1			Core Tox		
1126	20694	AA997048	Markers		ESTs
1129	3132	AA997191	1, J		EST
i			MM,		
			000, TTT,		
			General		·
			Core Tox		
1130	3145	AA997237	Markers		ESTs
1131	17343	AA997242	AA		ESTs
1132	3152	AA997253	ww	· · · · · · · · · · · · · · · · · · ·	EST
			General		201
			Core Tox	•	
			Markers,		
1			General		Rattus norvegicus Ratsg2 mRNA,
1134	19249	AA997342	Alternate		complete cds
1136	3168	AA997394	DDD		EST
					ESTs, Weakly similar to low
i			III, JJJ,		density lipoprotein receptor-
1			General		related protein 6; low density
	l		Core Tox		lipoprotein-related protein 6 [Mus
1138	3189	AA997438	Markers		musculus] [M.musculus]
		\			ESTs, Highly similar to 2120310B
					RNA polymerase II elongation
1120	17040	A A 007500	000		factor [Mus musculus]
1139	17246	AA997522	CCC		[M.musculus]
1140 1141	16619 21872	AA997544 AA997577	TT, DDD FF		EST
1143	12616	AA997577 AA997599	000		ESTs
1173	12010	~~331333			ESTs

TABL	<b>E</b> 1	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\		200	torney Docket 44921-5033-01000 Document No. 1985328.1
Sog i	ELEC:	Censent Acc or Refect ID	Model Code	وأستار وروى وسوماكا	Unigene Sequence Cluster Tille
					Rattus norvegicus putative G-
			General		protein coupled receptor RA1c
1144	3032	AA997671	Alternate	,	mRNA, complete cds
			BB, DD,		
			PP, QQ,	chemokine orphan	
1146	3452	AA997721	JJJ, NNN	receptor 1	chemokine orphan receptor 1
1147	3057	AA997731	RR		EST
	3265	AA997784	BB, CC		EST
1150	3268	AA997793	E		ESTs
1152	16071	AA997821	ZZ, AAA		ESTs
}			L, WW,		
1			SSS,		
1155	3302	AA997905	บบบ		ESTs
1156	3308	AA997929	Q, R		ESTs
1157	3722	AA997979	DD, KKK		ESTs
1158	3332	AA998006	ZZ, AAA		ESTs
	3346	AA998043	WW		ESTs
	3362	AA998092	OO, XX RR		ESTs
1163	24095	AA998102	KK		ESTs
1					ESTs, Highly similar to
					ORN_HUMAN Oligoribonuclease, mitochondrial precursor (Small
					fragment nuclease) (CGI-114)
1165	2084	AA998151	X, Y		[H.sapiens]
	16533	AA998174	ΩU .		ESTs
	6789	AA998207	F		ESTs
	3725	AA998222	EE, NNN		ESTs
1170	3730	AA998234	DD		ESTs
					ESTs, Moderately similar to
					JC2070 NADPH dehydrogenase
			X, Y, LLL,		(flavin) (EC 1.6.8.2) - human
1171	17470	AA998264	UUU	,	[H.sapiens]
1172	3744	AA998266	NN, 00		ESTs
1173	19458	AA998345	GGG		EST
			General		
			Core Tox		
			Markers,		
			General		
1178	17009		Alternate		ESTs
1179	3526		WW		ESTs
1181	12644		UUU		ESTs
4400			FFF,	ļ	
1182	3411		GGG		ESTs
	22737		BBB		ESTs
1184 1185	14404		EE		ESTs
1 102	3618		DDD		EST
1186	3460		BBB, CCC		ESTs
	13549		W		ESTs ESTs
			HH		ESTs
03	2000	. 3 1000000			LU13

TABL	E1	5.5 ²² .ea.; 		A STAN	torney Docket 44921-5033-91000 Document No. 1986328.1
S09 ID	ELEC :	Kaksad (D Vee or Kansen/i	Model Code	Known Gene Neme	Unigene Sequence Cluster Tille
1190	16821	AA999042	DD, EE, PP, QQ		ESTs
1191	3705	AA999054	ннн		ESTs
1193	3715	AA999103	K		ESTs
1194	3720	AA999138	RRR, SSS		ESTs
1195	3079	AA999169	QQ		ESTs
1201	25124	AB001453	RR		
1204	25134	AB004277	LL		
1213	12019	AB019693	М	HP33	HP33
1218	25160	AF004661	RR		
1010	-			Solute carrier family 11 member 2 (natural resistance- associated macrophage protein	Solute carrier family 11 member 2 (natural resistance-associated
1219	2012	AF008439	NN	2)	macrophage protein 2)
1224 1226	18624 20283	AF025308	7 00	- 1011111	
1227	25170	AF029357 AF030087	Z, AA DDD		
			I, L, NN, OO, PP, QQ, III,		
1228	23044	AF034218	111	hyaluronidase 2	hyaluronidase 2
1228	23045	AF034218	J, L, DD, EE	hyaluronidase 2	hyaluronidase 2
1229	7005	AF034237	W, PPP, QQQ		FOT-
1231	20188	AF034237 AF034900	Z, AA		ESTs
1239		AF079864	OOO, General Core Tox Markers, General Alternate	zinc finger protein	Rattus norvegicus putative G- protein coupled receptor RA1c mRNA, complete cds
1240	25203	AF079873	D	zinc finger protein 162	
1240	20200	VI-019012	R D, K, ZZ,	core binding factor	
	21957	AF087437	AAA	beta	ESTs
1245	25216		D, Z, AA		
1250	21757	AI007656	MM, TTT		ESTs
1252	22733	Al007668	C, DD, EE		ESTs
1253	22746	Al007672	B, W, CC		ESTs
1256	11361		General Alternate		ESTs
1257	1804		N, T, DD, EE		

TABL	31			. Ag	tornay Docket 44921-6033-01WO
	1	100000000000000000000000000000000000000	1	·	Document No. 1935328.1
S©@∙ <u>;</u>	@L@G	Constant Acc or	Model	to walking	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
(D)	10 Ko.	RefSeq ID	Code .	Known Gene Name:	elill relevid concuped chefold
			DD, KKK,		
1257	1805	AI007824	NNN		
	l		I, J, WW,		
			KKK,		
1261	11728	Al007884	NNN		ESTs
1263	4037	AI007942	UUU		ESTs
	23556	AI008205	Q, R		ESTs
	4063	AI008258	ww		ESTs
1272	13009	A1008380	WW		ESTs
			GGG,		
ļ	ŀ		ннн,		
4070	20422	A1000000	General		
1273 1274	26123 14737	AI008396 AI008416	Alternate		ESTs
12/4	14/3/	A10064 16	L		ESTs, Highly similar to G01922
			Ì		phosphogluconate
			•		dehydrogenase (decarboxylating)
					(EC 1.1.1.44) - human
1275	23917	AI008441	LLL		[H.sapiens]
12.0		7.11000 111	F, BB,		[i i.oapiono]
1276	4084	AI008504	CC		ESTs
					ESTs, Highly similar to
					synbindin; syndecan binding
					protein 2 [Mus musculus]
1278	24359	AI008536	F		[M.musculus]
1281	12438	AI008736	UU		ESTs
	4103	AI008740	TT		ESTs
1283	24112	A1008773	11		ESTs
			O, P, Q,		
1288	4115	A1008890	R		ESTs
1 1					ESTs, Highly similar to T00358
1000	0400	41000004			hypothetical protein KIAA0684 -
1289	8130	AI008894	HH		human (fragment) [H.sapiens]
			W, GG,		٠
			General		
1290	3365	Al008919	Core Tox Markers		ECT.
	6818	A1008919	L		ESTs ESTs
1231	0010	A1000931	000,		E318
			General		
l i			Core Tox		ļ
			Markers,		ļ
			General		
1294	13936	Al009021	Alternate		ESTs
			BB, CC,		
			000,		1
			General		
			Core Tox		
1295	4951	AI009026	Markers		ESTs

TABL	<b>E1</b>			× As	torney Doctat 44921-5033-01WO Document No. 1995323.1
Soq.	@r@c	Centank Accor	Model :		\$ 7.4. 1. W
	ID Ko.	Reණිලෙ ID .	ලාගුල	Known Cone Name	Unigene Sequence Cluster Title
1297	4261	AI009079	VV		ESTs
	24665	AI009098	CC, FF		ESTs
	22151	AI009115	Y, PP		ESTs
<b></b>					ESTs, Highly similar to RIKEN
			1		cDNA 2510048O06 [Mus
1301	15366	Al009132	F	A	musculus] [M.musculus]
1302	21595	Al009142	M		ESTs
			PPP,		
	16904	Al009156	QQQ		ESTs
1305	12704	Al009194	UU		ESTs
1307	3755	Al009208	A, B		ESTs
1308	3992	Al009222	L		ESTs
1310	15905	Al009274	S		ESTs
1					ESTs, Weakly similar to
					C37H5.3.p [Caenorhabditis
1311	7524	AI009350	F, R		elegans] [C.elegans]
1010			General		
1312		AI009362	Alternate		ESTs
1	4154	A1009467	MM, TTT	·	ESTs
1318	6826	AI009493	G, H		ESTs
4004	40500		CC, III,		-o
1321	10532 6831	A1009602	1111		ESTs
1323	21750	Al009644 Al009663	K, RR FF		ESTs ESTs
1323	21750	A1009003	ГГ		2018
1324	19358	Al009675	T, XX, YY		EST
1024	10000	7.1003073	C, DD,		
			KKK,		
			NNN,	,	
1325	22840	A1009676	RRR		ESTs
1327	21192	Al009732	C, HH		ESTs
			General		
			Core Tox		
1			Markers,		
			General		
1329	15089	AI009752	Alternate		ESTs
1331	6845	Al009781	SS	* ***	ESTs
					ESTs, Moderately similar to
					transmembrane 9 superfamily
					member 1 [Mus musculus]
	15593	A1009805	UUU		[M.musculus]
1334	24082	AI009815	BB, CC		ESTs
			CC, EE,		
			PP, SS,		
1335	22619	A1009825	III .		ESTs
			E, BB, III,		
	26133	A1009950	111		EST
1337	3657				ESTs
	6869	AI010025	CCC		EST
1339	16824	AI010027			ESTs

TABL	E1			A	tomay Doctet 44921-5033-011WO Document No. 1835323.1
		CONTRACT			
<b>Seq</b>	@L@C	Acc or	Modal	Manna Gana Mana	
(ID)	(ID K)0. ;	RefSeq ID .		Known Cene Name	Unigene Sequence Cluster Tille
1340	15258	Al010104	W		ESTs
1341	14491	AI010147	III, JJJ	<u> </u>	ESTs
1342	6881	Al010169	KK		ESTs
					ESTs, Highly similar to
İ	Į.				RANG_MOUSE Ran-specific
1					GTPase-activating protein (Ran
1					binding protein 1) (RANBP1)
1345	3534	AI010261	XX, YY		[M.musculus]
1346	14455	AI010277	S		ESTs
1349	7069	AI010301	000		ESTs
1350	6801	AI010316	X		ESTs
•					ESTs, Weakly similar to
1				İ	C16C10.11.p [Caenorhabditis
1351	12095	AI010339	U		elegans] [C.elegans]
1352	16307	AI010416	GG		ESTs
İ	1	·	A, B, W,		
			General		
	5466	AI010423	Alternate		ESTs
1354	18657	AI010435	W		ESTs
1355	6918	Al010445	DD, EE		EST
			DD, FF,		
			UU, WW,		
1358	6919	AI010461	KKK		ESTs
1361	6927	AI010542	ww		ESTs
1364	6957	AI010707	E		EST
1365	22884	AI010755	K		ESTs
1366	6986	AI010885	V, KKK		ESTs .
1					ESTs, Weakly similar to
					R08B4.3.p [Caenorhabditis
1367	8966	Al010944	ZZ, AAA		elegans] [C.elegans]
1368	6995	Al011003	AAA		ESTs
			SS, WW,		
			General		
1370	15679	AI011058	Alternate		ESTs
			MM, KKK,		
1372	6044	Al011285	TTT		ESTs
				synaptic vesicle	
1373	4268	Al011350	F	glycoprotein 2 b	synaptic vesicle glycoprotein 2 b
1374	7042	AI011387	ZZ, AAA		ESTs
ł			General		
1			Core Tox		
1378	3934	Al011510	Markers		ESTs
			000,		
			General		
		AI011556	Alternate		ESTs
1386		Al011746	0		ESTs
1387	21468	Al011749	GG		ESTs
1389	12745	Al011799	11		ESTs

TABL	물 <b>1</b> ·			Altorney Docket 44921-5093-01W0 Document No. 1935323.1		
<b>S</b> 99	@r@c	CONSTAL ACCOT	Model			
(ID)	(ID) (XO).	RefSeq ID	Code	Known Cene Name	Unigene Sequence Cluster Title	
					ESTs, Weakly similar to T31718	
ľ					hypothetical protein F44E7.9 -	
					Caenorhabditis elegans	
1390	2388	AI011806	K		[C.elegans]	
1394	13920	AI011930	ww		ESTs	
			General			
1395	4205	AI011982	Alternate		ESTs	
1396	12751	AI012074	W		ESTs	
					ESTs, Weakly similar to	
					Y33K_HUMAN Hypothetical 33.4	
	9349	AI012143	D		kDa protein [H.sapiens]	
1399	2341	AI012144	AAA		ESTs	
1400	3697	Al012160	GG		ESTs	
1405	2441	Al012231	A, B		ESTs	
1406	13569	AI012281	V		ESTs	
			AAA,	poly(ADP-ribose)		
1407	3957	AI012311	DDD	glycohydrolase	poly(ADP-ribose) glycohydrolase	
			E, CC, DD, UU, III, JJJ, KKK,		·	
1410	24200	AI012356	NNN		ESTs	
1411	19638	AI012366	RR		EST	
1412	7471	AI012379	NNN		ESTs	
1413	12758	AI012385	RR		ESTs	
1416	7247	AI012438	ННН		ESTs	
1419	2670	AI012552	III, JJJ, General Core Tox Markers, General Alternate		ESTs	
1.7.0	20.0	711012002	riteriote		ESTs, Moderately similar to	
1		1		·	dolichyl-phosphate	
					mannosyltransferase polypeptide	
1420	9723	AI012556	GG		3 [Homo sapiens] [H.sapiens]	
1421	5652	AI012562	ZZ, AAA		ESTs	
<del></del>	<del> </del>		† <del></del>	unconventional		
	1		1	myosin Myr2 I heavy	unconventional myosin Myr2 I	
1422	17489	AI012566	Р	chain	heavy chain	
1			<del></del>		ESTs, Weakly similar to S37744	
					endo-exonuclease yNucR - yeast	
	l				(Saccharomyces cerevisiae)	
1425	3961	AI012598	MM, TTT		[S.cerevisiae]	
1429	7171	Al012761	JJ, KK		ESTs	
					ESTs, Highly similar to	
					hypothetical protein FLJ10099	
1431	8594	AI012932	GG		[Homo sapiens] [H.sapiens]	
1434	14033	Al012979	ww. AAA		ESTs	

TABU	<b>3</b> 1			A	lorney Docket 44921-5038-01WC Document No. 1935323.1
	ELGE		Model Code	Known Cene Name	Unigene Seguenes Cluster Title
1435	10641	AI012995	Z, AA		ESTs
1.100	10011	7.110 12000			ESTs, Moderately similar to
j		1			N4AM_HUMAN NADH-
l				·	ubiquinone oxidoreductase
		İ			subunit B14.5a (Complex I-
1436	17054	AI013031	11		B14,5a) (CI-B14,5a) [H.sapiens]
		<del></del>	KK,		<u> </u>
l		•	General		
1			Core Tox		
1			Markers,		
İ			General		
1438	7199	AI013044	Alternate		ESTs
					ESTs, Moderately similar to
					hypothetical protein FLJ14621
1439	3191	Al013075	A, B		[Homo sapiens] [H.sapiens]
			Q, R, III,		
	21073	Al013090	<b>J</b> JJ		ESTs
	7248	Al013362	T		ESTs
	26147	AI013387	Υ		
1445	12793	Al013395	RR		ESTs
1446	19467	AI013397	Z, AA		ESTs
}			I, J, BB,		
1			00, LLL,		
1440	7005	41040057	General		FOT-
1449	7225	AI013657	Alternate V		ESTs ESTs
1450 1451	15130 17167	AI013676 AI013690	O, P	,	ESTs
1451	117107	A1013090	U, P		ESTs, Weakly similar to Human
					mRNA KIAA0066 predicted
					protein like [Caenorhabditis
1454	7281	AI013755	L		elegans] [C.elegans]
1455	2058	Al013756	QQ		ESTs
1			A, B, FF,		
			GGG,		
			000,		
			General		
			Core Tox		
1457	2799	AI013778	Markers		ESTs
1458	4066	Al013782	E		ESTs
			PP, QQ,		
	3260	AI013875	BBB		ESTs
	8585	AI013886	K		ESTs
	21454	AI013888	Z, AA		ESTs
	21074	AI013890	NN, 00		ESTs
	11547		11		ESTs
1468	15786	Al013924	PP, SS		ESTs
			EEE,		
	12779	Al013978	MMM		ESTs
1471	15936	AI013993	DD, EE		ESTs
1472	23646	AI014072	M		ESTs

TABL	<b>E</b> 1	* * * * * * * * * * * * * * * * * * *		· Al	torney Docket 44921-5033-011W0 Document No. 1935323.1
Seq :	ELEC	: inc:100) (; 100) - Ulderwor	Model .	Known Cene Name	Unigene Sequence Civeter Title
1473	7214	AI014145	YY		ESTs
1474	12431	Al014149	К	<del></del>	ESTs
1475	6277	AI014154	XX		ESTs
1415	0211	71014104	000,		1013
1	1		General		
1			Core Tox		
			Markers,		
1,470	7044		General		
1476	7344	AI028942	Alternate	<u> </u>	ESTs
1477	7345	A1028948	N FF		ESTs
1478	7362	AI029026	M, EE		ESTs
1470	24022	A1020057	E, KKK,		COT-
1479	21933	A1029057	บบบ		ESTs
1481	6792	A1029066	D		ESTs
1482	7384	AI029143	NN, 00	! 	ESTs
1483	7393	Al029191	FF		ESTs
1484	7402	AI029211	D		EST
	3647	A1029285	ZZ, AAA		ESTs
1487 1488	7639 7448	Al029292 Al029434	L, Z, AA JJ, KK		ESTs
	2668		CCC		ESTs
1490	2000	Al029455	CCC		ESTs Madagadaly signilar to
					ESTs, Moderately similar to
	1		ļ		transmembrane 9 superfamily
1492	15594	A1029672	ccc		member 1 [Mus musculus]
1493	7514	AI029672 AI029694	JJ, KK		[M.musculus] ESTs
1493	1314	A1029094	33, KK		ESTs, Moderately similar to
	İ				hypothetical protein FLJ20399
1494	7517	A1029709	BBB	• •	[Homo sapiens] [H.sapiens]
1495	7380	Al029723	Q, R, W		ESTs
1435	7300	71023723	<u>α, π, νν</u>		2018
					ESTs, Highly similar to
					VAA1 MOUSE Vacuolar ATP
					synthase catalytic subunit A,
1				HMm:ATPase, H+	ubiquitous isoform (V-ATPase A
				transporting,	subunit 1) (Vacuolar proton pump
				lysosomal 70kD, V1	alpha subunit 1) (V-ATPase 69
1498	2108	AI029960	ZZ, AAA	subunit A, isoform 1	kDa subunit 1) [M.musculus]
	2310	AI029969	BB, OO		ESTs
1500	7574	Al029976	D		ESTs
			_ I, J,		
1			000,		
			General		
			Core Tox		
1501	7582	A1029996	Markers	·	ESTs
	7583		EE, KKK		EST
	7586		H		ESTs
1504	14492	Al030091	00		ESTs

TABL	<b>≣</b> 1 ·	*		¥ A	tomey Docket 44921-5083-91WO Miss. Document No. 1986323.1
509 10	ELEC	Conson: Ace or Refseo ID	Model Codo :	Known Cene Neme	Unigene Sequence Cluster Title
1505	7617	Al030170	OOO, General Core Tox Markers		ESTs
1506	7618	AI030172	Z, AA		ESTs
1508	7003	Al030259	W, EE, OOO, General Core Tox Markers		ESTs, Moderately similar to hypothetical protein MGC12904 [Homo sapiens] [H.sapiens]
1509	6553	AI030271	RRR	**************************************	ESTs
1510	5856	AI030284	DDD		ESTs
1511	6192	AI030301	LL, SS		ESTs
1512	7681	Al030449	S		ESTs, Moderately similar to methyltransferase-like 1 (S. cerevisiae) [Mus musculus] [M.musculus]
1513	10710	Al030494	GG, HH, JJJ, KKK U, EEE,		ESTs
1514	2997	AI030545	MMM		ESTs
	7736	Al030545	E		EST
1517	7745	AI030001	MM, TTT		ESTs
1519	21172	Al030700	KK		ESTs
			I, J, T, General Core Tox		
	2911	A1030835	Markers		ESTs EST
1521 1522	10748 19560	Al030839 Al030921	D D		EST
	7825	Al030921	VV		ESTs
1527	7831	Al031025	RRR		ESTs
1528	5350	Al043611	M		ESTs
1	7860	Al043662	M. SS		ESTs
	19617	AI043664	D, RR		EST
1532	7882	Al043720	<del>                                      </del>		EST
	7584 5263	Al043724 Al043745	JJ, General Alternate SS, TT		ESTs ESTs
1535	2901	Al043752	FFF		ESTs
1537	7893	Al043761	General Core Tox Markers FFF, General Core Tox		EST
1538	7903	Al043805	Markers		ESTs
1539	10805	AI043840	Z, AA		EST
1541	3899	AI043904	В		ESTs

TABL	<b>E</b> 1	: .		tomay Docket 44921-5038-011WG
Soq ID 771	ID KJO. GFGC	Centenk Accor Rowce ID		Unigeno Sequence Cluster Tille
			K, X, Y,	
			SSS,	
1542	7926	AI043913	UUU	ESTs
1543	7938	AI043953	JJ, KK	EST
1544	17625	AI043961	D	 EST
1546	19121	AI044101	NN	 ESTs
1547	5386	AI044137	RR	
1548	5396	Al044176	EE	 EST
1549	5419	AI044225	D	ESTs
1551	4892	AI044292	E, NN	ESTs
1553	5464	AI044345	F, FFF	ESTs
1554	5465	AI044348	XX, PPP, QQQ, General Alternate	ESTs, Moderately similar to hypothetical protein FLJ11218 [Homo sapiens] [H.sapiens]
1555	21228	AI044404	11	 ESTs
1556	18986	AI044478	C	ESTs
1557	5523	AI044568	KKK, NNN	ESTs
1559	9889	AI044621	U, GG	 ESTs
1560	9893	AI044643	RR	ESTs
1562	19300	AI044706	F, S	EST
1567	22179	AI044700	D D	 ESTs .
1568	9924	AI044915	RR	 ESTs
1569	4047	AI044947	Q, R	 ESTs
1570	5662	AI044987	AA	 ESTs
1370	13002	A1044307	~	ESTs, Moderately similar to
1571	6740	AI045003	General Alternate	hypothetical protein DJ167A19.1 [Homo sapiens] [H.sapiens]
1572	9940	AI045008	X, Y	ESTs
1573	24290	AI045040	RRR, SSS, UUU, General Alternate	ESTs, Weakly similar to T15251 / hypothetical protein K07B1.4 - Caenorhabditis elegans [C.elegans]
1574	5684	AI045056	L	ESTs
1575	3406	AI045083	N	ESTs, Moderately similar to Y256_HUMAN HYPOTHETICAL PROTEIN KIAA0256 [H.sapiens]
1576	5696	AI045116	S	 ESTs
			General	
1577	20444	A1045118	Alternate	ESTs
1579	5703	AI045136	S	ESTs
1580	9963	Al045144	J, S	EST, Moderately similar to A34372 complement C6 precursor - human [H.sapiens]
1585	20524		E, JJJ, NNN	ESTs
1587	18932	AI045451	F	ESTs
1588	5809	AI045488	RR	EST

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TABLI	31	17.		AS	lomey Docket 44921-5038-01WC Document No. 1935828.1
S00. (D):	id ko: Grec'	CONSINT ACCOT RefSeq (D.A.	Coco. :: Model	emell eneo awankl	Unigene Sequence Cluster Title
					ESTs, Highly similar to Y233 HUMAN Hypothetical
1589	10008	AI045546	AA		protein KIAA0233 [H.sapiens]
1590	5824	AI045555	X	,	ESTs
1000	UULT	7.10-10000	<u> </u>		ESTs, Weakly similar to T25443
					hypothetical protein B0261.4 -
					Caenorhabditis elegans
1591	12825	AI045672	MM, TTT		[C.elegans]
1592	5873	AI045767	GGG		ESTs
1595	5886	AI045807	EE		ESTs
1596	5890	AI045836	D		ESTs
1597	8701	AI045945	KK		ESTs
1598	10053	AI045948	ww		ESTs
			CC, III,		
1599	6825	A1045972	บบบ		ESTs
			:		EST, Weakly similar to
					Glutaredoxin, Zinc finger, C3HC4
					type (RING finger)
					[Caenorhabditis elegans]
1601	10055	AI058291	NN, 00		[C.elegans]
			General Core Tox		
1602	16765	AI058319	Markers		ESTs
					ESTs, Moderately similar to
					uncharacterized bone marrow
					protein BM033 [Homo sapiens]
	8025	AI058365	O, P		[H.sapiens]
	8627	AI058453	RR		ESTs
1608	8065	AI058509	W		ESTs
1609	8068	AI058524	M		ESTs
1610	8177	AI058603	BBB		ESTs
1612	8113	AI058669	RR		ESTs
					ESTs, Highly similar to MTR3 MOUSE Myotubularin-
1613	10084	AI058674	Т		related protein 3 [M.musculus]
	3090	AI058074 AI058730	II, VV		ESTs
	10093	AI058746	DDD		ESTs
	8143	AI058759	AA, FFF		ESTs
1617	10103	AI058821	L .		EST
1618	18178		N		ESTs
	4789	AI058889	MM, TTT		ESTs
1621	5549		LLL		ESTs
			KKK, General Core Tox		
	8600	AI058956	Markers		ESTs
	8202	AI058990	Q, R		ESTs
	8206		W		ESTs
	4155		MM, TTT		ESTs
1626	8220	AI059046	НН		ESTs

TABL	멸이 : ''' :		*	. A	tomay Docket 44921-5033-011WC Document No. 1935323.1
		Kare and			
Seq.	@L@C .	Accor Reference	Model .	Known Gene Mame	Unigene Sequence Cluster Tille
	8221	AI059061			ESTs
	8230	AI059061	JJ, KK JJ, KK		
	8232	AI059117	D	·	ESTs
	8283	<u> </u>	K		ESTs
		A1059290			ESTs
1633	8285	AI059298	XX		ESTs
			LL,		
4004	0000	41050050	General		
	8303	A1059352	Alternate		ESTs
	8314	A1059386	Q, W	· · · · · · · · · · · · · · · · · · ·	ESTs
1638	10200	AI059444	Z, UUU		ESTs
					ESTs, Moderately similar to
					POL3_MOUSE Retrovirus-related
1					POL polyprotein (Endonuclease)
1639	14518	AI059477	N		[M.musculus]
	8344	AI059511	A, B		EST
	19230	AI059604	II, UUU		ESTs
	8392	AI059638	RR		ESTs
	8422	AI059723	N, UUU		EST
	9383	AI059824	HH	•	ESTs
1645	8457	AI059835	HH		ESTs
			DD, EE,		-
			HH, PP,		
1646	10270	AI059856	QQ		ESTs
			General		
1647	10281	AI059947	Alternate		ESTs
			B, UUU,		
			General		
	8490	AI059962	Alternate		ESTs
	8494	AI059968	II		ESTs
1651	8500	AI059983	LL		ESTs
			000,		ESTs, Moderately similar to
			General		RIKEN cDNA B230118H07 [Mus
1653	8520	A1060052	Alternate		musculus] [M.musculus]
			E, BB, III,		
		AI060071	JJJ		ESTs
			X, Y		ESTs
1656	23776	AI060224	11		ESTs
					ESTs, Weakly similar to T28787
					hypothetical protein C41D11.5 -
					Caenorhabditis elegans
1657	8116	Al060271	V		[C.elegans]
T					
			WW, DDD		ESTs
			QQ		EST
1660	3498		MM, TTT		ESTs
			I, J, DD,		
			ww,		
	l	l	General	i	
	,		O0110101	7	
		A1069920	Alternate C		ESTs

_	_	_	
~	_	7	
- •	-	•	-

TABL	≣1	, ,		A	tomey Docket 44921-5033-01000 Document No. 1995323.1
Seq ID	10 Kg. ;	(Constant Acc or : Roßeg (D)	Model	Known Cene Neme	Unigene Sequence Clueter Tille
			·		ESTs, Weakly similar to S.pombe hypothetical protein C1D4.09C like [Caenorhabditis
1663	10363	AI069986	A, B		elegans] [C.elegans]
1664	8710	AI070058	AA		ESTs
1666	8789	AI070073	М		ESTs
			ZZ, AAA, PPP, QQQ, General Core Tox Markers, General		
1668	8808	AI070132	Alternate		ESTs
1670	8809	AI070134	PP, QQ		ESTs
1672	7743	AI070233	V, NN		ESTs
1673	24372	AI070241	XX		ESTs
1674	16905	AI070275	GG		ESTs
1675	10396	AI070294	X, Y		ESTs
1676	4437	Al070308	Q, R	HMm:genes associated with retinoid-IFN-induced mortality 19	ESTs, Highly similar to genes associated with retinoid-IFN-induced mortality 19; RIKEN cDNA 2700054G14 gene [Mus musculus] [M.musculus]
1677	8864	AI070319	K		ESTs
1679	8874	AI070336	VV		ESTs
1680	23137	A1070408	Q, R		ESTs
1681	10418	AI070411	JJ, KK		EST
1682	14424	AI070421	Q, II		ESTs
•					ESTs, Highly similar to PSD7_MOUSE 26S proteasome non-ATPase regulatory subunit 7 (26S proteasome regulatory subunit S12) (Proteasome subunit p40) (Mov34 protein)
1683	9767	AI070459	XX, YY		[M.musculus]
1685	8931	AI070531	FF		ESTs
	10155		PPP,		
1690	10472	AI070809	QQQ		ESTs
1691	9012	A1070879	FFF, OOO, General Core Tox Markers	·	EST

TABL	<b>E</b> 1		AVID A STAN		tomey Docket 44921-5033-01WO Document No. 1935323.1
809 ; ID	id no.	Consonia Accor: Resseq ID		Known Cene Name	Unigene Sequence Cluster Title
			A, B, GGG, HHH, PPP, General Core Tox		,
1692	9016	AI070903	Markers		EST
1693	8720	Al071023	N		ESTs, Weakly similar to YG5I_YEAST Hypothetical 29.9 kDa protein in APL6-MES1 intergenic region [S.cerevisiae]
1695	11006	AI071155	D		ESTs
1696	18792	AI071177	General Core Tox Markers		ESTs
1697	9583	AI071185	A, B, CC, NN, OO		ESTs
1699	16799	AI071197	T		ESTs
1701	11019	AI071240	X, Y		EST
					ESTs, Moderately similar to A57050 K-glypican precursor -
	9079	AI071251	L, NN		mouse [M.musculus]
	11024	Al071285	D, V		ESTs
	11057	Al071509	SS		ESTs
1706 1707	9668 9669	Al071538 Al071563	W E		ESTs ESTs
1708	5695	Al071566	PP, QQ		ESTs, Weakly similar to SYBSR threonine synthase (EC 4.2.99.2) yeast (Saccharomyces cerevisiae) [S.cerevisiae]
1709	22929	Al071578	B, Z, II, FFF, GGG, HHH, OOO, General Core Tox Markers		ESTs, Moderately similar to S29993 P311 protein - mouse [M.musculus]
1709	22930	AI071578	FFF, GGG, OOO, General Core Tox Markers		ESTs, Moderately similar to S29993 P311 protein - mouse [M.musculus]
1710	9720	A1071727	O, P		EST
1711 1712	11097 9735	Al071749 Al071773	YY		EST ESTs
	9772	Al071773	FF		EST
11117	10112	1, 4101 1000	, , ,		1

TABL	<b>E</b> 1			: A	tomey Docket 44021-5033-011WO Document No. 1935323.1
	T	(Centank	li .	1	I Distribution that he seed 23.1
ବରଗ	Grec	Accor	Moddl.		A.C.
(D) ::-	(ID) (X)0-1	Rossog ID	ලිලේල -	Known Cone Mame	Unigene Sequence Civeter Title
	8711	AI071934	N	rate and economical series	ESTs
1717	9788	Al071958	T		ESTs
1717	9700	AI07 1956			
1		1.			ESTs, Weakly similar to U2af50-
1710	9800	A1070044	-,-,		P1 [Drosophila melanogaster]
1719	19000	Al072014	ZZ		[D.melanogaster]
1			W, LLL,		
1			RRR,		
4720	0005	A1070004	SSS,		507
1720 1722	9805 13426	AI072034 AI072081	บบบ		ESTs
1722	13426	AIU72081	I, J, RR	·····	ESTs
			Ì		ESTs, Weakly similar to
1	]				2118405G hexaprenyl
1	}				pyrophosphate synthetase
1704	9196	41070404			[Saccharomyces cerevisiae]
1724	9196	AI072121	11	<u> </u>	[S.cerevisiae]
					ESTs, Weakly similar to T26686
		1	H, V,		hypothetical protein Y38F1A.6 -
4705	20400	A1070044	General		Caenorhabditis elegans
1725	20123	AI072214	Alternate		[C.elegans]
	ŀ				ESTs, Weakly similar to T08793
1			General		hypothetical protein
1700	0045		Core Tox		DKFZp586F0422.1 - human
1726	9245	A1072278	Markers		(fragment) [H.sapiens]
1728	14231	AI072358	GG, HH		ESTs
1729 1730	10866		K		ESTs .
1730	18877	Al072393	JJ		ESTs
					ESTs, Highly similar to S43484
ł					heterogeneous nuclear
1732	17680	AI072403	vv		ribonucleoprotein F - human
1732	17000	A1072403	General		[H.sapiens]
			Core Tox		
			Markers,		
			General		
1733	9292	AI072485	1	;	FOT-
1734	10893		Alternate N		ESTs
1754	10093		PPP,		EST
1735	10902		QQQ		EST
1733	10302		General		ESTs
				•	1
1736	9331		Core Tox Markers	ļ	CCT-
	9336		GGG		ESTs
	6548		PP, QQ		EST
	9348		T T		ESTs EST
11,40	3373	7 1107 2007	·		
			i		ESTs, Moderately similar to RGR MOUSE RPE-retinal G
			:		
1741	9368	AI072706	_		protein-coupled receptor [M.musculus]
	5000	71012100	<u>-                                      </u>	1	[ivi.iriusculus]

TABL	<b>E1</b>	•		₹.AX	iomey Deciet 44921-5033-01W0 Decument No. 1955328.1
Soq ID	@F@C:		Model Code	Mnown Cene Manie	Unigano Seculoneo Cheter Tille
	9372	AI072712	KK, BBB, RRR, SSS	•	ESTs
1743	10918	AI072733	I, J, DD, EE, JJJ		EST
1744	16813	AI072746	VV		EST
1745	9384	AI072751	НН		ESTs
1746	9385	AI072755	JJ, KK		ESTs
1748	9432	AI072914	KKK		EST
1749	15518	AI072945	ZZ, AAA		ESTs
1750	22269	AI072965	RR		ESTs
1751	10940	AI072998	V		EST
	9469	AI073023	D		ESTs
1753	9471	AI073035	ZZ, AAA		ESTs
1754	10944	A1073039	E, RR		ESTs
1	9475	AI073059	FFF, SSS, UUU		ESTs
1756	7074	AI073086	FFF		ESTs
1757	5091	AI073092	C, LL		ESTs
1758	10958	AI073105	DD, EE		ESTs
1759	10968	AI073207	RR		ESTs
1760	5340	AI073239	Z, AA		ESTs
1761	23124	Al100785	M, OOO, General Alternate		ESTs, Highly similar to germ cell- less homolog (Drosophila) [Mus musculus] [M.musculus]
1762	9190	AI100835	I, DDD		ESTs
1764	10594	AI100878	Q, R		ESTs, Highly similar to hypothetical protein EST00098 [Homo sapiens] [H.sapiens]
1765 1767	4444 5687	AI100882 AI101006	B, V, BB, CC NN		ESTs, Highly similar to HSCO protein [Mus musculus] [M.musculus] ESTs
1768	11942	AI101094	RR		ESTs
1770		Al101113	D, V		ESTs
1771		Al101150	T, LL, TT		ESTs
1772	21913	AI101181	L		ESTs
1773		Al101229	OO, OOO, General Core Tox Markers		ESTs
1774	2220	AI101258	XX, YY		ESTs
1775	11742	AI101262	General Core Tox Markers	•	ESTs
			NN, OO,	HMm:Rho, GDP dissociation inhibitor	ESTs, Highly similar to I49687 GDP-dissociation inhibitor -
1776	5421	Al101270	VV	(GDI) beta	mouse [M.musculus]

TABL	图 1			A	lorney Docket 44921-5033-011WO
800) ID	id ka: Gree	Conson: Accor Rasson ID	Model Code	Kinown Gene Name	elili istavid esnaupos Seginu
1777	7870	Al101319	Υ	•	ESTs
-		İ	G,		ESTs, Weakly similar to
i			General		W06D4.4.p [Caenorhabditis
1779	4650	Al101582	Alternate		elegans] [C.elegans]
	<u> </u>		T, RRR,		
			SSS,		
1780	5597	AI101622	บบบ		ESTs
1781	2295	AI101674	PP, QQ		ESTs
1783	5074	AI101695	С		ESTs
					ESTs, Highly similar to ubiquitin-
		<b>i</b>			like 5 [Mus musculus]
					[M.musculus], ESTs, Moderately
Į.	ļ				similar to F46F11.4.p
1					[Caenorhabditis elegans]
1784	11213	AI101864	v, xx		[C.elegans]
1785	2042	Al101921	O, P, PP		ESTs
					ESTs, Highly similar to cDNA
					sequence AB012808; organic
1					cation transporter BOCT [Mus
1786	21965	AI101977	S		musculus] [M.musculus]
			III, LLL, OOO,		
1			บบบ.		
1			General		
			Core Tox		
1787	14208	AI102017	Markers		ESTs
1793	21592	AI102065	Q, R		ESTs
1794	18565	Al102073	T		ESTs
1795	6213	AI102190	LL		ESTs
1796	11463	AI102236	Z, AA		ESTs
			PPP,		
1797	10227	AI102248	QQQ		ESTs
					ESTs, Moderately similar to
}					BI54_MOUSE BRAIN PROTEIN
1798	22099	AI102258	บบบ		I54 [M.musculus]
1799	9522	AI102382	RRR		ESTs
1800	3320	AI102482	RR		ESTs
1804	11563	AI102560	NNN		ESTs
1805	19769	AI102570	<b>E</b> 10 111		
1806	21056	AI102570 AI102574	E, III, JJJ LLL		ESTs
1809	17510	AI102574 AI102595			ESTS
1009	17510	M1102090	ZZ, AAA		ESTs, Highly similar to proline
1			N 77		rich protein expressed in brain
1910	15515	AI102612	M, ZZ, AAA		[Mus musculus] [M.musculus]
1810 1811	19011	Al102612 Al102618	E, SS		ESTs
1812	23837		KKK		ESTS
1012	23031	71102020	W,	Λ	LUIS
1			VV, General		İ
1816	8837	AI102849	Alternate		ESTs
<del></del>	0001				

TABL	<b>3</b> 1		7.4		tomey Docket 4X121-5033-01WO
					Document No. 1935323.1
800	രാ രര	CONSTRUCTION OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF TH	North		A PARTY OF THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE
නු කුලල් .	00 C/O	Acc or Refseq ID.		Norma Goro Norgo	Unigane Sequence Cluster Title
10 % 2.	יאיסיאו הח	ਅਤਾਲਤਰੀ ਜਨ [ਾ] ਂ		(vznacýn čejnia menija:	Confidence eractorances consisted united
l			U,		
l			General		
			Core Tox		
1817	11228	Al102871	Markers		ESTs
1820	11723	Al102896	K		ESTs
			JJ, NN,		i-o-
1821	6541	AI102905	00		ESTs
1822	22628	AI102955	T, KKK		ESTs
1823	24229	AI102972	N		ESTs
			C, DD,		FOT
1824	13222	AI102977	EE		ESTs
			·		ESTs, Weakly similar to T20117
	Ì				hypothetical protein C50F4.11 -
1005	0704				Caenorhabditis elegans
1825	8784	AI103007	RRR		[C.elegans]
4000	10050	11100050	BB, CC,		507
1826	10659	AI103059	NNN		ESTs
					ESTs, Moderately similar to
4007	0040				selective hybridizing clone [Mus
1827	2316	Al103084	LL V		musculus] [M.musculus]
1829	15128	AI103098	V		ESTs
					ESTs, Highly similar to JC6067
4024	47750	A140224C	1414 TTT		CCAAT-binding factor CBF1 -
1831	17753	AI103246	MM, TTT		mouse [M.musculus]
			Canada		ESTs, Weakly similar to
1832	24181	AI103320	General Alternate		Y40B1B.7.p [Caenorhabditis
1834	1807	Al103365	YY		elegans] [C.elegans]
1034	1007	A1103363	7 1		ESTs, Weakly similar to T31650
					hypothetical protein Y57A10A.cc -
					Caenorhabditis elegans
1835	5197	AI103376	вв, сс		[C.elegans]
1033	3131	A1103370	MM, TTT,		[O.elegaris]
l	ļ		General		
1838	4355	AI103410	Alternate		ESTs
1840	17168	Al103441	00		ESTs
<del></del>					ESTs, Moderately similar to
					RP29 HUMAN Ribonuclease P
1841	15841	AI103465	MM, TTT		protein subunit p29 [H.sapiens]
	21579	Al103572	W		ESTs
	2752	Al103641	Q, R		ESTs
1849	17553	AI103643	X, Y		ESTs
1851	4856	AI103708	O .		ESTs
			-		ESTs, Highly similar to S37488
					gene T10 protein - mouse
1855	17762	AI103854	Н		[M.musculus]
1856	7434	Al103954	Z, AA		ESTs
1859	26213	AI104113	T T	-	
1861	20542		KKK		
1862	11738		LL	,	ESTs
	•				

TABL	<b>3</b> 1			A	torney Docket 44921-5038-01WC
		Cansania.	·		Document No. 1935323.1
S00 [D .	(ID K10°) (GTGC	Acc or Reference	Modal Codo	Known Cene Name	Unigene Sequence Cluster Title
					ESTs, Highly similar to
	İ				presenilins associated rhomboid-
					like protein; hypothetical protein
	04750				PRO2207 [Homo sapiens]
1864	21752	AI104250	LL		[H.sapiens]
1865	5907	AI104261	N	<u> </u>	ESTs
1866	7184	AI104297	F, II		ESTs
			ł		ESTs, Highly similar to RIKEN
1868	7223	AI104373	LLL, UUU		cDNA 2810428I15 [Mus
1871	7006	AI104373	W		musculus] [M.musculus] ESTs
1874	18235	Al104403	Z		ESTs
1877	15019	Al104552	PP, QQ		ESTs
1878	4782	Al104570	D D		ESTs
10.0	11.02	74101070	NN, OO,		2013
			GGG,		
			General		
			Core Tox		
1880	2484	AI104675	Markers		ESTs
			NN, EEE,		
1883	8273	AI104908	ммм		ESTs
					ESTs, Highly similar to RAN
					guanine nucleotide release factor
	23836	AI105088	CCC		[Mus musculus] [M.musculus]
1888	5246	AI105144	Z, AA		ESTs
	i				
			HH, 000,		
			General		
4000	44400	A1405445	Core Tox		
1889	11492	AI105145	Markers		ESTs
1891	17768	AI105196	HH, KKK		ESTs
1892 1894	2196 13231	AI105243 AI105376	J Z, AA		ESTs
1094	13231				ESTs
			M, FFF, GGG,		
			General		ESTs, Moderately similar to
			Core Tox		S29993 P311 protein - mouse
1895	22931	AI105417	Markers		[M.musculus]
	22948	Al105417	C		ESTs
	9141	AI111407	JJ, KK		ESTs
	4013	Al111441	PP, QQ		ESTs
	8305	Al111695	Z, AA		ESTs
	3309	Al111725	<del>UUU</del>		ESTs
	9047		HH		ESTs
					ESTs, Weakly similar to T33164
					hypothetical protein T26C12.1 -
					Caenorhabditis elegans
1906	24275	Al111854	RRR		[C.elegans]
		, , , , ,	1	l	[O.Ologano]

TABL	<b>匿</b> 1			A	tomey Doctet 44921-5033-011WO Document No. 1935323.1
500 D::::	ID Ko4.	COMBONI AGG OT ROSCO ID ::	Model :	Emeki ened axoniki	Unigene Sequence Cluster Title
100000	3.5				ESTs, Weakly similar to
					FKB5 MOUSE 51 kDa FK506-
			1		binding protein (FKBP51)
l		Ì	l, J,		(Peptidyl-prolyl cis-trans
			General		isomerase) (PPiase) (Rotamase)
1907	2539	AI111960	Alternate	Ì	[M.musculus]
1909	19219	AI112059	RR		ESTs
1910	12909	AI112074	RR		ESTs
			A, B, II,		
1	l		NN, OO,		•
j	1		XX, EEE,		
1	İ		FFF,		
	ļ		ммм,		
			000.		·
1	İ		General		
	ł		Core Tox		
1911	4914	AI112086	Markers		ESTs
			V, BB,		
Ì			CC, LL,		
			NN, OO,		
			EEE,		
1912	22522	AI112092	MMM		ESTs
			000,		
			General		
			Core Tox		
1913	4143	AI112107	Markers		ESTs
			A, B, Q,		
1914	14560	Al112111	R	<u> </u>	ESTs A SECTION
Ī					ESTs, Weakly similar to A55169
1015	4464	A1442444	0 0		pre-T-cell receptor alpha chain
1915	4161	Al112141	O, P 000,		precursor - mouse [M.musculus]
	1		General		
			· ·	seizure related gene	
1916	9754	AI112194	Markers	6	seizure related gene 6
1919	9654	Al112416	DDD		ESTs
1920	2482		II		ESTs
1921	11376	Al112863	0, P		ESTs
			- ' - '	<u> </u>	ESTs, Moderately similar to
					ALKB HUMAN Alkylated DNA
1			Q, R,		repair protein alkB homolog
1922	12965	AI112926	MM, TTT		[H.sapiens]
			G, GGG,		
1			General		
1	]		Core Tox		
1923	14512	Al112964	Markers		ESTs
1924	12969	Al112969	Q		ESTs
1927	6555		M, SS		ESTs
1931	17253	Al136523	D, E		ESTs

TABL	롤 1			AND AND AND AND AND AND AND AND AND AND	torney Docket 44921-5033-01WO Document No. 1985328.1
Seq [D ;		Kesseg ID	Model Code	Mnown Cene Name	Unigene Sequence Cluster Title
			PP, LLL,		
4000	0505	41400000	SSS,		
	9595 8985	Al136630 Al136672	UUU RR		ESTs
1934	11301	Al136709	HH		ESTs ESTs
1334	11301	A1130709	BBB,		2018
1935	9373	Al136714	DDD DDD		ESTs
					ESTs, Weakly similar to
					B0432.8.p [Caenorhabditis
1937	3488	Al136830	GG		elegans] [C.elegans]
					ESTs, Highly similar to
			GG, HH,		carcinoma related gene [Mus
	23851	AI136862	UUU		musculus] (M.musculus)
	12142	Al136972	E		ESTs
1945	22722	Al137211	JJ, FFF		ESTs
					ESTs, Weakly similar to Yeast
1046	14015	A1127222	C		YIP1 protein like [Caenorhabditis
1946	14915	Al137232	C		elegans] [C.elegans]
			A, B, NNN,		
			General		
			Core Tox		
			Markers,		
			General		
1948	22234	Al137344	Alternate		ESTs
			U, HH,		
1949	9192	AI137345	XX, YY		ESTs
					ESTs, Highly similar to
1					NUCG_MOUSE Endonuclease
				HMm:endonuclease	G, mitochondrial precursor (Endo
1951	19064	Al137443	E, HH	G	G) [M.musculus]
			LL, BBB,		
			RRR,		
			SSS,		
1050	24464	A4407400	General		
1953	21164	AI137488	Alternate		ESTs
j					ESTs, Weakly similar to T30021
					hypothetical protein K08F11.4 - Caenorhabditis elegans
1956	17369	Al137572	NN		[C.elegans]
	.,,,,,,		General		[O.Gicyaria]
1957	6638		Alternate		ESTs
	5104		RR		ESTs
			E, EE,		
1963	14459		XX, YY		ESTs
			J		ESTs
1965	12030	Al137976	FFF		ESTs

TABL	E1:		220020	, A	lomey Dockel 44921-5083-91WC Document No. 1935323.1
	ī — — ·	Kon:ank	i i	- 10.3	
<b>Seq</b>	10 Ko.	Accor Refseq ID	Model Gade	දුණුවේ දැනුන්වූ	Unigene Sequence Cluster Tille
٠, .	ا محمود جدد	aceses is .		Solitano Solosos Incolares	ont teaches enterpres one guite
			M, FF,		
		Į	ННН,	l	
1060	22492	A1144E06	General	avantin 1	overtin 1
1969 1970	23183 23187	AI144586	Alternate	evectin-1	evectin-1 ESTs
1970		AI144591 AI144612	PP, QQ		ESTS
1972	5993 2264	AI144741	SS		ESTs
1972	1	Al144741	HH		ESTs
1973	6291	A1144797	I, LL		ESTs, Highly similar to
1					SYR HUMAN ARGINYL-TRNA
		1			SYNTHETASE (ARGININE
ļ					TRNA LIGASE) (ARGRS)
1974	7887	AI144832	S, PPP		[H.sapiens]
1975	10529	AI144877	M		ESTs
1976	8880	Al144936	UUU		ESTs
1978	13018	AI145424	KK		ESTs
1370	13010	A1143424	IKK		ESTs, Weakly similar to
					YJ05 CAEEL HYPOTHETICAL
	-				85.1 KD NUCLEASE C41D11.5
1979	5235	Al145569	s		[C.elegans]
1373	0200	A1143303	NNN,		[C.elegans]
		]	General		
		)	Core Tox		
		i	Markers,		
]			General		·
1980	24170	AI145601	Alternate		ESTs
1982	23631	AI145650	O, P		ESTs
1002	20001	1		· · · · · · · · · · · · · · · ·	ESTs, Weakly similar to T31511
Ì		]	MM, TTT,		hypothetical protein Y116A8C.9 -
i .		ļ	General	1	Caenorhabditis elegans
1983	8634	Al145722	Alternate		[C.elegans]
			General		[c.c.oguoj
	}		Core Tox		ESTs, Weakly similar to T21659
	1		Markers.		hypothetical protein F32D8.4 -
			General		Caenorhabditis elegans
1984	8339	Al145761	Alternate		[C.elegans]
			M, GGG,		
			General		
			Core Tox		
	1		Markers,		
	1		General		
1985	5874	AI145801	Alternate		ESTs
			M,		
l	1		General		ESTs, Moderately similar to
			Core Tox		RIKEN cDNA 1110025H10 [Mus
1987	18522	AI145870	Markers	(	musculus] [M.musculus]

TABL	<b>E</b> 1			AS	tomey Doctet 44921-5033-01WG
71	1	(Consont			Document No. 1935323.1
S00 ID	GLEC SOLID		Model :	Known Cene Neme	Unigane Sequence Civeter Tille
			FFF, OOO, General Core Tox		
1989	11576	Al146177	Markers		ESTs ESTs, Weakly similar to Yeast hypothetical 52.9 KD protein like [Caenorhabditis elegans]
1992	18473	AI168975	x, TT		[C.elegans]
1993	11551	AI168981	O, P		ESTs
1994	2060	Al168996	ww	<del></del>	ESTs
1995	22559	AI169007	FFF		ESTs
1997	21523	Al169104	Ħ		ESTs, Highly similar to A26774 platelet factor 4 precursor - rat [R.norvegicus]
1999	16484	Al169116	QQQ		ESTs
			NN, EEE, MMM, General Core Tox		
2000	10984	AI169156	Markers		ESTs
2001	23075	AI169166	General Core Tox Markers		ESTs Highly similar to \$22262
2004	12979	AI169177	NNN		ESTs, Highly similar to S33363 gly96 protein - mouse [M.musculus] ESTs, Highly similar to G33_RAT
2005	806	Al169231	O, P		GENE 33 POLYPEPTIDE [R.norvegicus]
2006	5038	Al169239	Z, AA		ESTs
2007	15323	Al169255	RR		ESTs
			XX, YY, General Core Tox		
	24162	AI169279	Markers		ESTs
2010	22986	AI169291	S		ESTs
2011	7497	Al169302	JJ, PPP, QQQ		ESTs, Highly similar to S27393 sphingomyelin phosphodiesterase (EC 3.1.4.12), acidic, splice form 1 precursor - mouse [M.musculus]
2012	13910	AI169308	NNN		ESTs ESTs, Weakly similar to T29315 hypothetical protein F36D4.5 - Caenorhabditis elegans
2020	24163	AI169430	K, L		[C.elegans]
2022	6623	AI169595	FF.		ESTs

TABL	≣1			A	tornay Docket 44921-5093-01W0
			7	,	Document No. 1935323.1
Seq ID ::	ELEC	© 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Model Code	Known Cene Name	Unigano Sequence Cluster Title
				Serine protease	
ļ				inhibitor, kanzal type	
			1	1/ Trypsin inhibitor-	Serine protease inhibitor, kanzal
			T, PP,	like protein,	type 1/ Trypsin inhibitor-like
2024	24592	AI169622	QQ	pancreatic	protein, pancreatic
2028	11429	AI169706	G		ESTs
			LL, GGG,		
			UUU,		Rat cytochrome P450IB3
	00.400	41400705	General		(P450IIB subfamily) mRNA,
2029	20466	AI169735	Alternate		complete cds
2032	4274	AI169829	E		ESTs
1			A, H, II, FFF,		
			HHH, PPP,		
			QQQ,		
			General		
	1		Core Tox		
2035	3916	AI169947	Markers		ESTs
2000	10010	71103347	YY, PPP,		2013
2036	5954	AI169984	QQQ		ESTs
2000	10001	/	A,		12010
			General		
			Core Tox		
2038	5899	AI170038	Markers		ESTs
2039	21185	AI170056	В		ESTs
2040	21254	AI170059	D		ESTs
2041	22014	AI170117	RRR		ESTs
2044	15102	AI170298	RR		ESTs
2047	2729	AI170363	Z, AA		ESTs
2048	5297	Al170379	W		ESTs
2049	22707	AI170384	LLL		ESTs
2050	19728	AI170394	FFF		ESTs
2051	18744	Al170407	PP, QQ		ESTs
2052	7106	Al170446	AA		ESTs
					ESTs, Highly similar to RIKEN
					cDNA 2610206B05 [Mus
2057	17778	Al170538	ZZ, AAA		musculus] [M.musculus]
	1				ESTs, Moderately similar to
			HH,		hypothetical protein
0050	0404		General		AF053356_CDS3 [Homo sapiens]
2059	6164	AI170597	Alternate		[H.sapiens]
					ESTs, Weakly similar to
					DRNG_RAT
		l i			DEOXYRIBONUCLEASE
					GAMMA PRECURSOR (DNASE
			BB 66		GAMMA)
2060	13364	A1170606	PP, QQ,		(DEOXYRIBONUCLEASE I-LIKE
2060	13364	AI170606	<u>п</u>		3) (DNASEY) [R.norvegicus]

TABL	≣1	·		· AG	torney Docket 44921-5033-911WO Document No. 1985828.1
S09 ID: };	ELEC:	Centank Acc or. RefSeq ID :	Model Code	Kinown Cene Neime	Unigene Seguenee Cluster Tülg
					ESTs, Highly similar to DAZ associated protein 1 [Homo
2061	6272	AI170617	z		sapiens] [H.sapiens]
2063	12698	AI170665	XX		ESTs
2064	5057	AI170671	RR, SS		ESTs
2065	10593	Al170673	ZZ		ESTs
2068	9757	AI170693	A, B, Q, R, U, BBB, CCC		ESTs
	11686		RR		ESTs, Weakly similar to DD21_MOUSE Nucleolar RNA helicase II (Nucleolar RNA helicase Gu) (RH II/Gu) (DEAD- box protein 21) [M.musculus]
2069 2070	23612	AI170715 AI170751	I KK		ESTs
2070	4868	AI170751	III, JJJ		ESTs
2073	18905	AI170770	YY		ESTs, Highly similar to NUCM_HUMAN NADH- ubiquinone oxidoreductase 49 kDa subunit, mitochondrial precursor (Complex I-49KD) (CI- 49KD) [H.sapiens]
2074	3803	AI170773	X, Y, Z		Rattus norvegicus 250 kDa estrous-specific protein mRNA, partial cds
2075	3023	AI170795	G		ESTs
2076	1902	AI170809	A, B, Z, AA, PPP, QQQ C, MM,		ESTs
2077	22204	AI170820	TTT		ESTs
2079	2811	AI171090	FF, BBB, CCC, RRR, SSS	3-hydroxy-3- methylglutaryl CoA lyase	3-hydroxy-3-methylglutaryl CoA lyase
2079	2812	AI171090	BBB, CCC	3-hydroxy-3- methylglutaryl CoA lyase	3-hydroxy-3-methylglutaryl CoA lyase
2080	2131	Al171091	11		ESTs, Weakly similar to T19999 hypothetical protein C47D12.2 - Caenorhabditis elegans [C.elegans]
2082	18660	AI171262	KKK, NNN		ESTs
2086	11426	AI171305	НН, ИИ, ОО, III, ЈЈЈ		ESTs, Moderately similar to PTN3_HUMAN Protein tyrosine phosphatase, non-receptor type 3 (Protein-tyrosine phosphatase H1) (PTP-H1) [H.sapiens]

TABL	<b>3</b> 1			. As	tomey Doctet 44921-5033-91W0 **** Document No. 1983323.1
Seq	ELEC	CONSINK ACCO Reference	Model		Unigene Sequence Cluster Title
2087	3695	AI171307	T		ESTs
	17591	Al171354	III, JJJ, General Core Tox Markers		ESTs
2089	17391	A117 1354	Markers		ESTs, Moderately similar to
2091	6243	AI171367	BBB, CCC		HSPC154 protein [Homo sapiens] [H.sapiens]
2095	11813	AI171487	Z, AA		ESTs
2099	15345	AI171587	L, Z		ESTs
	9128	Al171611	I, J, L, Z, 000		ESTs
2101	24073	AI171632	X, Y		ESTs
					ESTs, Weakly similar to BVECAG apaG protein -
	11504	A1171652	E, KKK		Escherichia coli [E.coli]
	14357	AI171662	ZZ, AAA		ESTs
2107	2216	AI171745	ZZ		ESTs ESTs
2109	16005	AI171764	RR, FFF CC, UU, III, JJJ, KKK,		2015
2111	21209	AI171772	NNN		ESTs
2112	22745	AI171788	E		ESTs
2113	11708	AI171807	L, AA		ESTs ESTs, Weakly similar to FAD-1 like protein [Caenorhabditis
2114	11514	AI171855	Z, AA		elegans] [C.elegans]
2116	6524	AI171952	TT		ESTs
2119	6637	AI171975	DDD		ESTs, Moderately similar to I48672 p8 MTCP-1 - mouse
	22239	AI171982	Z, AA		[M.musculus]
2121	6645	AI171998	II		ESTs ESTs, Highly similar to
2125	3971	AI172050	ZZ, AAA, PPP, QQQ		Coordinates Of Rat Map Kinase Erk2 With An Arginine Mutation At Position 52 [R.norvegicus]
2126	19012	Al172056	X, DD, EE, SS, NNN, General Alternate		ESTs
			G, III,		
2127	11205	AI172057	วาว, บบบ		ESTs
2128	1411	AI172075	O, P		ESTs ·
2134	11438	Al172189	CC N, RR,		ESTs
2136	11888	AI172217	CCC		ESTs

Seq CLCC Acc or Model D No. RefSeq D Code Known Cene Name Uniga	
	والالا تفاوياكا ووسويتوج وسو
Core Tox	
2139 15016 AI172285 Markers ESTs	
	, Weakly similar to S43056
	thetical protein - mouse
	usculus]
GGG,	
	, Weakly similar to
	otilis YQJC protein like
	norhabditis elegans]
	egans]
2149 26222 AI172506 D General	
2150   13434   Al172552   Alternate   EST	
PPP,	
2151 13097 A1172600 QQQ ESTs	<b>:</b>
2152 8795 AI172618 Q, R ESTs	3
2153   22947   AI175008   LL   ESTs	
2155 8053 AI175033 E ESTs	
2156 2331 Al175045 C ESTs	
General	
2157 7134 Al175063 Alternate ESTs	
2158 4989 AI175087 O, P ESTs	
	s, Weakly similar to A53237 12 protein - fruit fly
	ophila melanogaster)
	ment) [D.melanogaster]
2164 4187 A1175346 S ESTs	
2168 14717 AI175477 S ESTs	
BB, III, JJJ, KKK,	
NNN,	
General	
Core Tox	
Markers,	
General	
2169 13353 AI175508 Alternate ESTs	
General	
2171 23536 Al175558 Alternate ESTs	
1 1 1 1	, Weakly similar to T15628
	thetical protein C25H3.9 -
	orhabditis elegans
	egans] , Weakly similar to A53237
	12 protein - fruit fly
	ophila melanogaster)
	nent) [D.melanogaster]
2174 14501 A1175778 QQ ESTs	

TABL		**		A	tomey Docket 4/1921-5093-01W0 Document No. 1995328.1
509 : ID :::	erec Grec	Constant Acc or Refseq ID	Modal Code	Known Cone Name	ellir relevie eneginu
			C, Z, DD,		
0475	00000	41475700	MM, WW,		ESTs
2175	22906	AI175790 AI175833	KKK, TTT VV		ESTs
2176	7262	A1175633	• • • • • • • • • • • • • • • • • • •		ESTs, Highly similar to JC1450
			\		fibroblast growth factor receptor 4
2179	13490	AI175948	ZZ, AAA		- rat [R.norvegicus]
2179	13490	A1173940	22, 777		ESTs, Highly similar to
			MM, AAA,		PM5P HUMAN Protein pM5
2182	22311	AI176007	TTT		precursor [H.sapiens]
2102	22311	A1170007	PPP,		precursor [ri.sapiens]
2183	6739	AI176016	QQQ		ESTs
2103	10739	A1170010	uuu -		ESTs, Weakly similar to T16696
	1				hypothetical protein R07E4.4 -
		į			Caenorhabditis elegans
2184	3114	AI176018	lww		[C.elegans]
2104	3114	A1170010	10000		ESTs, Weakly similar to retinoic
1			ww.		acid receptor responder
İ		ļ	PPP,		(tazarotene induced) 2 [Homo
10400	24.407	AI176061	QQQ		sapiens] [H.sapiens]
2186	21467 4585	AI176001			ESTs
2188 2189	6686	AI176121	Q, R ZZ		ESTs
2190	8742	AI176136	QQ		ESTs
2191	18581	AI176160	E		ESTs
2192	14159	AI176169	V		ESTs
2192	14133	A1170103	<u>'</u>		ESTs, Weakly similar to
1					T23D8.3.p [Caenorhabditis
2194	22011	AI176212	υυ		elegans] [C.elegans]
2196	21130	AI176298	w		ESTs
2198	13502	AI176320	L		ESTs
2100	10002	741110020			Rattus norvegicus MHC class I
					RT1.E protein mRNA, complete
2199	18936	A1176358	III, XX, YY		cds, haplotype u
2200	3014	Al176362	W		ESTs
2201	15015	AI176363	BBB		ESTs
	1.00.0		000,		
		İ	General		
ĺ			Core Tox		
2202	8387	AI176365	Markers		ESTs
2204	6138	AI176420	UU		ESTs
1	1		M, T,		
2207	26029	AI176460	KKK		
	1	0.400	<del> </del>		ESTs, Highly similar to 2016304A
]					motor protein [Homo sapiens]
2208	11488	AI176477	U		[H.sapiens]
2212	8609	AI176505	SS		ESTs
2213	15959	Al176540	Z		ESTs
	1.0000	1 55-75	<u> </u>	<u> </u>	

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S09 : ID :	ELEC:	COMBONI AGGOT REFEGUE	Model	Known Cene Name.	Unligenc Sequence Cluster Tille
	-		N, BBB,		ESTs, Weakly similar to
1			ccc,		T15B7.2.p [Caenorhabditis
2215	22139	AI176548	บบบ		elegans] [C.elegans]
			W, AA,		
1			вв, сс,		
1			III, JJJ,		
			KKK,		
]			NNN,		
2217	2161	AI176592	General Alternate		ESTs
2217	2101	A1170592	Alternate		1515
1			V, III, JJJ,		
1			000.		
1			General		
			Core Tox		
	2536	AI176616	Markers		ESTs
	15847	AI176638	Z, AA		ESTs
2221	15179	AI176675	ZZ		ESTs
2222	24313	A1476690	SSS, UUU		ESTs
2222	13697	AI176680 AI176718	111		ESTs
2223	13091	A1170710	333		ESTs, Highly similar to
ļ					hypothetical protein FLJ20580
2224	23547	AI176734	111		[Homo sapiens] [H.sapiens]
			III, JJJ,		
ļ			ккк,		
		ĺ	000,		ESTs, Moderately similar to
		3	General		KIAA1002 protein; clone
0005	44500	41470700	Core Tox		FLB5224 [Homo sapiens]
2225	11536	Al176739	Markers		[H.sapiens] ESTs, Weakly similar to
					BVECAG apaG protein -
2226	11505	AI176767	QQ		Escherichia coli [E.coli]
<del></del>			General		
2227	10187	A1176781	Alternate		ESTs
			GG, JJ,		
			KK, FFF,		
2228	18525	AI176792	GGG	<u></u>	ESTs
			E, BB,		
2220	21740	A1176910	GG, PP,		ESTs
2229	21740	AI176810	DD, EE,		1019
			UU, III,		1
2230	2557	AI176820	JJJ		ESTs
2231	23449	Al176828	C, L, HH		ESTs
			•	<del> </del>	ESTs, Weakly similar to T21364
					hypothetical protein F25H5.6 -
					Caenorhabditis elegans
2232	9712	AI176836	111		[C.elegans]

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8 1	WAR SO				1 % Dogaman Kop responsed
S00]	©L©C	Acc or	Model :		Unigeno Seguenco Cluster Tille
(I)	(D) (No	Resea (D)		Known Cene Kame	Müidəvə zədrəves Cirzisi, 11116
			KK, FFF,		
			General		COTo
	23299	AI176839	Alternate		ESTs ESTs
	6821	AI176841	Z SS		ESTs
2235 2236	19309 5579	AI176858 AI176863	E, UU		ESTs
2236	3379	A1170003	E, 00		ESTs, Weakly similar to BEM-
					1/BUD5 suppressor-like
		1	i		[Caenorhabditis elegans]
2237	12792	AI176883	DD, EE		[C.elegans]
2237	12/32	A1170003	DD, LL		[O.ciogunoj
	1		A, B, BB,		
			GGG,	·	
			General		
'		1	Core Tox		
2238	7697	AI176942	Markers		ESTs
2239	5460	AI176944	GGG		ESTs
2240	16917	Al176951	11		ESTs
	-		W, LLL,		
2243	15146	AI176969	sss		ESTs
2244	6861	AI176970	I, ZZ		ESTs
2245	14738	AI176993	L, GGG		ESTs
	<b> </b>		PPP,		
2247	2596	Al177031	QQQ		ESTs
			LLL, SSS,		
	3969	AI177055	UUU	<u> </u>	ESTs
2249	4383	Al177056	DD, EE		ESTs
2250	6473	AI177091	FFF		ESTs
	İ		GGG,		ESTs, Weakly similar to
1			General		OAF_DROME Out at first protein
			Core Tox		[Contains: Out at first short
2252	5943	AI177105	Markers		protein] [D.melanogaster]
2253	2487	AI177117	RR		ESTs
2254	14920	Al177120	K		ESTs
2255	6262	Al177125	III, JJJ		ESTs
2259	24221	Al177166	N		ESTs
0001	0500	A1477400	JJ, KK,		CCT.
2261	3528	AI177189	ННН		ESTs
2262	7163	AI177256	Υ		ESTs Weekly similar to
					ESTs, Weakly similar to GMCR MOUSE Granulocyte-
			1		macrophage colony-stimulating
			1		
			1		factor receptor alpha chain precursor (GM-CSF-R-alpha)
2202	12520	A1177000	l.,,		(GMR) [M.musculus]
2263	13539	AI177280	ww		ESTs .
2267	7975	AI177374		<del> </del>	ESTs
2268	1903	AI177377	B, X, Y	L	CO18

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809 , (D	id ko: Greë	Reser (: Assor (: Assor (:	Model Gode	Known Cone Name:	Onigene Sequence Circler Tille
2270	3071	Al177404	R, General Alternate		ESTs
2271	18095	Al177482	s	SH-PTP2 protein tyrosine phosphatase, non- receptor type 11	SH-PTP2 protein tyrosine phosphatase, non-receptor type
2276	14275	AI177748	ZZ, AAA		ESTs
2277	14425	AI177755	E, DD, EE, KKK, NNN		ESTs, Moderately similar to PBEF_HUMAN Pre-B cell enhancing factor precursor [H.sapiens]
2278	10611	AI177790	F, II, FFF		ESTs
2279	22037	AI177797	AA, General Alternate		ESTs
					ESTs, Highly similar to CDK1_MOUSE Cyclin-dependent kinase 2-associated protein 1 (CDK2-associated protein 1) (Putative oral cancer suppressor) (Deleted in oral cancer-1) (DOC-
2280	547	AI177871	F, II, FFF		1) [M.musculus]
2281	8638 5275	Al177875 Al177898	PP, QQ		ESTs ESTs, Weakly similar to T25144 hypothetical protein T22H6.6 - Caenorhabditis elegans [C.elegans]
2286	17706	Al178052	LL		ESTs
2289	3943	Al178179	FF		ESTs, Weakly similar to hypothetical protein FLJ21868 [Homo sapiens] [H.sapiens]
2292	17847	Al178214	C, FF, General Core Tox Markers		ESTs
2294 2297	5813 19720	Al178231 Al178259	General Core Tox Markers XX, YY		ESTs
2298	4073	AI178272	Y, SS		ESTs, Weakly similar to S51973 hypothetical protein YAL046c - yeast (Saccharomyces cerevisiae) [S.cerevisiae]
2299	7318	Al178278	E		ESTs, Weakly similar to S47857 basic protein, cytosolic - fruit fly (Drosophila melanogaster) [D.melanogaster]

TABL	<b>3</b> 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		A A	lomey Docket 44921-5053-01W0
S09 ID	ETGC	CONSONIA ACCO ROBSONIA	Model Code:	2.7	Unifono Sequence Cluster Tille
			DD, EE,		
2301	14561	AI178503	YY		ESTs
2302	18800	Al178504	O, P		ESTs
2303	13580	Al178507	00		ESTs
			L, OOO, General Core Tox		
2304	22197	AI178527	Markers		ESTs
2305	5921	AI178556	ZZ, AAA		ESTs
	13581	AI178602	SS		ESTs .
	4097	AI178635	O, VV		ESTs
	5200	AI178699	Q, R		ESTs
2311	5381	AI178734	ZZ		ESTs
2312	13166	Al178736	UU		ESTs
2314	17239	AI178763	F, II		ESTs
2316	21224	AI178778	YY		ESTs, Moderately similar to T14273 zinc finger protein 106 - mouse [M.musculus]
2317	9674	AI178784	С		ESTs
	14520	Al178785	General Alternate		ESTs, Moderately similar to POL3_MOUSE Retrovirus-related POL polyprotein (Endonuclease) [M.musculus]
2321	4576	Al178872	LL		ESTs
2327	4791	AI179106	HH		ESTs
2329	22436 2818	Al179139	Z, AA General Core Tox Markers, General Alternate		ESTs
2330	2010	AI179144	W, DD,		ESTs
2333	8477	Al179167	EE, NNN C, DD,		ESTs
2334	21568	Al179185	EE		ESTs
	26270	Al179218	RR		
2336	6303	Al179243	PPP, QQQ		Rat Rev-ErbA-alpha protein mRNA, complete cds
		Al179291	LLL, UUU		ESTs
2339	8849	AI179315	W		ESTs ESTs, Highly similar to RIKEN cDNA 0610040D20 [Mus
2341	19783	AI179388	L		musculus] [M.musculus] ESTs, Moderately similar to RB17 MOUSE Ras-related
2342	13614	Al179407	м		protein Rab-17 [M.musculus]
			S		ESTs
2344	15042	Al179422	A, B		ESTs
2345	13619	AI179464	C, Q, R, HH		ESTs

	31:	1 -1	14 49 44 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	A	torney Docket 44921-5033-01WO Document No. 1935323.1
100		Consoni;	3,0		elili ieteuk) eaasupes eaeglau
	22852	AI179478	V		ESTS
2347	2768	Al179481	BBB, CCC		ESTs
2348	23515	AI179498	I.		ESTs, Highly similar to SEC23B (S. cerevisiae) [Mus musculus]
2350	22961	AI179519	V, RR		ESTs
2351	13054	AI179560	General Alternate		ESTs
2352	15533	AI179569	RR		·
2254	44404	A1470C42		myeloid differentiation primary response	myeloid differentiation primary
2354	11484	AI179612	R	gene 116	response gene 116 ESTs, Highly similar to RIKEN cDNA 0610009B22 [Mus
2356	17865	AI179636	Υ		musculus] [M.musculus]
2358	7918	AI179750	FFF		ESTs
2359	6647	AI179795	Z, AA		ESTs
2360	14496	AI179833	L		ESTs
2361	3524	AI179840	RRR, SSS		ESTs
2365 2366	3049 18239	Al179892 Al179942	J B, CC	glucocorticoid- inducible protein	glucocorticoid-inducible protein
2367	9157	Al179947	нн		ESTs, Highly similar to 42 kD cGMP-dependent protein kinase anchoring protein; hypothetical testis-specific [Mus musculus] [M.musculus]
2375	16706	AI180032	CC		ESTs
2378	15447	AI180108	L		ESTs
2379	2246	AI180113	JJ, KK		ESTs
2382	18465	Al180187	BB, CC, PP		ESTs
2383	3587	Al180253	Q T		ESTs ESTs, Highly similar to RIKEN cDNA 1110036B12 [Mus musculus] [M.musculus]
2384	3134	Al180259 Al180292	EEE,		ESTs, Moderately similar to A23521 serum amyloid A3
2385 2391	7073	Al180292 Al180416	MMM UUU		precursor - mouse [M.musculus] ESTs
2391	3067	Al180426	нн		ESTs, Weakly similar to T26786 hypothetical protein Y40B1B.8 - Caenorhabditis elegans [C.elegans]
2393	23262	AI227688	HH, ZZ, AAA		ESTs
2394	11631	Al227690	SS		ESTs
		1			

TABL	€1			A A	tormay Docket 44921-5033-011WO Document No. 1935323.1
Sog :	(B) (A) (A) (A) (A) (A) (A) (A) (A) (A) (A	CONSIDER AGG OF BOSSON ID	Model Gode	Mary Gans Marins	Unigene Sequence Cluster Title
	(19 000 e );	الأغانجودا أتحارث		Rádia enesa regulas	ESTs, Weakly similar to T21344
i			1		hypothetical protein F25H2.1 -
					Caenorhabditis elegans
2395	23944	AI227705	w		[C.elegans]
		<u> </u>	000,	<del> </del>	
			General		
2396	13670	AI227734	Alternate		ESTs
					ESTs, Highly similar to
					EFER_HUMAN Eferin
2397	6765	Al227761	С		[H.sapiens]
					ESTs, Highly similar to UBX
ł					domain-containing 2 [Mus
2398	21890	AI227815	RR	<u> </u>	musculus] [M.musculus]
					ESTs, Weakly similar to
2200	04200	41007000	DD 00		BD3_MOUSE BRAIN PROTEIN
	24300 13981	AI227829	RR, SS W		D3 [M.musculus]
2401 2402	7324	Al227872 Al227885	F, II		ESTs ESTs
2402	7324	A1227605	F, II F, GG,		E318
2405	21288	AI227935	HH, LL		ESTs
2406	2226	Al227933	R		ESTs
2700	2220	A1227341	1		ESTs, Moderately similar to
	]		N, PPP,		T17453 ERG-associated protein
2408	4275	AI227972	QQQ		ESET - mouse [M.musculus]
2410	22901	AI228052	ZZ, AAA		ESTs
			PP, QQ, PPP,		
2412	18491	Al228195	QQQ		ESTs
2414	14539	Al228254	Τ		ESTs
2415	24256	Al228256	T		ESTs
					ESTs, Weakly similar to
					F09G2.8.p [Caenorhabditis
2416	14540	AI228269	YY		elegans] [C.elegans]
			General		
			Core Tox		
			Markers,		
2447	C745	A1000004	General		FOT-
2417	6715	AI228284	Alternate		ESTs .
			DD, 000,		
	\		General		
			Core Tox		
2418	12946	Al228291	Markers		ESTs
F	-2010		EE, FF,		
			III, JJJ,		
2420	8917		NNN		ESTs
			K, L, N,		
2421	15879		TT		ESTs
	13729		ННН		ESTs
2424	4424	Al228422	T		ESTs

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TABL					terney Docket 44921-5093-011W0 Document No. 1935323.1
S09 ID	@L@G : .	Consoni ; Accor Reisco ID ;	Model: Code	මගාද්ග ලෙනු කහතෙනි	Unigene Sequence Cluster Title
2425	17892	Al228438	RR		ESTs
2425	17032	A1220430	Z, AÄ,		2013
2426	13746	AI228502	RR		ESTs
2420	10740	AIZZOOOZ	000,		
			General		
			Core Tox		
2427	13749	AI228540	Markers		ESTs
					ESTs, Weakly similar to T16757
					hypothetical protein R144.3 -
					Caenorhabditis elegans
2428	16053	AI228596	J, Z		[C.elegans]
2430	22106	Al228628	ZZ, AAA		ESTs
			A, K, L,		
			N,		ESTs, Weakly similar to T20360
	İ		General		hypothetical protein D2030.9b -
			Core Tox		Caenorhabditis elegans
2431	6072	AI228630	Markers		[C.elegans]
			RRR,		
2433	6788	AI228646	UUU		ESTs Months similar to Month
			PPP,		ESTs, Weakly similar to Yeast
			QQQ,		YAE2 hypothetical protein
0404	40050	A 1000 C 40	General		[Caenorhabditis elegans]
2434	12252	A1228649	Alternate		[C.elegans] ESTs
2435	3557	Al228672	KK 000,		2015
			General		ESTs, Weakly similar to
			Core Tox		C32D5.6.p [Caenorhabditis
2436	13757	Al228676	Markers		elegans] [C.elegans]
2430	10707	AIZZOOTO	BBB,		ologanoj (o.ologanoj
2438	20388	AI228811	ccc		EST
2439	6721	Al228813	RR		ESTs
2440	16998	AI228829	UUU		EST
2441	11875	Al228846	D		ESTs
2442	6633	Al228931	C, TT		ESTs
					ESTs, Weakly similar to T26088
					hypothetical protein W02B12.7 -
					Caenorhabditis elegans
2443	2210	AI228963	FF		[C.elegans]
2444	13785	Al228970	MM, TTT		ESTs
2445	19513	AI229035	UU		ESTs
					ESTs, Moderately similar to
					retinoic acid induced 12; Clone
	23824	A1229059	ZZ, AAA	<b></b>	13u [Mus musculus] [M.musculus]
2447	22824	Al229074	М	<b> </b> -	ESTs
					ESTs, Highly similar to
					mitochondrial ribosomal protein
2440	10063	A1220466	00		S14; 1810032L21Rik [Mus
2448	19063	Al229166	RR	l	musculus] [M.musculus]

TABL	<b>≣</b> 1			A PART AND A PART AND A PART AND A PART AND A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART	tomey Docket 4/1921-5193-01W0 Document No. 1935823.1
Seq .	GLGC ID No	Centant Acc or RefSeq ID	Model Codo:	Known Cone Name:	Unigene Seguence Cluster Tille
Taxable San		0	PPP,		
2450	2748	Al229179	QQQ		ESTs
				·	Rattus norvegicus zinc finger
			PPP,		protein (pMLZ-4) mRNA, 3'
2453	15490	AI229253	QQQ		untranslated region
	<b> </b>		JJ, KK,		
2454	24013	AI229260	ннн		ESTs
2455	5107	Al229291	X, Y	•	ESTs
2458	19721	Al229387	RR, SS		EST
	<u> </u>		MM, ZZ,		
2459	13838	Al229416	TTT		ESTs
2460	21237	A1220420	ss		Rattus norvegicus Tclone4 mRNA
2460 2462	6945	Al229430 Al229467	G, H		ESTs
2402	0945	A1229407	В, п		ESTs, Weakly similar to
					mitochondrial ribosomal protein
Ì	i				L2a [Drosophila melanogaster]
2462	17183	A1220497			[D.melanogaster]
2463 2464	13846	Al229487 Al229493	I, J K		ESTs
2404	13040	A1229493	<u> </u>		ESTs, Moderately similar to
	1	•	R, DD,		JE0381 NADH dehydrogenase
	]		EE, III,		(ubiquinone) (EC 1.6.5.3) chain
2465	15426	Al229497	JJJ		NDUFB10 - human [H.sapiens]
2466	15193	A1229508	DDD		ESTs
2400	13133	A1223300	KKK,		12013
Ì			General		
2469	7067	AI229655	Alternate		ESTs
2470	2231	Al229664	JJ, KK		ESTs
2474	21446	Al229854	E	<u> </u>	ESTs
<del></del>	12	/ 122000 1			ESTs, Weakly similar to T26088
	]				hypothetical protein W02B12.7 -
					Caenorhabditis elegans
2475	11934	Al229905	cc		[C.elegans]
			O, NN,		
			00,		
			General		
2477	12551	Al230056	Alternate		ESTs
					ESTs, Weakly similar to T33304
'					hypothetical protein R01B10.5 -
1					Caenorhabditis elegans
2478	23048	AI230073	11		[C.elegans]
2480	2732	Al230136	V		ESTs
				··········	ESTs, Weakly similar to
					Deoxyribose-phosphate aldolase
1			General		[Caenorhabditis elegans]
2482	6629	AI230165	Alternate		[C.elegans]
2487	14450	Al230262	XX		ESTs
2489	13762	Al230326	С		ESTs
2491	2372	AI230373	Z		ESTs

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				-311-	
TABLE	₹1				tomay Docket 4/12/1-5033-01/WO Document No. 1935323.1
3.3	givin it	70000 = 1000 F			
899 ID: : :	erec erec	Rei§eg ID ÷ Rei§eg ID ÷ Rei§eg ID ÷	Modol Code	emell ened nivenl	Unigene Sequence Cluster Title
					ESTs, Weakly similar to zinc finger protein 364 [Mus musculus]
2493	13899	AI230424	RR, SS		[M.musculus]
2494	6560	AI230440	JJ, KK, HHH		ESTs
			General		
2497	20895	AI230549	Alternate W, MM,		ESTs
2498	13446	AI230625	TTT		ESTs
	18393	AI230632	A, B	-	ESTs
2500	14481	AI230697	BB, CC		ESTs
2501	18529	Al230716	W		ESTs
2301	10329	A12307 10	S,		
			General		
2502	17879	AI230741	Alternate		ESTs
	9171	Al230747	RR		ESTs
2304	3171	A1230141			
		_	C, W, MM, NNN, TTT, General	-	
	4731	AI230773	Alternate		ESTs
2511	23730	Al230915	RR		ESTs
0542	22402	A1220081	III, JJJ, NNN		ESTs
	23182 19315	AI230981 AI231010	V		EST
2516	16087	Al231010	Z		ESTs
2517	19082	Al231011	BB, CC		ESTs
			UU, FFF, GGG, General Core Tox		ESTs
2519	633	AI231127	Markers		ESTs, Moderately similar to
2502	12040	A1224402	77		SEC_HUMAN SEC protein [H.sapiens]
2522	13949	AI231193	ZZ QQ		ESTs
2524	3019	Al231218	H, General		
2525	6743	Al231219	Alternate		ESTs
2528	4272	Al231309	U, FF, LL, BBB, PPP, QQQ, RRR, SSS, UUU		ESTs
2020	7212	, 11201000		glucocorticoid-	
2529	3050	Al231321	z, aa	inducible protein	glucocorticoid-inducible protein

TABL	. Oct. 1		June 7 Al de 4 June 1	AG AG	terney Doctot 44221-5038-011W0
500 (D)	(C) (C) (C) (C) (C) (C) (C) (C) (C) (C)	Genienk Assor Refeed ID	Model Code	Kinowii Gene Neme	Unigéne Sequence Cluster Tille
			FFF,		
]			ннн,		
	ļ		General		
2531	13966	Al231421	Alternate		ESTs
2532	12343	Al231433	R		ESTs
2533	13967	Al231439	UUU ·		ESTs
					ESTs, Moderately similar to
					RIKEN cDNA 1110017G11;
	]				RIKEN cDNA 1110017G11 gene
2535	3581	Al231471	LL, LLL		[Mus musculus] [M.musculus]
2538	16321	AI231506	A, B		ESTs
1	1				ESTs, Weakly similar to T45057
1	1				hypothetical protein Y39B6B.ee
					[imported] - Caenorhabditis
2541	17172	AI231572	WW	<u> </u>	elegans [C.elegans]
05.40	10.400	11004770	DD, EE,		ESTs
2543	18402	Al231778 Al231797	KKK		ESTs
2546	6193	AI231797	LL		ESTs, Highly similar to T-
			;		complex expressed gene 2 [Mus
2547	2339	AI231798	s	,	musculus] [M.musculus]
2347	2339	A1231730	3		musculus) [W.musculus]
			AA, GGG,	`	
			General		
			Core Tox		
2548	14007	AI231808	Markers	·	ESTs
2549	7001	Al231814	V		ESTs
	<u> </u>		HH, MM,		
2550	15173	Al231846	TTT		ESTs
2555	24273	AI232033	AA		ESTs
2556	22995	AI232047	C		ESTs
2559	12366	AI232088	SS		ESTs
			G, S,		
	1		GGG,		
			PPP,		
2560	2587	AI232103	QQQ		ESTs
2563	11549	Al232174	Q, R		ESTs
					ESTs, Weakly similar to T27032
					hypothetical protein Y49A3A.1 -
0501	04040	.,,,,,,,,,,,	E, XX,		Caenorhabditis elegans
2564	21242	AI232230	YY		[C.elegans]
2565	14030	AI232248	T		ESTs
1				cytochrome b5, outer	autochromo hE cutor
2566	240	A1222256	l	mitochondrial membrane isoform	cytochrome b5, outer mitochondrial membrane isoform
2566	349	AI232256	I, J	memorane isolorm	ESTs, Weakly similar to T25417
					hypothetical protein T28D6.9 -
l	1		PPP,		Caenorhabditis elegans
2568	2913	AI232272	QQQ		[C.elegans]
2000	12313	MICUCAIC	uuu	<u> </u>	[O.cicyans]

Seg   SLGC   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Research   Researc	33-01W@ 1935328.1
RTC2_HUMAN PROBAL 37-TERMINAL PHOSPH.	
BB, CC, OO, PP, PHOSPHATE CYCLASE 2 (RNA-3'-PHOSPHATE CYCLASE 2) [H.sapiens	BLE RNA
DOC, PP, NNN   CYCLASE 2) [H.sapiens	ATE
2569   11720   Al232273   NNN   CYCLASE 2) [H.sapiens	
QQ, TT, DDD, GGG, General Core Tox	
DDD,   GGG,   General   Core Tox	<u>;]                                    </u>
Core Tox	
Core Tox	
2570   15955   Al232294   Markers   ESTs	
2571   6594   Al232296   GG   ESTs   ESTs, Highly similar to J   stomatin - mouse [M.mus   M.mus   ESTs   ESTs, Highly similar to J   stomatin - mouse [M.mus   ESTs   General   Core Tox   ESTs, Moderately similar   Core Tox   Markers, General   POL polyprotein (Endons   M.mus   POL polyprotein (Endons   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs, Weakly similar to hydrolase protein [M.mus   M.mus   ESTs, Weakly similar to hydrolase protein [Mus   M.mus   ESTs, Weakly similar to hydrolase protein [Mus   M.mus   ESTs, Weakly similar to hydrolase protein [Mus   M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   ESTs, Weakly similar to hydrolase protein [M.mus   M.mus   M.mus   M.mus   M.mus   M.mus   M.mus   M.mus   M.mus   M.mus   M.mus   M.mus	
ESTs, Highly similar to J stomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse [M.mustomatin - mouse	
2573   6430   Al232319   J	
III, JJJ,   General   Alternate   ESTs	
Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox	sculus]
2575	
General   Core Tox   ESTs, Moderately simila   POL3_MOUSE Retrovirus   POL polyprotein (Endone   M.musculus)	
Core Tox   Markers,   POL3_MOUSE Retrovirus   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endone   POL polyprotein (Endon	<del></del>
Markers,   General   POL3_MOUSE Retrovirus   POL3_MOUSE Retrovirus   POL polyprotein (Endone   M.musculus)	ır to
2576	
2577 3435 Al232354 MM, TTT ESTs  2579 14390 Al232385 LLL ESTs  TT,  General  2580 3143 Al232408 Alternate ESTs  BBB, UUU ESTs, Weakly similar to hydrolase protein [Mus now protein [Mus now protein [Mus now protein C35D10.4 in Core Tox protein C35D10.4 in Core Tox protein C35D10.4 in Core Tox protein C35D10.4 in Core Tox protein C35D10.4 in Core Tox protein C35D10.4 in Core Tox protein C35D10.4 in Core Tox protein C35D10.4 in Core Tox protein C35D10.4 in Core Tox protein C35D10.4 in Core Tox protein C35D10.4 in Core Tox protein C35D10.4 in Core Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D10.4 in Care Tox protein C35D1	uclease)
2579	
TT,   General   Alternate   ESTs   ESTs, Weakly similar to   hydrolase protein [Mus n   [M.musculus]   ESTs, Weakly similar to   hydrolase protein [Mus n   [M.musculus]   ESTs, Weakly similar to   YLC4_CAEEL Hypotheti   Core Tox   kDa protein C35D10.4 in   Chromosome III [C.elega   M,   General   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox	
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2580 3143 Al232408 Alternate ESTs  BBB, ESTs, Weakly similar to hydrolase protein [Mus n [M.musculus]]  ESTs, Weakly similar to hydrolase protein [Mus n [M.musculus]]  ESTs, Weakly similar to YLC4_CAEEL Hypotheti kDa protein C35D10.4 in chromosome III [C.elega M, General Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox Core Tox C	
BBB, UUU [M.musculus]  Sequence of the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein and the protein	
BBB, UUU [M.musculus]  September 1	serine
2581   14264   Al232409   UUU   [M.musculus]   ESTs, Weakly similar to   YLC4_CAEEL Hypotheti   KDa protein C35D10.4 in   Chromosome III [C.elega   M,   General   Core Tox   Core Tox   Core Tox   Chromosome III [C.elega   M,   General   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Core Tox   Cor	
General Core Tox Al232419  General Core Tox Markers  M, General Core Tox Chromosome III [C.elegal Core Tox Chromosome III [C.elegal M, General Core Tox	-
Core Tox kDa protein C35D10.4 in chromosome III [C.elega M, General Core Tox	
2582 18910 Al232419 Markers chromosome III [C.elega M, General Core Tox	
M, General Core Tox	
General Core Tox	nsj
Core Tox	
General	
2583 17703 Al232498 Alternate ESTs	
2586 14056 Al232529 V ESTs	
A, B, N,	
2588 20350 Al232552 WW EST	
FFF,	
GGG, General	
Core Tox	
2590 4440 Al232643 Markers ESTs	
2594 14278 Al232722 V ESTs	

TABU				A	iomey Docket 44921-5033-011WO , Document No. 1935323.1
8.7		CONSONS -		22.15	
			Model	Marchan Como Nama	0000000 Gommon Gommon 53000
na : :-	(D) K/O: ·	Ressen ID		Kinowi Gana Kenia	Unigene Sequence Cluster Title
2595	14073	AI232723	General Alternate		ESTs
	3885	AI232723	MM, TTT		ESTs
	11190	AI232810	YY		ESTs
200.	177.00		CC, JJ,		
2598	21871	Al232841	кк, ннн		ESTs
			F, T, U,		
			W, MM,		
	3917	A1232970	RR, TTT		ESTs
2601	23570	A1232979	PP, QQ		ESTs
2603	11815	A1232993	DDD PPP,		ESTs
2604	5355	AI233031	QQQ		ESTs
2004		71200001	<u> </u>		2013
			JJJ, 000,		
			General		
			Core Tox		
2607	6033	AI233081	Markers		ESTs
					ESTs, Moderately similar to
					PS0139 H-2 class I
2608	18794	AI233121	v		histocompatibility antigen T18 - mouse (fragment) [M.musculus]
2000	10/94	A1233121	BB, CC,		mouse (traginent) [wimusculus]
2610	14081	Al233164	NN		ESTs
			General		
2612	11561	AI233182	Alternate		ESTs
2613	13598	Al233194	E		ESTs
					ESTs, Highly similar to
			N, GG,	,	RS18_HUMAN 40S ribosomal
2644	15107	A1233220	PP, QQ, XX, YY		protein S18 (KE-3) (KE3)
2614	15107	A1233220	G, H,		[R.norvegicus]
			FFF,		
			General		
			Core Tox		
2617	15900	AI233262	Markers		ESTs
2621	14118	Al233367	H, P		EST
			R,		ESTs, Weakly similar to S44853
2622	7161	AI233407	General Alternate		K12H4.3 protein - Caenorhabditis elegans [C.elegans]
2622 2623	19655	Al233407 Al233460	ZZ, AAA		ESTs
	5794	Al233480	72, 744 TT		ESTs
			LL, LLL,		
	·		RRR,		
			SSS,		•
2625	14131	Al233493	บบบ		ESTs

Color		<b>E</b> 1 · · ·	1 1 2 2 2		A PART AND AND AND AND AND AND AND AND AND AND	tomey Doctet 44921-5033-01W0 Document No. 1985328.1
A, I, OOO, General Core Tox	S00.	@rec	AGE OF	Model	W	00.5
COO, General Core Tox	no; 🤃	In Kov.	kg80010%:	Good :: :	ranown constraints.	laividava žednavės rainaras ima
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Core Tox   Markers   ESTs		j		-		
2630   8549   Al233639   Markers   ESTs		i		1		·
2631   7837						
DD, MM, TTT, General Core Tox Markers   ESTs						
TTT, General Core Tox	2631	7837	A1233688			ESTs
Canaria						
Core Tox   Markers   ESTs				тт,		
2632 4670 Al233714 Markers ESTs 2637 22686 Al233753 Q, R, S General Core Tox Markers, General Alternate 2639 2822 Al233763 Alternate 2640 14153 Al233787 A, B ESTs 2641 2096 Al233801 C U, FF, 2643 15085 Al233829 RRR P11 protein P11 protein P11 protein P11 protein P11 protein P11 protein P11 protein ESTs 2644 4026 Al233835 OO, PP ESTs 2645 12655 Al233865 JJ ESTs 2646 21260 Al233885 TT ESTs 2647 21321 Al233902 UUU ESTs ESTs, Weakly similar to T19236 hypothetical protein C13C4,4 - Caenorhabditis elegans [C.elegans] ESTs 2652 Al233966 RR Spinocerebellar ataxia 10 homolog (human) ESTs 2653 22140 Al234098 W ESTs 2654 6532 Al234105 MMM ESTs 2655 14181 Al234107 UUU ESTs 2658 14190 Al23428 I, J ESTs 2657 ESTs 2658 14190 Al23428 I, J ESTs 2657 ESTs 2658 14190 Al234283 O, P, VV ESTs ESTs ESTS ESTS			1	General		
2637   22686   Al233753   Q. R. S   General   Core Tox   Markers, General   ESTs				Core Tox		
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Core Tox   Markers, General   ESTs	2637	22686	AI233753	Q, R, S		ESTs
Markers, General   Series				S .		
2639   2822   Al233763   Alternate   ESTs	<u> </u>			Core Tox		
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2640				General		
2641   2096   Al233801   C	2639	2822	AI233763	Alternate	1	ESTs
Column	2640	14153	Al233787	A, B		ESTs
2643   15085   Al233829   RRR	2641	2096	Al233801	С		ESTs
E. BB. CC, NN, OO, PP				U, FF,		
CC, NN, OO, PP	2643	15085	AI233829	RRR	P11 protein	P11 protein
2644         4026         Al233835         OO, PP         ESTs           2645         12655         Al233836         JJ         ESTs           2646         21260         Al233885         TT         ESTs           2647         21321         Al233902         UUU         ESTs           2648         4918         Al233941         T, GG         ESTs, Weakly similar to T19236 hypothetical protein C13C4.4 - Caenorhabditis elegans [C.elegans]           2649         10972         Al233956         PP, QQ         ESTs           2650         14167         Al233966         RR         ESTs           2652         21281         Al234090         BB, III         Spinocerebellar ataxia 10 homolog (human)           2653         22140         Al234098         W         ESTs           2653         22140         Al234105         MMM         ESTs           2655         14181         Al234107         UUU         ESTs           2655         14181         Al234128         I, J         ESTs           2658         14190         Al23428         ZZ, AAA         ESTs           2661         2765         Al234283         O, P, VV         ESTs				E, BB,		
2645         12655         AI233836         JJ         ESTs           2646         21260         AI233885         TT         ESTs           2647         21321         AI233902         UUU         ESTs           2648         4918         AI233941         T, GG         ESTs, Weakly similar to T19236 hypothetical protein C13C4.4 - Caenorhabditis elegans [C.elegans]           2649         10972         AI233956         PP, QQ         ESTs           2650         14167         AI233966         RR         ESTs           2650         14167         AI234090         BB, III         (human)         spinocerebellar ataxia 10 homolog (human)           2653         22140         AI234098         W         ESTs           2654         6532         AI234105         MMM         ESTs           2655         14181         AI234107         UUU         ESTs           2655         14181         AI234107         UU         ESTs           2657         14187         AI234147         V         ESTs           2658         14190         AI234283         O, P, VV         ESTs				CC, NN,		
2646         21260         Al233885         TT         ESTs           2647         21321         Al233902         UUU         ESTs           2648         4918         Al233941         T, GG         ESTs, Weakly similar to T19236 hypothetical protein C13C4.4 - Caenorhabditis elegans [C.elegans]           2649         10972         Al233956         PP, QQ         ESTs           2650         14167         Al233966         RR         ESTs           2652         21281         Al234090         BB, III         (human)         spinocerebellar ataxia 10 homolog (human)           2653         22140         Al234098         W         ESTs           2654         6532         Al234105         MMM         ESTs           2655         14181         Al234107         UUU         ESTs           2655         14187         Al234147         V         ESTs           2658         14190         Al23428         Z, AAA         ESTs           2661         2765         Al234283         O, P, VV         ESTs	2644	4026	AI233835	00, PP		ESTs
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ESTs, Weakly similar to T19236 hypothetical protein C13C4.4 - Caenorhabditis elegans [C.elegans]  2649 10972 Al233956 PP, QQ ESTs  2650 14167 Al233966 RR ESTs  2652 21281 Al234090 BB, III (human) spinocerebellar ataxia 10 homolog (human)  2652 2140 Al234098 W ESTs  2654 6532 Al234105 MMM ESTs  2655 14181 Al234107 UUU ESTs  2656 22233 Al234128 I, J ESTs  2657 14187 Al234187 V ESTs  2658 14190 Al234218 ZZ, AAA ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTs  ESTS	2646	21260	Al233885	TT		ESTs
hypothetical protein C13C4.4 - Caenorhabditis elegans   C.elegans	2647	21321	Al233902	UUU		ESTs
Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis eleg	·					ESTs, Weakly similar to T19236
Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis eleg						
2648       4918       Al233941       T, GG       [C.elegans]         2649       10972       Al233956       PP, QQ       ESTs         2650       14167       Al233966       RR       ESTs         2652       21281       Al234090       BB, III       (human)       spinocerebellar ataxia 10 homolog (human)         2653       22140       Al234098       W       ESTs         D, V, BB, CC, NN, OO, PP, EEE, III, OO, PP, EEE, III, Al234107       EUUU       ESTs         2655       14181       Al234107       UUU       ESTs         2656       22233       Al234128       I, J       ESTs         2658       14190       Al234218       ZZ, AAA       ESTs         2661       2765       Al234283       O, P, VV       ESTs	1					Caenorhabditis elegans
2649       10972       Al233956       PP, QQ       ESTs         2650       14167       Al233966       RR       ESTs         2652       21281       Al234090       BB, III       (human)       spinocerebellar ataxia 10 homolog (human)         2653       22140       Al234098       W       ESTs         D, V, BB, CC, NN, OO, PP, EEE, III, OO, PP, EEE, III, Al234107       ESTs       ESTs         2655       14181       Al234107       UUU       ESTs         2656       22233       Al234128       I, J       ESTs         2658       14190       Al234218       ZZ, AAA       ESTs         2661       2765       Al234283       O, P, VV       ESTs	2648	4918	Al233941	T, GG		
2650       14167       Al233966       RR       ESTs         2652       21281       Al234090       BB, III       (human)       spinocerebellar ataxia 10         2653       22140       Al234098       W       ESTs         D, V, BB, CC, NN, OO, PP, EEE, III, OO, PP, EEE, III, Al234107       EUUU       ESTs         2654       6532       Al234105       MMM       ESTs         2655       14181       Al234107       UUU       ESTs         2656       22233       Al234128       I, J       ESTs         2657       14187       Al234147       V       ESTs         2658       14190       Al234283       O, P, VV       ESTs	2649	10972	Al233956	PP, QQ		
Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocerebellar   Spinocereb		14167	AI233966			
Alexa					spinocerebellar	
2652       21281       Al234090       BB, III       (human)       homolog (human)         2653       22140       Al234098       W       ESTs         D, V, BB, CC, NN, OO, PP, EEE, III, Al234105       MMM       ESTs         2654       6532       Al234105       MMM       ESTs         2655       14181       Al234107       UUU       ESTs         2656       22233       Al234128       I, J       ESTs         2657       14187       Al234147       V       ESTs         2658       14190       Al234283       O, P, VV       ESTs         2661       2765       Al234283       O, P, VV       ESTs					1 *	spinocerebellar ataxia 10
2653 22140 Al234098 W ESTs  D, V, BB, CC, NN, OO, PP, EEE, III,  2654 6532 Al234105 MMM ESTs  2655 14181 Al234107 UUU ESTs  2656 22233 Al234128 I, J ESTs  2657 14187 Al234147 V ESTs  2658 14190 Al234218 ZZ, AAA ESTs  2661 2765 Al234283 O, P, VV ESTs	2652	21281	A1234090	вв, ш		
D, V, BB, CC, NN, OO, PP, EEE, III, MMM ESTs  2654 6532 AI234105 MMM ESTs  2655 14181 AI234107 UUU ESTs  2656 22233 AI234128 I, J ESTs  2657 14187 AI234147 V ESTs  2658 14190 AI234218 ZZ, AAA ESTs  2661 2765 AI234283 O, P, VV ESTs					· · · · · · · · · · · · · · · · · · ·	
CC, NN, OO, PP, EEE, III,  2654 6532 Al234105 MMM ESTs  2655 14181 Al234107 UUU ESTs  2656 22233 Al234128 I, J ESTs  2657 14187 Al234147 V ESTs  2658 14190 Al234218 ZZ, AAA ESTs  2661 2765 Al234283 O, P, VV ESTs				D, V, BB.		
OO, PP, EEE, III, 2654 6532 Al234105 MMM ESTs ESTs ESTs 2655 14181 Al234107 UUU ESTs ESTs 2656 22233 Al234128 I, J ESTs 2657 14187 Al234147 V ESTs 2658 14190 Al234218 ZZ, AAA ESTS 2661 2765 Al234283 O, P, VV ESTS						
EEE, III,   ESTs	1					
2654       6532       Al234105       MMM       ESTs         2655       14181       Al234107       UUU       ESTs         2656       22233       Al234128       I, J       ESTs         2657       14187       Al234147       V       ESTs         2658       14190       Al234218       ZZ, AAA       ESTs         2661       2765       Al234283       O, P, VV       ESTs						
2655       14181       Al234107       UUU       ESTs         2656       22233       Al234128       I, J       ESTs         2657       14187       Al234147       V       ESTs         2658       14190       Al234218       ZZ, AAA       ESTs         2661       2765       Al234283       O, P, VV       ESTs	2654	6532	Al234105			ESTs
2656       22233       Al234128       I, J       ESTs         2657       14187       Al234147       V       ESTs         2658       14190       Al234218       ZZ, AAA       ESTs         2661       2765       Al234283       O, P, VV       ESTs	2655					
2657     14187     Al234147     V     ESTs       2658     14190     Al234218     ZZ, AAA     ESTs       2661     2765     Al234283     O, P, VV     ESTs						
2658     14190     Al234218     ZZ, AAA     ESTs       2661     2765     Al234283     O, P, VV     ESTs	2657					
2661 2765 Al234283 O. P. VV ESTs					·	
	2661					
	2662	14197	Al234292	CCC		ESTs

TABL				e de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de l	tomey Docket 44921-5033-01WC Document No. 1935323.1
Seq ID :::	ര്ദ്ദരം	Conson; Accor §; Roßeg ID	Medal	Known Cene Name	Unigene Sequence Civeter Title
2663	14202	Al234326	LLL, SSS, UUU		EST
			A, B, DD, EE, PP, III, NNN, General		
2664	17664	A1234496	Alternate		ESTs
2666	7782	AI234515	D		ESTs
2668	26313	Al234599	SS		
2670	16960	Al234666	SS		ESTs
2671	18999	Al234677	R, W		ESTs
2672	23964	Al234748	11		ESTs
2673	9015	Al234810	General Alternate		ESTs
2674	23583	AI234819	W, III, JJJ		ESTs -
2676	2594	Al234843	Z		ESTs, Moderately similar to Yeast LPG22P protein like [Caenorhabditis elegans] [C.elegans]
					ESTs, Weakly similar to Human mRNA KIAA0066 predicted protein like [Caenorhabditis
2678	7282	Al234962	Z, AA		elegans] [C.elegans]
2679	8850	Al235059	Q, R, W		ESTs
2682	5316	Al235219	XX, YY		ESTs
2685	15181	Al235234	บบบ		ESTs
2686	6632	Al235277	S		ESTs
2689	14725	AI235306	HH		ESTs
2692	22805	Al235403	S	•	ESTs, Highly similar to adaptor- related protein complex AP-3, delta subunit [Mus musculus] [M.musculus]
	21874		SS		ESTs
2694	23228	Al235446	RRR		ESTs
2700	19052	Al235675	E V, ZZ,		ESTs
2704	14766	AI235886	AAA EEE,		ESTs
2705	14767		MMM, OOO, General Core Tox Markers		ESTs, Weakly similar to RIKEN cDNA 2410005O16 [Mus musculus] [M.musculus]
0700			RRR, SSS,		ESTs, Highly similar to RIKEN cDNA 2510027N19 [Mus
		AI235898	บบบ		musculus] [M.musculus]
2707	26330	Al235911	D		

	7			AV.	tomey Docket 44921-5033-01WC 
509 ID ::	id no. Grec	Conson: Acc or Refer 10	Modd Code	T	Unigene Sèquence Cluster Tills
			DD, III, JJJ, NNN, General		
2710	14776	Al235950	Core Tox Markers		ESTs
2711	15836	Al235951	PP, QQ		ESTs, Moderately similar to N4BM_HUMAN NADH-ubiquinone oxidoreductase subunit B14.5b (Complex I-B14.5b) (CI-B14.5b) [H.sapiens]
			KKK, PPP, QQQ, General Core Tox		
2713	14312	AI236036	Markers G, GGG,		ESTs
2715	19732	AI236066	ннн		ESTs
					ESTs, Moderately similar to S15785 heat-stable antigen- related hypothetical protein HSA-
2718	15467	AI236106	QQ		C - mouse [M.musculus]
2719	11431	AI236120	Q, R, PPP, QQQ		ESTs ·
2720	23230	Al236146	C, DD		ESTs
2721	14594	AI236152	11		ESTs
2722	14878	Al236188	М		EST
2723	9009	AI236223	General Alternate		ESTs, Highly similar to cullin 4A [Homo sapiens] [H.sapiens]
2724	12964	Al236227	XX, YY		ESTs
2725	14887	Al236243	N, PP, QQ, XX		EST, Moderately similar to 0806162D protein COII [Mus musculus] [M.musculus]
2727		AI236280	G, H	protein S	protein S
2729	18610	Al236307	G, H		ESTs
2732			DD, EE		Rattus norvegicus retinol dehydrogenase type II mRNA, complete cds
2733	19075	AI236473	Q, II		ESTs
2737		AI236590	E, DD, EE		ESTs
			Q, T		ESTs
2739	6567	AI236608	ZZ, AAA		ESTs
2741	17248	AI236635	M, X, Y		ESTs, Highly similar to 2120310B RNA polymerase II elongation factor [Mus musculus] [M.musculus]

TABL	Eq			A	tomey Docket 4X921-5933-91W0 
960 10	elec Dixo.	Refseq ID	Moම්ම :	Known Cone Kamë.	Unigano Soquance Cluster Tille
					ESTs, Moderately similar to RHG4_HUMAN Rho-GTPase-activating protein 4 (Rho-GAP
2742	13462	AI236683	C		hematopoietic protein C1) (P115) [H.sapiens]
2744	18783	AI236746	C, DD, MM, TTT		ESTs
2745	16609	AI236748	Z, AA		ESTs, Moderately similar to CENB_MOUSE MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) [M.musculus]
2746	16859	AI236753	DD, NNN		ESTs
2747	22443	AI236761	Q		ESTs
2748	24388	Al236772	R		ESTs
2749	23855	AI236773	PP, QQ		ESTs
2751	23081	AI236778	ZZ, AAA		ESTs
2752	14232	AI236794	N		ESTs ESTs, Highly similar to
2754	17455	Al236818	AA, SS		FKBX_MOUSE 65 kDa FK506-binding protein precursor (FKBP65) (FKBPRP) (Peptidylprolyl cis-trans isomerase) (PPiase) (Rotamase) (Immunophilin FKBP65) [M.musculus]
2755	23595	AI236834	Q, R		ESTs
2756	18303	AI236863	ww		Rattus norvegicus retinol dehydrogenase type II mRNA, complete cds.
2758	17323	AI236936	$\overline{v}$		ESTs
2759 2764	5059 14811	AI236947 AI237026	W, EEE, MMM TT		ESTs ESTs
L			AAA		ESTs
2767	13336		Z, AA		ESTs
	4175		UUU		ESTs
2770	14937		XX, III, JJJ		ESTs, Weakly similar to T23655 hypothetical protein M01F1.3 - Caenorhabditis elegans [C.elegans]
2771	4937		Z		ESTs
2772	14911	AI237403	L		ESTs
			Y		ESTs
	12956	AI237580	Z, LL		ESTs
2777	18267	AI237595	SS		ESTs
2778	22038		General Core Tox Markers		ESTs

TABU	<b>3</b> 1			AG	torney Docket 44921-5033-91WC Document No. 1935328.1
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			I, T, DD,		
1			III, JJJ,		
1 1			NNN,		
1			000,		,
1			General		
			Core Tox		
2779	15170	Al237618	Markers		ESTs
2781	23860	AI237684	Н		ESTs
			0 5 111		
0700	4 40 40	41007000	O, P, NN,		COT-
2782	14840	Al237698	00, VV		ESTs
2792	14520	A1227749	General Alternate		ESTs
2783 2784	14528 14842	AI237718 AI237724	C		ESTs
2785	14844	Al237782	S, Z, AA		13
2787	14656	Al237820	P		ESTs
2707	14030	A1237020	A, B,		2013
2789	5046	Al237855	SSS		ESTs
2790	14850	AI237880	RR		ESTs
2791	6127	A1638960	K, JJ, KK		ESTs
2791	6128	AI638960	JJ, KK		ESTs
2793	25855	Al639002	D, L		
	7176	AI639029	D, W, GG	l	ESTs
2796	24205	AI639045	UU		ESTs
					ESTs, Highly similar to Nedd4
			NN, OO,		WW binding# protein 4; Nedd4
1			EEE,		WW-binding protein 4 [Mus
2797	10071	AI639058	МММ		musculus] [M.musculus]
0700	05000	41000070	T, TT,		
2798	25883 19900	Al639076 Al639079	NNN		EST
2799	16514	Al639079 Al639093	D RR		ESTs
2800 2801	7170	Al639102	JJ, KK		ESTs
2001	7 170	A1039102	33, KK		2013
			F, III, JJJ,		
İ			KKK,		
1			000,		
1			General		
			Core Tox		
2802	19952	AI639108	Markers		ESTs
1		1	E, Y, MM,		ESTs, Highly similar to
1	l		ww,		CFAB_MOUSE Complement
			BBB,		factor B precursor (C3/C5
2803	5545	Al639117	CCC, TTT		convertase) [M.musculus]
2804	13882	Al639120	LL		ESTs
2805	25907	Al639167	Q		ESTs

TABU	<b>ਭ</b> 1			A	tomey Decket 44921-5033-01WO Document No. 1995928.1
		Conson!			
	@L@C		Model .	3.4.	
(D)	(D) (X)6.	RefSeq ID	Code	Known Cene Name	Unigene Sequence Cluster Title
	20615	AI639176	D		ESTs
2807	25915	Al639195	K		
	19795	AI639197	RR		EST
	19749	AI639203	ZZ, AAA		ESTs
	25928	AI639236	K		
2811	25930	AI639245	D		
2812	20614	A1639246	LLL		ESTs
2813	19962	AI639248	X, Y		
2814	17082	AI639255	TT		ESTs
			C, N, O,		
2814	17083	AI639255	Р		ESTs
			Q, R,		
2815	25934	A1639257	ww		
2816	25938	Al639281	D		ESTs
2817	3787	AI639324	ZZ, AAA		ESTs
			Y, ZZ,		
2817	3788	A1639324	AAA		ESTs
2819	25964	AI639352	Y		
2820	20026	Al639354	GG	•	EST
2821	25971	AI639365	K		
2822	18295	AI639381	LLL		ESTs
2823	25983	AI639390	K		
2825	10097	AI639425	K		ESTs
2825	10098	AI639425	D ·		ESTs
				eukaryotic translation	
				initiation factor 2B,	eukaryotic translation initiation
				subunit 3 (gamma,	factor 2B, subunit 3 (gamma,
2826	799	AI639441	UU	58kD)	58kD)
2827	19870	Al639462	V		ESTs
					ESTs, Moderately similar to
			AA, BBB,		Y039 HUMAN HYPOTHETICAL
2829	20402	A1639489	ccc		PROTEIN KIAA0039 [H.sapiens]
2830	5998	Al639501	LLL		ESTs
			A, B,		
			GGG,		ESTs, Weakly similar to T13607
			ннн,		hypothetical protein 87B1.3 - fruit
			General		fly (Drosophila melanogaster)
2831	20056	A1639504	Alternate		[D.melanogaster]
			G, H, O,		
2847	25257	D13623	T, 00		
2851	20384	D17349	TT, DDD		·
2854	25270	D26498	D		
	25276	D28966	CC		
2863	25287	D38069	K, X, Y		
				nuclear receptor	
			JJ, KK,	subfamily 0, group B,	nuclear receptor subfamily 0,
2874	970	D86580	ннн	member 2	group B, member 2
2875	19420	D86711	X, Y		ESTs
			OO, EEE,		
2878	25313	D87991	MMM		

Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   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the state of the state of the state of the state of the state of the state of the s	tomay Docket 44921-5033-011WC Document No. 1985323.1
Z, AA, MM, SS, TTT	S00 :	elec .	Consenia Age or	Model		
MM, SS, TTT	(D)	In Kid		@@@****	known ceus haws:	Muidava sadravas ciratat utila
2882   25805   E01050   TTT						
2889   22543   H31117   D				MM, SS,		
2890   21863   H31128   D						
2892   4333		_L	<del></del>			
2893   20514   H31489   P   ESTs   ESTs   Highly similar to Ral-A   exchange factor RalGPS2 [Mus musculus] [M.musculus]   ESTs, Highly similar to Ral-A   exchange factor RalGPS2 [Mus musculus] [M.musculus]   ESTs, Highly similar to ORN   HUMAN Oligoribonuclease mitochondrial precursor (Small fragment nuclease) (CGI-114)   H.s.apiens]   EST   ESTs, Weakly similar to S28312   hypothetical protein F02A9.4   Caenorhabditis elegans   CCC   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ES						
III, JJJ, KKKK,						
14933	2893	20514	H31489	1.		
14933						
ESTs, Highly similar to   ORN_HUMAN Oligoribonuclease mitochondrial precursor (Small fragment nuclease) (CGI-114)   H. X. Y. HHH   H. Sapiens]   EST   ESTs, Weakly similar to S28312 hypothetical protein F02A9.4 - Caenorhabditis elegans   C. Ceegans]   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs	2004	44022	1124500	•	•	
CRN_HUMAN Oligoribonuclease mitochondrial precursor (Small fragment nuclease) (CGI-114)   H, X, Y, HHH   H, Sapiens]   EST	2894	14933	H31588	000		
Mitochondrial precursor (Small fragment nuclease) (CGI-114)						
12613	1	İ		•		
12613						
Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Babar   Baba	2005	12612	U24620			
BBB,   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   ESTs   ESTs, Weakly similar to ESTs, Weakly similar to END3_CAEEL Probable endonuclease III homolog (DNA-(Apurinic or apyrimidinic site) lyase) [Caelegans]   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caen						
BBB,   CCC   Caenorhabditis elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.elegans   C.	2090	4349	1040	00		
BBB,   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabditis elegans   Caenorhabdit			İ			
2898 16588 H31711 CCC [C.elegans]  2901 4364 H31887 CCC ESTs  2902 10530 H31897 DD, EE ESTs  2904 12485 H31964 C ESTs  2906 20684 H32977 PPP ESTs  2907 4395 H33149 K, FF ESTs, Weakly similar to F38A5.1.p [Caenorhabditis elegans] [C.elegans]  2908 16524 H33219 ZZ, AAA ESTs  ESTs, Weakly similar to END3_CAEEL Probable endonuclease III homolog (DNA-(Apurinic or apyrimidinic site) lyase) [C.elegans]  2909 4397 H33255 E  KKK, OOO, General Core Tox Markers, General Core Tox Markers, General Core Tox Markers, General Core Tox Markers ESTs  2910 10184 H33426 Alternate ESTs  F, Q, R, U, HH, UU, DDD, LLL ESTS  2911 4407 H33528 LLL ESTS  2912 4414 H33629 ZZ, AAA ESTS				RRR		
2901   4364	2898	16588	H31711			
2901   4364   H31887   CCC   ESTs	2000	10000	1101711			[O.elegans]
2902   10530   H31897   DD, EE   ESTs	2901	4364	H31887			FSTs
2904   12485   H31964   C						
2906   20684   H32977   PPP   ESTs   ESTs, Weakly similar to   F38A5.1.p [Caenorhabditis   elegans] [C.elegans]   ESTs   ESTs, Weakly similar to   F38A5.1.p [Caenorhabditis   elegans]   C.elegans]   ESTs   ESTs, Weakly similar to   END3_CAEEL Probable   endonuclease III homolog (DNA-(Apurinic or apyrimidinic site)   lyase) [C.elegans]   KKK, OOO, General   Core Tox   Markers, General   Core Tox   Markers, General   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   E						
ESTs, Weakly similar to F38A5.1.p [Caenorhabditis elegans] [C.elegans]	2906					
F38A5.1.p [Caenorhabditis elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.elegans]   C.ele						
2907   4395   H33149   K, FF   elegans] [C.elegans]   ESTs   ESTs, Weakly similar to END3_CAEEL Probable endonuclease III homolog (DNA-(Apurinic or apyrimidinic site)   lyase) [C.elegans]   ESTs   ESTs, Weakly similar to END3_CAEEL Probable endonuclease III homolog (DNA-(Apurinic or apyrimidinic site)   lyase) [C.elegans]   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTs   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   ESTS   EST						
2908   16524   H33219   ZZ, AAA   ESTs	2907	4395	H33149	K, FF		
END3_CAEEL Probable endonuclease III homolog (DNA-(Apurinic or apyrimidinic site) lyase) [C.elegans]  KKK, OOO, General Core Tox Markers, General Alternate  ESTs  General Alternate  F, Q, R, U, HH, UU, DDD, LLL ESTs  END3_CAEEL Probable endonuclease III homolog (DNA-(Apurinic or apyrimidinic site) lyase) [C.elegans]  ESTs  ESTs  ESTs  ESTs	2908	16524	H33219	ZZ, AAA		
endonuclease III homolog (DNA- (Apurinic or apyrimidinic site) lyase) [C.elegans]  KKK, OOO, General Core Tox Markers, General 2910 10184 H33426 Alternate  ESTs  General Alternate  F, Q, R, U, HH, UU, DDD, LLL ESTs  endonuclease III homolog (DNA- (Apurinic or apyrimidinic site) lyase) [C.elegans]  ESTs  ESTs						ESTs, Weakly similar to
2909   4397	Į.					
2909   4397   H33255   E						•
KKK, OOO, General Core Tox Markers, General 2910 10184 H33426 Alternate ESTs  General 2910 10185 H33426 Alternate ESTs  F, Q, R, U, HH, UU, DDD, 2911 4407 H33528 LLL ESTs  ESTs  ESTs						
OOO,     General     Core Tox     Markers,     General 2910 10184 H33426 Alternate ESTs  General 2910 10185 H33426 Alternate ESTs  F, Q, R, U, HH, UU, DDD, 2911 4407 H33528 LLL ESTs  ESTs  ESTs	2909	4397	H33255			lyase) [C.elegans]
General Core Tox Markers, General 2910 10184 H33426 Alternate ESTs  General 2910 10185 H33426 Alternate ESTs  F, Q, R, U, HH, UU, DDD, 2911 4407 H33528 LLL ESTs  ESTs  ESTs						
Core Tox Markers, General 2910 10184 H33426 Alternate ESTs  General Alternate ESTs  General Alternate ESTs  F, Q, R, U, HH, UU, DDD, UU, DDD, 2911 4407 H33528 LLL ESTs  2912 4414 H33629 ZZ, AAA ESTs			: :	· ·		
Markers, General 2910 10184 H33426 Alternate ESTs  General 2910 10185 H33426 Alternate ESTs  F, Q, R, U, HH, UU, DDD, LLL 2911 4407 H33528 LLL 2912 4414 H33629 ZZ, AAA ESTs						
General Alternate ESTs  General Alternate  2910 10184 H33426 Alternate  General ESTs  F, Q, R, U, HH, UU, DDD, LLL ESTs  2911 4407 H33528 LLL ESTs  2912 4414 H33629 ZZ, AAA ESTs						
2910 10184 H33426 Alternate ESTs  General Alternate ESTs  F, Q, R, U, HH, UU, DDD, 2911 4407 H33528 LLL 2912 4414 H33629 ZZ, AAA ESTs						
General Alternate ESTs  F, Q, R, U, HH, UU, DDD, LLL ESTs  2912 4414 H33629 ZZ, AAA ESTs	2040	10104	U2240E			FOT-
2910 10185 H33426 Alternate ESTs  F, Q, R, U, HH, UU, DDD, 2911 4407 H33528 LLL ESTs  2912 4414 H33629 ZZ, AAA ESTs	2910	10184	⊓3342b			ESIS
F, Q, R, U, HH, UU, DDD, 2911 4407 H33528 LLL ESTs 2912 4414 H33629 ZZ, AAA ESTs	2040	10105	H33436			EST
U, HH, UU, DDD, 2911 4407 H33528 LLL ESTs 2912 4414 H33629 ZZ, AAA ESTs	2310	10100	1133420	Alternate		EOIS
U, HH, UU, DDD, 2911 4407 H33528 LLL ESTs 2912 4414 H33629 ZZ, AAA ESTs				E O B	İ	
UU, DDD, 2911 4407 H33528 LLL ESTs 2912 4414 H33629 ZZ, AAA ESTs	d				1	
2911 4407 H33528 LLL ESTs 2912 4414 H33629 ZZ, AAA ESTs			1			
2912 4414 H33629 ZZ, AAA ESTs	2911	4407				FSTs
			H33723			EST

TABL	31			AS	tomey Docket 4/4221-5033-01000 Document No. 1985323.1
	er ee	Geneent Ass or Refeed ID	00-0-0		Oliff, retervice encourage.
2914	9597	H33832	XX, YY		
2914	9598	H33832	U		
2918	12974	H34243	SS		ESTs
			K, L, X, HH, II, TT, DDD,		
2919	12155	J00728	LLL		
2920	25050	J01435	HH, NNN		
2920	25319	J01435	FF		
2921	25051	J01436	S, HH, NNN		
2935	12156	K00996	K, X, TT, DDD, LLL, RRR, UUU	cytochrome P450, 2b19	cytochrome P450, 2b19
2936	12157	K01721	K, L, X, FF, TT, DDD, LLL, UUU	cytochrome P450, 2b19	cytochrome P450, 2b19
			S, GG,		
2939	25325	K03045	ss	·	
2939	25326	K03045	GG		
1	12158	L00320	X, TT, DDD, RRR		
2943	25327	L00686	DDD		
2946	15378	L05541	E, GG, III, JJJ, General Alternate Z, AA, General		
2947	25343	L07407	Alternate		
	25350 25363	L10669 L13235	D UUU	Phosphorylase, glycogen; muscle (McArdle syndrome)	
2954	25366	L14003	UU		
2307	20000		I, J, T, PP, III, KKK, NNN, OOO, General Core Tox Markers, General	<del>-</del>	,
2958	25370	L16995	Alternate		
2959	25371	L17077	D, RR		

TABL	<b>3</b> 9		in April 1		(omey Docket 44921-5088-01WO
ت ده					Document No. 1935023.1
10) : i ·	ID Nort	CONSINT ACCO ROSSOCID	Model Code	Known Cene Name	Unigene Sequence Cluster Title
2962	25052	L22190	A, E, W, BB, EEE, JJJ, MMM	Y	
2963	43	L23413	D, M, T, NN, UU, III, JJJ, UUU	sulfate anion transporter	sulfate anion transporter
2977	25055 25055	L46593 M11251	V A, B, X, TT, DDD, LLL, RRR		
2985	17086	M13011	V, FFF		
2986	18480	M13100	RR		ESTs
2986	20625	M13100	RR		
2986	20626	M13100	RR, SS		
2986	20630	M13100 M13101	RR		
2987	25399 25056	M13234	RR K, X, Z, TT, DDD, LLL		
2991	25400	M14776	K, N, TT, DDD		
2996	25412	M18530	XX		
2997	25413 17274	M18531 M18854	X, Y PP, QQ		Rat T-cell receptor active beta- chain C-region mRNA, partial cds, clone TRB4
2999	20464	M20406	N, QQ, UU, HHH, PPP, QQQ, General Alternate		Rat cytochrome P450IIB3 (P450IIB subfamily) mRNA, complete cds
3002	20481	M22631	II, XX, YY	Propionyl Coenzyme A carboxylase, alpha polypeptide	
3003	1476	M22756	RR	24-kDa subunit of mitochondrial NADH dehydrogenase	24-kDa subunit of mitochondrial NADH dehydrogenase
3013 3020	16305 25439	M33312 M35826	E, M, GG S, SS	Cytochrome P450 IIA1 (hepatic steroid hydroxylase IIA1) gene	Cytochrome P450 IIA1 (hepatic steroid hydroxylase IIA1) gene
3032	17130	M62992	O, P		
3037 3041	1223 19730	M75281 M81183	SS, III, JJJ LL, LLL		ESTs
	1				

TABL			* **		tomey Docket 44921-5033-01W0 Document No. 1935323.1
809 (D	@L@C	Kaisag id Acc or Raisag id	Model Code	emien enco avean	Unigene Sequence Cluster Tille
				ATPase, Na+K+ transporting, beta polypeptide 2 (Atp1b2), mRNA. 4/2002 Length =	•
3063	25049	NM_012507	GG	1764	
			т, xx,	fructose-1,6- bisphosphatase 1 (Fbp1), mRNA. 10/2002 Length =	
3079	16895	NM_012558	YY, DDD E, CC,	1357 Fibrinogen, gamma	Fructose-1,6- biphosphatase
3080	25317	NM 012559	DD, EE, III, JJJ, NNN	polypeptide (Fgg), mRNA. 11/2000 Length = 1358	
3080	20017	NW_012339	G, H, I,	Mannose binding protein A, serum (Mbpa), mRNA. 11/2000 Length =	
3092	25204	NM_012599	J, XX	717	
3096	23524	NM_012615	OOO, General Alternate	Ornitine decarboxylase (Odc1), mRNA. 11/2000 Length = 2442	
3101	18619	NM_012645	т, п	RT1 class lb gene (RT1Aw2), mRNA. 11/2002 Length = 1540	RT1 class I gene
3101	18725	NM 012645	F, LL,	RT1 class lb gene (RT1Aw2), mRNA. 11/2002 Length = 1540	
3101	10725	14W_012U43	Aireillare	RT1 class lb gene, H2-TL-like, grc region (RT1-N1), mRNA. 11/2000	
3102	18637	NM_012646	QQ, XX	Length = 1179	RT1 class I gene
3112	24589	NM_012674	NN, EEE, MMM	Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic (Spink1), mRNA. 11/2000 Length = 2338	Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic

TABL	इ१			M.	torney Docket 44921-5033-01W0 - :: Document No. 1935323.1
S09 [D::::]	ID Ko.	CEMEDINI ACC OT RC(SOG ID	Model Code	eijien eies woon	Unigane Sequence Cluster Title
3116	16306	NM 012692	JJ, KK, FFF, HHH, PPP, QQQ, General Alternate	Cytochrome P450 IIA1 (hepatic steroid hydroxylase IIA1) gene (Cyp2a1), mRNA. 11/2000 Length = 1687	Cytochrome P450 IIA1 (hepatic steroid hydroxylase IIA1) gene, Cytochrome P450 IIA2
		_	JJ, VV, XX, YY, HHH, PPP, QQQ, General	Cytochrome P450 IIA2 (Cyp2a2), mRNA. 11/2000	
3117	24707	NM_012693	Alternate	Length = 2259 Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length =	Cytochrome P450 IIA2  Sulfotransferase hydroxysteroid
3119	10622	NM_012695	N, YY	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length =	gene 2 Sulfotransferase hydroxysteroid
3119	10624	NM_012695		1000 Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length =	gene 2 Sulfotransferase hydroxysteroid
3119	10625 10626	NM_012695 NM_012695	N N, II, UUU	1000 Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length =	gene 2 Sulfotransferase hydroxysteroid gene 2
3119	18717		N	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Rat senescence marker protein 2A gene, exons 1 and 2
3119	18719		M, N, UUU	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Rat senescence marker protein 2A gene, exons 1 and 2

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TABL	ાં લ	3		ANG	torney Docket 4/1921-5033-01W0 Document No. 1935323.1
Seq (D,:	id ko Grec	Lace or Ace or Redien	Model (Code :-	Known Cene Name	Uniteni Sequence Cluster Title
3119	18860	NM_012695	×	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Rattus norvegicus mRNA for hydroxysteroid sulfotransferase subunit, complete cds
3119	18861	NM_012695	N	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Rattus norvegicus mRNA for hydroxysteroid sulfotransferase subunit, complete cds
				Thyroid hormone responsive protein (spot14) (Thrsp), mRNA. 4/2002	
3122	26032	NM_012703	FF E, BB, CC, DD,	Length = 453	
3133	20354	NM_012741	NN, OO, PP, EEE, III, KKK, LLL, MMM, NNN, UUU	K-kininogen, differential splicing leads to HMW Kngk (Kng_v1), mRNA. 11/2002 Length = 2100	
3154	11136	NM_012839	MM, FFF, TTT	cytochrome c, somatic (Cycs), mRNA. 11/2002 Length = 318	•
3158	25336	NM_012850	RR	Growth hormone - releasing receptor (Ghrhr), mRNA. 11/2000 Length = 1629	
0450	40000		General Core Tox	Hydroxysteroid dehydrogenase 17 beta, type 1 (Hsd17b1), mRNA. 11/2000 Length =	
3159	18960	NM_012851		Thyroid stimulating hormone receptor (Tshr), mRNA. 11/2002 Length =	ESTs
3167	25284	NM_012888	HH	5270	•

TABL	€1			·	tomey Docket 44921-5033-911WO Document No. 1935323.1
Seq . ID :	ELEC	CONSTAL ACC OT ROSSOGID	Model Code:	Known Cone Name	Unigene Sequence Cluster Title
3177	6107	NM_012915	G, H, O, P, XX, YY, PPP, QQQ	ATPase inhibitor (rat mitochondrial IF1 protein) (Atpi), mRNA. 11/2000 Length = 833	ATPase inhibitor (rat mitochondrial IF1 protein)
3177	6108	NM_012915	G, H, Y, General Alternate	ATPase inhibitor (rat mitochondrial IF1 protein) (Atpi), mRNA. 11/2000 Length = 833	ATPase inhibitor (rat mitochondrial IF1 protein)
3177	6109	NM_012915	F, J, M, S, EE, HH, SS, NNN	ATPase inhibitor (rat mitochondrial IF1 protein) (Atpi), mRNA. 11/2000 Length = 833	ATPase inhibitor (rat mitochondrial IF1 protein) EST, Moderately similar to
3179	19302	NM_012930	BBB, CCC	palmitoyltransferase 2 (Cpt2), mRNA. 11/2002 Length = 2296	CPT2_RAT CARNITINE O- PALMITOYLTRANSFERASE II, MITOCHONDRIAL PRECURSOR (CPT II)
3186	956	NM_012976	L, MM, RR, TTT	Lectin, galactose binding, soluble 5 (Galectin-5) (Lgals5), mRNA. 11/2000 Length = 872	Lectin, galactose binding, soluble 9 (Galectin-9)
3208	14997	NM_013059	JJJ, KKK,	alkaline phosphatase, tissue- nonspecific (Alpl), mRNA. 11/2002 Length = 2415	Tissue-nonspecific ALP alkaline phosphatase
3212	16924	NM_013069	Z, AA	CD74 antigen (invariant polpypeptide of major histocompatibility class II antigen- associated) (Cd74), mRNA. 11/2000 Length = 1150	CD74 antigen (invariant polpypeptide of major histocompatibility class II antigenassociated)
3212	16926	NM_013069		CD74 antigen (invariant polpypeptide of major histocompatibility class II antigen- associated) (Cd74), mRNA. 11/2000 Length = 1150	CD74 antigen (invariant polpypeptide of major histocompatibility class II antigenassociated)

TABL	<b>E</b> 1		Application of the second	A	tomey Docket 44921-5093-011WO Document No. 1935323.1
Seq [D	ELEC ID No.:	CONSINK ACCO RCESION	Model .	Known Cene Name.	Unigene Sequence Civeter Title
				CD74 antigen (invariant polpypeptide of major histocompatibility class II antigen- associated) (Cd74), mRNA. 11/2000	
3212	25676	NM_013069	X, Y, QQ	Length = 1150 Hemoglobin, alpha 1	
3217	26047	NM_013096	TT	(Hba1), mRNA. 11/2000 Length = 556	•
3217	26150	NM 013096	М, Т	Hemoglobin, alpha 1 (Hba1), mRNA. 11/2000 Length = 556	
3229	25567	NM_013156	A, B, C, E, Q, W, MM, OOO, TTT	Cathepsin L (Ctsl), mRNA. 11/2002 Length = 1386	
3238	20728	NM_013217	UU, PPP, QQQ	afadin (AF-6), mRNA. 11/2000 Length = 5957	afadin .
3238	20729	NM_013217	1	afadin (AF-6), mRNA. 11/2000 Length = 5957	afadin
3254	25546	NM_017023	RR SS	Potassium inwardly- rectifying channel, subfamily J, member 1 (Kcnj1), mRNA. 11/2002 Length = 2069	
3264	18973	NM_017060	•	Hras-revertant gene 107 (Hrev107), mRNA. 10/2002 Length = 966	ESTs, Moderately similar to S14234 hypothetical protein - mouse [M.musculus]
3271	1261	 NM_017077	Q, R, MM, TTT	Hepatocyte nuclear factor 3 gamma (Hnf3g), mRNA. 11/2000 Length = 1497	
3310	6071	NM_017220		6-pyruvoyl- tetrahydropterin synthase (Pts), mRNA. 11/2002 Length = 1176	ESTs, Weakly similar to T20360 hypothetical protein D2030.9b - Caenorhabditis elegans [C.elegans]

TABL	E1	•		A	iomey Docket 44921-5033-91W0 Document No. 1935323.1
809 (D)	. ID Ko.	(CALEAR) AGE OT REFSEQ (D)	(Cocio)	Known Gene Name	Unigene Sequence Cluster Title
				6-pyruvoyl- tetrahydropterin synthase (Pts), mRNA. 11/2002	
3310	21903	NM_017220	K, N, TT	Length = 1176	cytochrome P450, 2c37
3311	18967	NM_017222	RR	solute carrier family 10, member 2 (SIc10a2), mRNA. 11/2002 Length = 4269	ESTs
3322	20913	NM_017272	M, TT, LLL, SSS, UUU	aldehyde dehydrogenase family 1, subfamily A4 (Aldh1a4), mRNA. 11/2002 Length = 2024	aldehyde dehydrogenase family 1, subfamily A4
3322	20914	NM_017272	TT, DDD, LLL, SSS,	aldehyde dehydrogenase family 1, subfamily A4 (Aldh1a4), mRNA. 11/2002 Length = 2024	aldehyde dehydrogenase family 1, subfamily A4
3335	26109	NM 017306	U, FF, XX, YY, BBB, RRR, SSS	dodecenoyl- coenzyme A delta isomerase (Dci), mRNA. 11/2002 Length = 987	EST
	20564			sodium-coupled ascorbic acid transporter 1 (SVCT1), mRNA. 11/2000 Length =	
3338			SSS, TTT, UUU, General	CAMP responsive element modulator (Crem), mRNA. 10/2002 Length =	CAMP responsive element
3344	355	NM_017334	L, DD, FFF, GGG, HHH,	CAMP responsive element modulator (Crem), mRNA. 10/2002 Length =	CAMP responsive element
3344	356 16148		U, FF, LL,	436 acyl-coA oxidase (RATACOA1), mRNA. 11/2000	modulator acyl-coA oxidase

TABL	<b>E</b> 1.		24 H 4	A	iomey Docket 44921-5099-01WO Document No. 1935923.1
Seq : ID ::	id kot: Græc	Consens Acc or Reseal	Model Code	Known Cone Name	Unigene Sequence Cluster Title
			J, U, DD, EE, FF, II, LL,	acyl-coA oxidase (RATACOA1), mRNA. 11/2000	
3345	16150	NM_017340	RRR	Length = 3741	acyl-coA oxidase
3350	26379	NM_019129	Z, AA	Insulin (Ins1), mRNA. 11/2000 Length = 333	
3351	25322	NM_019130	AA	Insulin 2 (Ins2), mRNA. 11/2000 Length = 333	
3364	1173	NM_019184	T, V, CC, OO, GGG, PPP, QQQ	Cytochrome P450, subfamily IIC (mephenytoin 4- hydroxylase) (Cyp2c), mRNA. 11/2002 Length = 1856	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
3364	1174	NM_019184	DD, TT	Cytochrome P450, subfamily IIC (mephenytoin 4- hydroxylase) (Cyp2c), mRNA. 11/2002 Length =	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
3392	20750	NM_019301	C	Complement receptor related protein (Cr1), mRNA. 11/2000 Length = 1811	
3423	26349	NM 021576	ss	5 nucleotidase (Nt5), mRNA. 11/2002 Length = 3152	
3434	25579	NM_021750	Т	cysteine-sulfinate decarboxylase (Csad), mRNA. 11/2000 Length = 2413	
3440	20182	NM_021840	M, II	histone 2a (H2a), mRNA. 1/2001 Length = 393	
3453	18216	NM 022241		prostaglandin D2 receptor (Ptgdr2), mRNA. 12/2000 Length = 1315	prostaglandin D2 receptor
3458	. 10369	NM_022271	Z, AA,	sertolin (LOC64038), mRNA. 12/2000	sertolin

TABL	<b>E</b> 1			A	tomey Docket 44921-5033-011WO Document No. 1935323.1
S99 ID	(L) (1) (1) (1) (1) (1) (1) (1) (1) (1) (1	(CONSON) ACC OT ROSSON ID	(6009) (10000)	Known Cene Name	Unigene Sequence Cluster Title
3496	20935	NM 022595	UU	kinase substrate HASPP28 (Haspp28), mRNA. 1/2001 Length = 1220	kingge aubetrate HASDD29
3490	20933		00	protein phosphatase 2C (AF095927), mRNA. 1/2001	kinase substrate HASPP28
3500	21204	NM_022606	D	Length = 1318 ribosomal protein	protein phosphatase 2C
3511	25303	NM_022699	v	L30 (Rpl30), mRNA. 11/2002 Length = 392	
3515	17500	, NM 022866	NN	solute carrier family 13 (sodium- dependent dicarboxylate transporter), member 3 (SIc13a3), mRNA. 11/2002 Length = 3239	sodium-dependent high-affinity dicarboxylate transporter 3
3516	23606	NM 022867		microtubule- associated proteins 1A/1B light chain 3 (MPL3), mRNA. 1/2001 Length = 861	microtubule-associated proteins 1A/1B light chain 3
	23608		C, DD, EE, HH, KKK, General Core Tox Markers, General Alternate	microtubule- associated proteins 1A/1B light chain 3 (MPL3), mRNA. 1/2001 Length = 861	microtubule-associated proteins 1A/1B light chain 3
3518	18630	NM 022921	O, P, XX, YY	RT1 class lb gene, locus M3 (RT1-M3), mRNA. 11/2002 Length = 1341	RT1 class lb gene, locus M3
		_		unconventional myosin Myr2 I heavy chain (Myr2), mRNA. 2/2001 Length =	unconventional myosin Myr2 I
3530	17487	NM_023092	X, Y	SECIS binding protein 2 (Sbp2),	heavy chain
3533	14468	NM_024002	нн	mRNA. 2/2001 Length = 3240	SECIS binding protein 2

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0 C-YEAR	-d5 U			$^{\circ}$	iomey Docket 44921-5033-01000 Document No. 1986323.1
809 ID . :	ID KJS. GLGC	Conteni Accor Refer ID	Code :		Unigene Sequence Cluster Title
				cytochrome b5, outer mitochondrial membrane isoform	
3562	348	NM_030586	Υ	(omb5), mRNA. 3/2001 Length = 845	cytochrome b5, outer mitochondrial membrane isoform
3565	15120	NM 030833	וננג	interferon-inducible protein 16 (LOC80875), mRNA. 4/2001 Length = 630	interferon-inducible protein 16
				interferon-inducible protein 16 (LOC80875), mRNA.	interverent-inducible protein 10
3565	15121	NM_030833	Р	4/2001 Length = 630	interferon-inducible protein 16
3573	7872	NM 030985	F, H, LL, LLL, OOO, SSS, General Alternate	angiotensin receptor 1a (Agtr1a), mRNA. 11/2002 Length = 1450	ESTs
3573	25453	NM_030985	F, LLL, SSS, General Alternate	angiotensin receptor 1a (Agtr1a), mRNA. 11/2002 Length = 1450	
3592	17269	NM_031057	General Alternate	methylmalonate semialdehyde dehydrogenase gene (Mmsdh), mRNA. 4/2001 Length = 2059	methylmalonate semialdehyde dehydrogenase gene
3598	1404	NM_031087	DD, EE	presenilin-2 (Psen2), mRNA. 4/2001 Length = 2088	presenilin-2
3599	1175	NM 031093	F, T, V, BB, TT, DDD, FFF, PPP,	#NAME? (Rala),	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
	21623			cytoplasmic beta- actin (Actx), mRNA. 4/2001 Length =	(mephenytoin 4-nyoroxyiase)
	15359	NM_031144 NM_031335		1128 polymerase II (LOC83503), mRNA. 4/2001 Length = 470	polymerase II

TABI	El	14.0	14.7	A	iomey Docket 44921-5033-011W0 Document No. 1933323.1
800 (D)	. ELGC	Consent Accor RefSeq ID	 Model "Eode	Known Cene Name	Unigene Sequence Cluster Title
3634	634	NM_031509	K, V, NN, TT, DDD, EEE, MMM	Glutathione-S- transferase, alpha type (Ya) (Gsta1), mRNA. 5/2001 Length = 1178 Glutathione-S-	Glutathione-S-transferase, alpha type (Ya)
3634	635	NM_031509	M, NN, TT, DDD, EEE, MMM	transferase, alpha type (Ya) (Gsta1), mRNA. 5/2001 Length = 1178	Glutathione-S-transferase, alpha type (Ya)
3634	25069	NM_031509	G, K, Y, TT, LLL, UUU	Glutathione-S- transferase, alpha type (Ya) (Gsta1), mRNA. 5/2001 Length = 1178	
3634	25525	NM_031509		Glutathione-S- transferase, alpha type (Ya) (Gsta1), mRNA. 5/2001 Length = 1178	Glutathione-S-transferase, alpha type (Ya)
3640	25058	NM_031533	D, RR	Androsterone UDP- glucuronosyltransfera se (Ugt2b2), mRNA. 5/2001 Length = 1593	·
3654	15803	NM_031593	T, PP, QQ	synaptic vesicle protein 2C (Sv2c), mRNA. 8/2001 Length = 2622 amyloid beta (A4)	synaptic vesicle protein 2C
3688	21646	NM 031781	V	precursor protein- binding, family A, member 3 (X11-like 2) (Apba3), mRNA. 5/2001 Length =	amyloid beta (A4) precursor protein-binding, family A, member 3 (X11-like 2)
3695	15759		PP, QQ	activin beta E (Inhbe), mRNA. 5/2001 Length = 2600 vascular endothelial	activin beta E
3703	8384	NM_031836	RR	vascular endothelial	vascular endothelial growth factor
3703	8386	NM_031836		growth factor (Vegf), mRNA. 11/2002 Length = 645	vascular endothelial growth factor

TABL	<b>E</b> 1			. A	tomay Docket 44921-5033-01WO Document No. 1935323.1
509 [D:::):	ELEC ELEC	©m:m; Acc or Re⁄Seq D ;;	Model Code	Known Cene Name	Unigana Sequenca Cluster Tille
3713	8661	NM_031971	С, К, Q, GG, НН	Heat shock protein 70-1 (Hspa1a), mRNA. 5/2001 Length = 2455	Heat shock protein 70-1
				26S proteasome, subunit p112 (PSMD1), mRNA. 5/2001 Length =	·
3717	25611	NM_031978	UU	vesicle associated protein (VAP1), mRNA. 7/2001	
3732	21103	NM_033021	D, JJ, KK	Length = 4422 vesicle associated protein (VAP1), mRNA. 7/2001	vesicle associated protein
3732	21104	NM_033021	Z, AA	Length = 4422 Hemoglobin, beta (Hbb), mRNA.	vesicle associated protein
3734	25469	NM_033234	M, T, HH, XX, YY	12/2001 Length = 620 interferon gamma inducing factor	
3757	9214	NM_053374	EEE, MMM	binding protein (Igifbp), mRNA. 11/2002 Length = 626	interferon gamma inducing factor binding protein
3757	9215	NM_053374	EEE, MMM	interferon gamma inducing factor binding protein (Igifbp), mRNA. 11/2002 Length = 626	interferon gamma inducing factor binding protein
3758	11092	NM_053381	RR	mRNA. 11/2002 Length = 4174	ESTs, Weakly similar to I54060 Na+,K+ -ATPae beta2 subunit - rat (fragment) [R.norvegicus]
3764	14621	NM_053437	L, BBB, CCC	diacylglycerol O- acyltransferase 1 (Dgat1), mRNA. 11/2002 Length = 1751	diacylglycerol acyltransferase
3786	20708	NM_053543	Q, R, W, PPP	neurochondrin (Ncdn- pending), mRNA. 11/2001 Length = 3730	neurochondrin

TABL	<b>E</b> 1	. 4	2000年		tomey Docket 44921-5033-01WC Document No. 1935328.1
900	GLGC.	Consoni Assor	Mocel :	100	
<b>Seq</b>	ID No.	Rosson ID.		Known Cone Name	Unigene Sequence Cluster Tille
				beta-carotene 15, 15-	
				dioxygenase (Bcdo),	
			E, LL,	mRNA. 11/2002	beta-carotene 15, 15'-
3810	18644	NM_053648	NNN	Length = 2207	dioxygenase
				Rho interacting protein 3 (Rhoip3),	ľ
	[		DD, EE,	mRNA. 11/2001	
3832	15103	NM_053814	NNN	Length = 3286	Rho interacting protein 3
				N-Acetyltransferase-	
				2 (Nat2), mRNA.	
				10/2002 Length =	
3841	25073	NM_053854	T	1385	
Ì				glutathione reductase	
			G, K, L,	(Gsr), mRNA. 11/2001 Length =	
3849	17090	NM 053906	X X	1428	glutathione reductase
	-		G, K, L,	glutathione reductase	
			х, тт,	(Gsr), mRNA.	
			DDD,	11/2001 Length =	
3849	17091	NM_053906	บบบ	1428	glutathione reductase
				glutathione reductase	
	ĺ			(Gsr), mRNA. 11/2001 Length =	
3849	17092	NM 053906	DDD	1428	glutathione reductase
				endoplasmic	giacaone veagotaeo
				retuclum protein 29	
				(Erp29), mRNA.	
	40770			11/2001 Length =	
3855	19772	NM_053961	HH	4529	
				endoplasmic retuclum protein 29	
			_	(Erp29), mRNA.	
				11/2001 Length =	
3855	26264	NM_053961	RR	4529	ESTs
				neuraminidase 3	
				(Neu3), mRNA.	
3873	26267	NM 054010	SS	11/2001 Length = 2307	
3073	20201	14101_034010	JJ	2301	
[				nuclear receptor	
				subfamily 0, group B,	
			-	member 2 (Nr0b2),	İ
				mRNA. 11/2001	nuclear receptor subfamily 0,
3884	968	NM_057133	ннн	Length = 1111	group B, member 2
				nuclear receptor	
				subfamily 0, group B,	
İ				member 2 (Nr0b2),	1
			JJ, KK,	mRNA. 11/2001	nuclear receptor subfamily 0,
3884	969	NM_057133	ннн	Length = 1111	group B, member 2

TABL	E 1	1		A	tomey Docket 44921-5033-011WO Document No. 1985323.1
	ELEC BLOS.	CONSTANT ASS OF CONSTANT	Model :	Known Cene Name	Unigene Sequence Cluster Title
3892	17391	NM_057207	YY	synaptic vesicle glycoprotein 2 b (Sv2b), mRNA. 4/2002 Length = 6004 ATP-binding cassette, sub-family	synaptic vesicle glycoprotein 2 b
3900	18779	NM_080581	Т	C (CFTR/MRP), member 3 (Abcc3), mRNA. 11/2002 Length = 5174 diacylglycerol kinase,	ESTs
3908	7595	NM_080787	ZZ, AAA	alpha (80 kDa) (Dgka), mRNA. 11/2002 Length = 3043	diacylglycerol kinase, alpha (80kD)
3918	18764		NNN	complement component factor h (Cfh), mRNA. 1/2002 Length = 4256 mitofusin 2 (Mfn2), mRNA. 11/2002	13G1 - mouse [M.musculus]
3930	23348	NM_130894 NM_130894	DD, EE, DD, EE, NNN	Length = 4160 mitofusin 2 (Mfn2), mRNA. 11/2002 Length = 4160	mitofusin 2 mitofusin 2
3936	4956	NM_133315	JJ, KK, XX, YY	solute carrier family 39 (iron-regulated transporter), member 1 (Slc39a1), mRNA. 11/2002 Length = 2129	solute carrier family 39 (iron- regulated transporter), member 1
3936	4957	NM_133315	JJ, KK, HHH	solute carrier family 39 (iron-regulated transporter), member 1 (Slc39a1), mRNA. 11/2002 Length = 2129	solute carrier family 39 (iron- regulated transporter), member 1
3938	22501	NM_133394	A, B	putative zinc finger protein SERZ-1 (Serz-1), mRNA. 3/2002 Length = 2677	putative zinc finger protein SERZ- 1
3939	21576		PPP,	LYRIC (Lyric), mRNA. 3/2002 Length = 2234	LYRIC

TABL	<b>E</b> 1.			A	tomay Docket 44221-5028-01WQ Document No. 1935323.1
Seq. ID	(ID KJS. :	Consent Acc or Rowood ID	Model Code	Known Cone Name	Unigene Sequence Cluster Title
3939	21577	NM 133398	нн	LYRIC (Lyric), mRNA. 3/2002 Length = 2234	LYRIC
		_		myeloid differentiation primary response gene 116 (Myd116),	
3947	11483	NM_133546	Q, W	mRNA. 3/2002 Length = 2225 myeloid	myeloid differentiation primary response gene 116
3947	18043	NM_133546	Q	differentiation primary response gene 116 (Myd116), mRNA. 3/2002 Length = 2225	myeloid differentiation primary response gene 116
3949	17886	NM 133561	U, RRR, SSS, General Alternate	brain protein 44-like (Brp44I), mRNA. 11/2002 Length = 901	brain protein 44-like
3949	17887	NM 133561	GGG, HHH, RRR, UUU, General Core Tox Markers, General Alternate	brain protein 44-like (Brp44l), mRNA. 11/2002 Length = 901	brain protein 44-like
3959	19384	NM_134326	QQ, YY	Albumin (Alb), mRNA. 3/2002 Length = 1956	EST
3963	17337	NM_134351	Q, WW	methionine adenosyltransferase II, alpha (Mat2a), mRNA. 3/2002 Length = 1337	ESTs
3967	2367	NM_134410	CC, DD, EE, NNN	Mg87 protein (Mg87), mRNA. 3/2002 Length = 1330	Mg87 protein
3967	2368	NM_134410	U, CC, DD, NNN	Mg87 protein (Mg87), mRNA. 3/2002 Length = 1330	Mg87 protein
3971	6397	NM_134458	D	nuclear receptor coactivator GT198 (Gt198), mRNA. 3/2002 Length = 721	nuclear receptor coactivator GT198

TABL	<b>13</b> 1				itomey Docket 44921-5038-01W0 Document No. 1935323.1
<b>Seq</b>	ei.ec	Consens,		and the contract of	
10 ¢:		Accor Reason ID		Smown Gene Name	Unicere Sequence Cluster Thic
	,			3-alpha-	
				hydroxysteroid	
İ				dehydrogenase	•
		]		(LOC191574),	
			LL, RRR,	mRNA. 4/2002	3-alpha-hydroxysteroid
3978	48	NM_138547	บบบ	Length = 2466	dehydrogenase
				3-alpha-	
				hydroxysteroid	1
1				dehydrogenase	
	1		1	(LOC191574),	
				mRNA. 4/2002	3-alpha-hydroxysteroid
3978	25475	NM_138547	ww	Length = 2466	dehydrogenase
		1		apolipoprotein E	
				(Apoe), mRNA.	
2002	10404	100000	S, DD,	11/2002 Length =	
3983	16401	NM_138828	EE, SS	936	
1		į		membrane and	
1				microfilament-	
}				associated protein p58 (LOC207121),	
	İ		•	mRNA. 5/2002	
3997	17573	NM 139039	PP, QQ	Length = 2003	ESTs
-	17070	11111_100000	11, 00	spermatogenesis-	1313
l	1		ļ	related protein (Srp)	
l			MM, TTT,	(LOC246042),	
			General	mRNA. 5/2002	spermatogenesis-related protein
4009	10018	NM_139186	Alternate	Length = 1016	(Srp)
				spermatogenesis-	
ŀ	1			related protein (Srp)	
	ļ	•		(LOC246042),	
			General	mRNA. 5/2002	spermatogenesis-related protein
4009	10019	NM_139186	Alternate	Length = 1016	(Srp)
	]		) 	phosphatidic acid	
	1			phosphatase type 2c	
	1		A B	(Ppap2c), mRNA.	
4011	16592	NM 139252	A, B, HHH	5/2002 Length = 1603	phosphatidic acid phosphatase
7011	10032	14W_139232	ппп	LRP16 protein	type 2c
				(Lrp16), mRNA.	
				11/2002 Length =	Rattus norvegicus LRP16-like
4016	12450	NM_139337	F	1030	protein mRNA, complete cds
				peroxisomal Ca-	F. C.C. T. T. T. T. T. GOTTIPIOLO GOS
		·		dependent solute	
				carrier-like protein	
				(Pcscl), mRNA.	
			C, MM,	11/2002 Length =	ľ
4024	6988	NM_145677	П	3150	ESTs

TABL	E 1	, se	nik pilik	, A	iomey Docket 44921-5659-9100 Document No. 1935323.1
Seq (D	@L@C [D K)o.	CONSING AGE OF ROSER	Model Code	Known Cene Name	Unigene Sequence Cluster Title
				G protein-coupled receptor 37-like 1 (Gpr37l1), mRNA.	
4030	20046	NM_145784	O, P	11/2002 Length = 2451	ESTs
4030	20050	NM_145784	НН	G protein-coupled receptor 37-like 1 (Gpr37I1), mRNA. 11/2002 Length = 2451	ESTs, Highly similar to T17310 hypothetical protein DKFZp434B168.1 - human (fragment) [H.sapiens]
4030	20608	NNA 145794	E, V, W, BB, CC, PP, QQ, SS, UU, EEE, III, JJJ, KKK, LLL, MMM, NNN, SSS,	G protein-coupled receptor 37-like 1 (Gpr37I1), mRNA. 11/2002 Length =	· •
4030	20698	NM_145784	UUU U, FF, LL, CCC, RRR, SSS,	2451 G protein-coupled receptor 37-like 1 (Gpr37I1), mRNA. 11/2002 Length =	
4030	21355	NM_145784	บบบ	2451 G protein-coupled	ESTs
4030	21904	NM 145784		receptor 37-like 1 (Gpr37I1), mRNA. 11/2002 Length = 2451	
4030	26320	NM_145784		G protein-coupled receptor 37-like 1 (Gpr37I1), mRNA. 11/2002 Length = 2451	
4031	11440	NM 145790	ccc	Lipogenin (Lipogenin), mRNA. 11/2002 Length = 1265	ESTs
4031	14664	NM 145790	Q, R	Lipogenin (Lipogenin), mRNA. 11/2002 Length = 1265	·
	25644	NM_147136		rRNA promoter binding protein (LOC257642), mRNA. 11/2002 Length = 1038	ESTs

TABL	<b>E</b> 1		•	: A0	torney Docket 44921-5093-91WO Document No. 1985323.1
(ID	(C) n	Modd : Code ::··	Known Cene Name	Unigene Sequence Cluster Title	
4034	683	NM_147206	м	cytochrome P450 3A9 (CYP3A9), mRNA. 11/2002 Length = 2101	Rattus norvegicus cytochrome P450 3A9 mRNA, complete cds
4038	23070	NM_148891	GGG	N- myristoyltransferase 1 (Nmt1), mRNA. 11/2002 Length = 1491	ESTs, Highly similar to NMT1_MOUSE Glycylpeptide N-tetradecanoyltransferase 1 (Peptide N-myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase 1) (NMT 1) (Type I N-myristoyltransferase) [M.musculus]
				G protein-coupled receptor 56 (Gpr56), mRNA. 11/2002	
4040	6274	NM_152242	SS QQ, TT,	Length = 2949 testosterone 6-beta- hydroxylase (CYP3A2), mRNA. 10/2002 Length =	ESTs Rattus norvegicus Sprague Dawley testosterone 6-beta- hydroxylase, cytochrome P450/6- beta-A, (CYP3A2) mRNA,
4045	17995	NM_153312	DDD, FFF		complete cds
4047	11755	NM 153314	т	glucuronosyltransfera se 2B3 precursor, microsomal (UDPGT), mRNA. 10/2002 Length =	
			G, EEE,	Na/Pi cotransporter 4 (Rnpt4), mRNA. 10/2002 Length =	*
4049	5920 25565	NM_153622 NM 153821	MMM D	2316 paired mesoderm homeobox 1 (Pmx1), mRNA. 10/2002 Length = 1375	ESTs
	25064	S45392	H, K, S, FF, PP, QQ, KKK	•	
4060 4061	25481 25495	S46798 S59892	F, HH, NNN ZZ, AAA		
4062	25496	S59893	R, ZZ, AAA, PPP, QQQ		
4064	25500	S63458	FF, RRR, SSS, UUU		

TAB	UE 1				temey Docket 44921-5038-01000 Document No. 1935323.1
<b>Seq</b>	(10 Kg. )	COMBANK Ace or Refer ID.	Modal . Codo : ; .		Unigene Sequence Civeter Title
			A, B,		
4065	3244	S63519	General Alternate		ESTs
4066		S63521	FF, LL		E31\$
4067	25507	S67316	Z, AA		
					ESTs, Moderately similar to N4BM_HUMAN NADH-ubiquinone oxidoreductase subunit B14.5b (Complex I-
4068	15832	S68589	MM, TTT		B14.5b) (CI-B14.5b) [H.sapiens]
4070	25513	S69315	D		
4072	25518	S70011	JJ, KK, HHH		
4073	7554	S70803	М		ESTs .
4073	25520	S70803	E		
4075	25066	S75280	ww		
4078	25550	S79213	J, CC, II,	protein phosphatase 1, regulatory (inhibitor) subunit 2	
4081	25559	S81025	М	(*************************************	
4083	25071	S83436	JJ, KK		
4090	357	U04835	C, K, MM, GGG, TTT C, F, G, S, XX,	CAMP responsive element modulator	CAMP responsive element modulator
4092	15462	U06230		protein S	protein S
4098	17281	U10697	M, BB, NN	carboxylesterase 1	carboxylesterase 1
4103	9520	U17837	UU		ESTs
4108	90	U20796	T		Rattus norvegicus nuclear receptor Rev-ErbA-beta mRNA, partial cds
4400	25500	1104740	H, PPP,		
4110	25589 22196	U21718 U21719	QQQ B, HHH, PPP, QQQ, General Alternate		ESTs
4111		U21720	RR		
4112	25591	U21721	VV		
4116	17480	U31598	NN, OO, VV		R.norvegicus mRNA for RT1.Ma
4121	,		M, DD, EE, WW		Rattus norvegicus retinol dehydrogenase type II mRNA, complete cds

TABL	E1			. As	torney Docket 44921-5033-011WO Document No. 1935323.1
	 @L@C	CONSTRUCT ACCOR	Model Carle		Unigene Sequence Cluster Title
٠.٠	. us. uos	liveneese irai			Rattus norvegicus retinol
4121	18302	U33500	N, DD, EE, WW		dehydrogenase type II mRNA, complete cds
4122	25078	U33540	QQQ, General Alternate		
4124	797	U38253	General Alternate	eukaryotic translation initiation factor 2B, subunit 3 (gamma, 58kD)	eukaryotic translation initiation factor 2B, subunit 3 (gamma, 58kD)
4133	772	U48288	PP, QQ, SS	A-kinase anchoring protein	A-kinase anchoring protein
4135	738	U49058	PP, QQ	CTD-binding SR-like protein rA4	
4142	25607	U53873	RR, SS, WW		
4152	25618	U64705	R		
4161	25629	U70270	PP, QQ		
4164	957	U72741	L, MM, WW, TTT	Lectin, galactose binding, soluble 9 (Galectin-9)	Lectin, galactose binding, soluble 9 (Galectin-9)
4164	958	U72741	F, MM, WW, TTT	Lectin, galactose binding, soluble 9 (Galectin-9)	Lectin, galactose binding, soluble 9 (Galectin-9)
4167	25632	U75405	11	(Galectin-5)	3 (Galectin-3)
4172	25643			growth arrest specific	
4175	25647	U77829 U83119	H, Q, R RR	5	
4180	22005	U96490	A, B	liver protein	liver protein
4180	22006	U96490	RR	liver protein	liver protein liver protein
4182	819	X02284	Y, SS	iiver protein	iiver proteiii
			E, DD,		
4185	20168	X03347	EE		
4189 4189	25662 25663	X05472 X05472	RR		
			X, Y A, B, V,		
4191	25084		LL		
4193	25671	X07686	RR		
4197	25675	X14181	G, H, EEE, MMM		
4201	25678	X14848	V .		
4202	25679	X15013	D, H, DDD		
4209 4214	25087 25689	X51615	WW, LLL, UUU A, B, T		
1217	20009	7.02010	7, U, I		•

Terrando de					
TABL	<b>E</b> 1			lpha	iomey Docket 44921-5063-01WC Document No. 1995323.1
V see		Conson's		1.2	The Bridge
Seq ;	@L@C	Acc or	Model	2 0 0 0 tab	- 3 6 -
	(ID) Klo.: -	RefSeq ID	Codo :	Known Cone Name	Unigano Sequenco Chuster Title
			BB, CC,		
			DDD, III,		
			JJJ,		
1			General		
4216	25691	X53504	Alternate		
4222	20308	X56327	RR, SS		
					ESTs, Highly similar to
	ŀ				RS18_HUMAN 40S ribosomal
					protein S18 (KE-3) (KE3)
4224	15106	X57529	GG		[R.norvegicus]
			s, cc,		
]			000,	Protein kinase, cAMP	
			General	dependent, catalytic,	
4225	25701	X57986	Alternate	alpha	,
			F, I, K, II,		
	1		TT, WW,		
4230	25705	X59375	FFF		
4232	25707	X59677	Z, AA	·-···	
4234	25717	X61296	RR		
4240	25723	X62327	X, Y		
			X, GG,		
			TT, XX,		
4242	25725	X62660	DDD		
4247	25091	X65190	D		
			DDD,		
			PPP,		
4262	16272	X76456	QQQ		
4267	25742	X80130	UU		·
1			A, E, II,		
				keratin complex 1,	
	25747	X81448	VV, GGG	acidic, gene 18	
	25754		Z, AA		
	25756		RR, SS		
			SS		
4279	25768		N, UU		
4000	05377	1	V, FF,	oxidative stress	
	25777		00	induced	oxidative stress induced
	25797		E		
	2387		N AAA		ESTs
4295	26099	AA963133	ZZ, AAA	—	

TABL	E2 ·			Aliomay Doctor 4/1921-5033-0/1WO
	.	(Centank	1	<u> </u>
Seq [[	D GLGG	Acc or	Model	
Ko.	ID Koz	Rewestern :	Codo :	Pathways
1		4		Activation of Csk by cAMP-dependent Protein Kinase
1				Inhibits Signaling through the T Cell Receptor,
				Activation of cAMP-dependent protein kinase, PKA,
ĺ	1			Attenuation of GPCR Signaling, CCR3 signaling in
1				Eosinophils, ChREBP regulation by carbohydrates
ľ	}		}	and cAMP, Erk1/Erk2 Mapk Signaling pathway,
}			İ	Phospholipase C-epsilon pathway, Signaling Pathway from G-Protein Families, Transcription
3353	15977	NM_019132	s	Pathway from G-Protein Families, Transcription factor CREB and its extracellular signals
	1			Activation of PKC through G protein coupled receptor,
1			1	Angiotensin II mediated activation of JNK Pathway via
		1		Pyk2 dependent signaling, Apoptotic Signaling in
			İ	Response to DNA Damage, Attenuation of GPCR
		1.		Signaling, BCR and Bioactive Peptide Induced
	1			Signaling Pathways, CCR3 signaling in Eosinophils,
l				EGF, Growth Hormone, and CXCR4 Signaling
	1	ļ		Pathways, Effects of calcinurin in Keratinocyte
				Differentiation, Fc Epsilon Receptor I Signaling in
1				Mast Cells, Ion Channel and Phorbal Esters Signaling Pathway, Links between Pyk2 and Map Kinases,
1	l			PDGF and Phospholipase C Signaling Pathways,
				PKC-catalyzed phosphorylation of inhibitory
1			1	phosphoprotein of myosin phosphatase, Pertussis
i			1	toxin-insensitive CCR5 Signaling in Macrophage,
				Phospholipase C d1 in phospholipid associated cell
		1		signaling, Regulation of elF4e and p70 S6 Kinase,
		]		Signaling Pathway from G-Protein Families, TPO
1			,	Signaling Pathway, Thrombin signaling and protease-
	ĺ			activated receptors, Transcription factor CREB and its
3124	24545	NM 012713	D	extracellular signals, T Cell and Trka Receptor Signaling Pathways, egf, g-Secretase mediated
		1		Adhesion Molecules on Lymphocyte, B Lymphocyte
				Cell Surface Molecules, CTL mediated immune
				response against target cells , Cells and Molecules
				involved in local acute inflammatory response,
l		}		Monocyte and its Surface Molecules, Neutrophil and
2405	2554	NA 040007		Its Surface Molecules, T Cytotoxic Cell Surface
3185	2554	NM_012967	VV	Molecules, T Helper Cell Surface Molecules
		]		Adhesion Molecules on Lymphocyte, B Lymphocyte
1		1		Cell Surface Molecules, CTL mediated immune response against target cells , Cells and Molecules
<b> </b>	1	]		involved in local acute inflammatory response,
1	1	]		Monocyte and its Surface Molecules, Neutrophil and
			W, BB, CC,	Its Surface Molecules, T Cytotoxic Cell Surface
3185	2555	NM_012967	NN, OO, PP	Molecules, T Helper Cell Surface Molecules

TABLE	2 :		200	Altomay Docket 44921-5033-01140  Document No. 1935323.1
S09 (D No. : :	elec D Ka.	ind: 1997 Acc or Reference:	Model ; Code ;	Palliways
				Adhesion Molecules on Lymphocyte, Cells and Molecules involved in local acute inflammatory response, Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Monocyte and its Surface Molecules, PTEN dependent cell cycle arrest and apoptosis, Ras-
2266	14989	Al177366	ннн	Independent pathway in NK cell-mediated cytotoxicity
4244	25089	X63594	I, J	AKT Signaling Pathway, ATM Signaling Pathway, Acetylation and Deacetylation of RelA in The Nucleus, Activation of PKC through G protein coupled receptor, CD40L Signaling Pathway, Double Stranded RNA Induced Gene Expression, Erythropoietin mediated neuroprotection through NF-kB, HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5 Death Receptors, Influence of Ras and Rho proteins on G1 to S Transition, NF-kB Signaling Pathway, Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells, Signal transduction through IL1R, T Cell Receptor Signaling Pathway, TNF/Stress Related Signaling, TNFR2 Signaling Pathway, The 41BB-dependent immune response, Toll-Like Receptor Pathway, interact6-1
		X63594		AKT Signaling Pathway, ATM Signaling Pathway, Acetylation and Deacetylation of RelA in The Nucleus, Activation of PKC through G protein coupled receptor, CD40L Signaling Pathway, Double Stranded RNA Induced Gene Expression, Erythropoietin mediated neuroprotection through NF-kB, HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5 Death Receptors, Influence of Ras and Rho proteins on G1 to S Transition, NF-kB Signaling Pathway, Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells, Signal transduction through IL1R, T Cell Receptor Signaling Pathway, TNF/Stress Related Signaling, TNFR2 Signaling Pathway, The 41BB-dependent immune response, Toll-Like Receptor Pathway, interact6-1

TABLE	2			Altomey Docket 44921-5033-01140 Document No. 1995323.1
	©L©C :	Constant Acc or RefSeq ID	Model Code	Pathways
3205	16683	NM_013052	w, ss, ннн	AKT Signaling Pathway, Cell Cycle: G2/M Checkpoint, Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphphorylation, RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage, Regulation of BAD phosphorylation, Role of nicotinic acetylcholine receptors in the regulation of apoptosis, Signal Dependent Regulation of Myogenesis by Corepressor MITR, cdc25 and chk1 Regulatory Pathway in response to DNA damage
			W, JJ,	AKT Signaling Pathway, Cell Cycle: G2/M Checkpoint, Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphphorylation, RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage, Regulation of BAD phosphorylation, Role of nicotinic acetylcholine receptors in the regulation of apoptosis, Signal Dependent Regulation of Myogenesis by Corepressor MITR, cdc25 and chk1
1424	3203	NM_013052 Al012595	GGG, HHH Q, R, General Alternate	Regulatory Pathway in response to DNA damage AKT Signaling Pathway, ChREBP regulation by carbohydrates and cAMP, Erk1/Erk2 Mapk Signaling pathway, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Regulation of ck1/cdk5 by type 1 glutamate receptors, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, WNT Signaling Pathway, mTOR Signaling Pathway
3257	3202	NM_017039	B, Q, R, WW, General Alternate General	AKT Signaling Pathway, ChREBP regulation by carbohydrates and cAMP, Erk1/Erk2 Mapk Signaling pathway, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Regulation of ck1/cdk5 by type 1 glutamate receptors, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, WNT Signaling Pathway, mTOR Signaling Pathway
1362	17524	AI010568	Core Tox	AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of eIF4e and p70 S6 Kinase

TABLE	2			Alitomey Docket 44921-5033-011440 Document No. 1935323.1
Gora ila	@1 @6	CONSTANT.	Worden .	
No: : : : : : : : : : : : : : : : : : :	ELEC.	Acc or RefScq ID	(COGO	Palliways
			B, H, S,	
1			LLL, PPP,	
1			QQQ, General	
			Core Tox	
l			Markers,	
			General	AKT Signaling Pathway, Growth Hormone Signaling
3274	10886	NM_017094	Alternate	Pathway, Regulation of eIF4e and p70 S6 Kinase
			A, B, T, FF,	
			NN, 00,	
			General	AKT Signaling Pathway, Growth Hormone Signaling
3274	10887	NM_017094		Pathway, Regulation of elF4e and p70 S6 Kinase
			D, U, FF, BBB, RRR,	·
777	21010	AA925306	SSS RKK,	Alanine and aspartate metabolism
-	21010	74.02000	C, I, J, X,	Alanine and aspartate metabolism, Alkaloid
			EE, MM,	biosynthesis I, Arginine and proline metabolism,
			UU, WW,	Carbon fixation, Cysteine metabolism, Glutamate
			KKK, TTT,	metabolism, Malate-aspartate shuttle, Phenylalanine
			General	metabolism, Phenylalanine, tyrosine and tryptophan
3083	20744	NM_012571	Alternate	biosynthesis, Tyrosine metabolism
				Alanine and aspartate metabolism, Alkaloid
		•		biosynthesis I, Arginine and proline metabolism,
				Carbon fixation, Cysteine metabolism, Glutamate
			General	metabolism, Phenylalanine metabolism,
3230	17628	NM_013177		Phenylalanine, tyrosine and tryptophan biosynthesis, Tyrosine metabolism
			, atomato	Alanine and aspartate metabolism, Aminoacyl-tRNA
3429	23424	NM_021680	E	biosynthesis
			E, GG, III,	Alanine and aspartate metabolism, Aminoacyl-tRNA
4093	1583	U07201	111	biosynthesis, Nitrogen metabolism
			A, B, I, L, Y,	
			MM, HHH,	
] [			KKK, 000,	Alonino and annudate sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate the sentate t
			TTT,	Alanine and aspartate metabolism, Arginine and
3626	4234	NM 031330		
			, atomato	
4194	20597	X12459	C, YY, BBB	amino groups
			A, B, I, J, L,	
	l			Alamina and annual description
	Į			, , ,
3424	18727	NM 021577		
				amino groups
			General	Alanine and aspartate metabolism. Carbon fixation
3587	21094	NM_031039		Glutamate metabolism
4194	20597 18727	NM_021577	A, B, I, J, L, MM, WW, BBB, KKK, OOO, TTT, General Alternate HH, XX, General	Alanine and aspartate metabolism, Arginine and proline metabolism, Urea cycle and metabolism of amino groups  Alanine and aspartate metabolism, Carbon fixation,

TABL		V	¥ 1	Altomay Docket 4K921-5953-01W0 Document No. 1935323.1
	ELEC,	Centanii Ace or Reseal	Model ; Codo	Pathways
				Alanine and aspartate metabolism, Carbon fixation,
3587	21096	NM_031039		Glutamate metabolism
			M, VV,	
1	· i		DDD, GGG,	Ì
			LLL, UUU, General	
1			Core Tox	Alanine and aspartate metabolism, Citrate cycle (TCA
4118	1478	U32314	Markers	cycle), Pyruvate metabolism
11.0	1.470	002014	M, X, VV,	cycle), 1 yravate metabolism
			DDD, GGG,	
			LLL, UUU,	
1			General	
			Core Tox	Alanine and aspartate metabolism, Citrate cycle (TCA
4118	1479	U32314	Markers	cycle), Pyruvate metabolism
			MM, VV,	Alanine and aspartate metabolism, Glycine, serine
1944	24803	AI137065	TTT	and threonine metabolism
			MM, PP,	
2040	0.4707	D42007	QQ, RR,	Alanine and aspartate metabolism, Glycine, serine
2848	24797	D13667	TTT	and threonine metabolism
2882	24799	E01050	X, Y, MM, SS, TTT	Alanine and aspartate metabolism, Glycine, serine and threonine metabolism
2002	24133	L01030	F, N, MM,	and theornie metabolism
ļ			SS, BBB,	Alanine and aspartate metabolism, Glycine, serine
3563	24798	NM 030656	CCC, TTT	and threonine metabolism
			MM, RR,	Alanine and aspartate metabolism, Glycine, serine
3563	24800	NM_030656	SS, TTT	and threonine metabolism
			MM, VV,	Alanine and aspartate metabolism, Glycine, serine
3563	24801	NM_030656	TTT	and threonine metabolism
1			I, J, CC, II,	Alkaloid biosynthesis I, Histidine metabolism,
1,550	4404	A1044C40	General	Phenylalanine metabolism, Tryptophan metabolism,
1558	1431	Al044610	Alternate	Tyrosine metabolism
ł			TT, DDD, General	
			Core Tox	
	1			Alkaloid biosynthesis I, Histidine metabolism,
			General	Phenylalanine metabolism, Tryptophan metabolism,
3046	1430	M84648	Alternate	Tyrosine metabolism
				Alkaloid biosynthesis I, Phenylalanine metabolism,
			C, D, I, J,	Phenylalanine, tyrosine and tryptophan biosynthesis,
3109	24825	NM_012668	NNN	Tyrosine metabolism
				Alkaloid biosynthesis II, Arginine and proline
				metabolism, Glycine, serine and threonine
				metabolism, Histidine metabolism, Phenylalanine
3521	16184	NM 022935	Z, AA	metabolism, Tryptophan metabolism, Tyrosine metabolism, beta-Alanine metabolism
	1,0104	1411_02230	<u>-, ~~</u>	Alkaloid biosynthesis II, Arginine and proline
				metabolism, Glycine, serine and threonine
]				metabolism, Histidine metabolism, Phenylalanine
				metabolism, Tryptophan metabolism, Tyrosine
4163	25083	U72632	RR	metabolism, beta-Alanine metabolism

TABLE	₹2 ·	1		- Aliomay Docket 44921-5063-011W0 Document No. 1935323.1
Seq (D No.	ID No. Grec	Keisen ID Reisen ID	Modal Goda	Pathways
3096	23522	NM_012615	A	Alkaloid biosynthesis II, Arginine and proline metabolism, Urea cycle and metabolism of amino groups  Alkaloid biosynthesis II, Arginine and proline
3096	23523	NM_012615	B, H, I, J	metabolism, Urea cycle and metabolism of amino groups
3246	1958	NM_016994	L, S, HH	Alternative Complement Pathway, Cells and Molecules involved in local acute inflammatory response, Classic Complement Pathway, Complement Pathway, Lectin Induced Complement Pathway
4212	1959	X52477	S, HH, MM, SS, TTT	Alternative Complement Pathway, Cells and Molecules involved in local acute inflammatory response, Classic Complement Pathway, Complement Pathway, Lectin Induced Complement Pathway
153	16756	AA818089	G, H	Aminoacyl-tRNA biosynthesis, Glycine, serine and threonine metabolism
2300	6502	AI178283	xx	Aminoacyl-tRNA biosynthesis, Phenylalanine, tyrosine and tryptophan biosynthesis
1684	2838	Al070511	G, Н	Aminoacyl-tRNA biosynthesis, Valine, leucine and isoleucine biosynthesis
3336	23130	NM_017307	V, FF	Aminophosphonate metabolism, Glycerolipid metabolism, Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3823 2842	7927 1515	NM_053765 D10233	I, U, X, Y, DDD, LLL	Aminosugars metabolism
2042	1313	10233	O, P	Aminosugars metabolism  Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Glycolysis
3130	1371	NM_012734	D, V, GG	Pathway, Starch and sucrose metabolism  Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Starch
3131	11839	NM_012735	Z, AA, NNN	and sucrose metabolism Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannose metabolism, Galactose
3445	17100	NM_022179	F	metabolism, Glycolysis / Gluconeogenesis, Starch and sucrose metabolism
3445	17101	NM_022179	JJ, KK, FFF, HHH	Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Starch and sucrose metabolism
3256	24861	NM_017033	T	Aminosugars metabolism, Erythromycin biosynthesis, Galactose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway, Starch and sucrose metabolism, Streptomycin biosynthesis

TABLE	2		\$1.7°	Altorney Docket 44921-6033-011WC Document No. 1985323.1
Seq ID Ko: : :	erec Ors:	1368360 ID Ace or Confident	Model Codo	Pathways
				Aminosugars metabolism, Erythromycin biosynthesis, Galactose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway, Starch and sucrose
3256	24862	NM_017033		metabolism, Streptomycin biosynthesis
3555	9929	NM_024392	U, EE, XX, YY, RRR, SSS	Androgen and estrogen metabolism
3555	9931	NM 024392	U, RRR, SSS	Androgen and estrogen metabolism
			U, FF, LL, CCC, RRR,	Androgen and estrogen metabolism
3555 3107	25070 21087	NM_024392 NM_012661	SSS FFF	Androgen and estrogen metabolism
			F, T, GG,	Androgen and estrogen metabolism, Bile acid
2930	20429	J05035	GGG, LLL F, T, GG,	biosynthesis
			GGG, General	Androgen and estrogen metabolism, Bile acid
2930	20430	J05035	Alternate	biosynthesis Androgen and estrogen metabolism, C21-Steroid
3086	17292	NM_012584	K, GGG	hormone metabolism
3272	23660	NM 017080	T, U, RRR, SSS	Androgen and estrogen metabolism, C21-Steroid hormone metabolism, Visceral Fat Deposits and the Metabolic Syndrome
3879	5492	NM 057105	G, K, GG, HH, WW, DDD	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
3879	5493	NM 057105	G, K, GG, HH, TT, WW, DDD	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
3879	15124	NM 057105	J, K, L, N, S, U, FF, GG, HH, TT, LLL,	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
3879	15125	NM_057105	K, L, M, N, U, FF, GG, PP, QQ, TT, LLL, SSS,	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
3879	15126	NM_057105	I, J, K, L, M, N, U, X, Y, GG, HH, LLL, SSS, UUU	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism

TABLE	2	7.		Attorney Doctor 44921-5098-0100 Document No. 1985328.1
Seq (D No		Conseni Acc or Refseq ID	ලිමෙම	Pathways
3879	15127	NM 057105	HH, TT, LLL, SSS,	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
3640	14633	NM 031533		Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
4047	14632	NM_153314		Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
4047	11755	NM_153314	тт	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
3165	4282	NM_012883	R, General Alternate	Androgen and estrogen metabolism, Sulfur metabolism
3119	18718	NM_012695	X, Y	Androgen and estrogen metabolism, Sulfur metabolism
3119	18717	NM_012695	N	Androgen and estrogen metabolism, Sulfur metabolism
3119	18719	NM_012695	M, N, UUU	Androgen and estrogen metabolism, Sulfur metabolism
				Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Anthrax Toxin Mechanism of Action, Bioactive Peptide Induced Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down
3316	17562	NM_017245	VV	regulates the MAP kinase pathway Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Anthrax Toxin Mechanism of Action, Bioactive Peptide Induced Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down
3932	17560	NM_133283		regulates the MAP kinase pathway Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Anthrax Toxin Mechanism of Action, Bioactive Peptide Induced Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway

TABLE	2	,		Aliomey Docket 4/1921-5033-01/WO Document No. 1935323.1
0	@L@C	Gewren?	00-0-0	
		Acc or RefSeq ID.:	Model Code	(Poll)mayo
1000 172	id Ko.	ाज्याद्यक्षती (ग्र _ि र.	Good (1	Pathways
				Angiotensin II mediated activation of JNK Pathway via
1				Pyk2 dependent signaling, Anthrax Toxin Mechanism
1				of Action, Bioactive Peptide Induced Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, Integrin
				Signaling Pathway, Links between Pyk2 and Map
1			Î	Kinases, MAPKinase Signaling Pathway,
			I, J, RRR,	Phosphorylation of MEK1 by cdk5/p35 down
3932	21848	NM_133283		regulates the MAP kinase pathway
0002	2.0.0	1		Angiotensin II mediated activation of JNK Pathway via
ľ				Pyk2 dependent signaling, Anthrax Toxin Mechanism
				of Action, Bioactive Peptide Induced Signaling
l				Pathway, Erk1/Erk2 Mapk Signaling pathway, Integrin
1				Signaling Pathway, Links between Pyk2 and Map
ļ				Kinases, MAPKinase Signaling Pathway,
				Phosphorylation of MEK1 by cdk5/p35 down
3932	21849	NM_133283	U, RRR	regulates the MAP kinase pathway
1				Angiotensin II mediated activation of JNK Pathway via
1				Pyk2 dependent signaling, BCR, EGF, EPO,
				Erk1/Erk2 Mapk, IGF-1, and CXCR4 Signaling
]				Pathways, Bioactive Peptide Induced Signaling
				Pathway, CCR3 signaling in Eosinophils, Erk and PI-
				3 Kinase Are Necessary for Collagen Binding in
1				Corneal Epithelia, Fc Epsilon Receptor I Signaling in
				Mast Cells, Growth Hormone Signaling Pathway, IL-2,
				IL-3, and IL-6 signaling pathways, IL-2 Receptor B Protein Interaction Pathway, Influence of Ras and
				Rho proteins on G1 to S Transition, Inhibition of
				Cellular Proliferation by Gleevec, Insulin Signaling
				Pathway, Integrin Signaling Pathway, Links between
				Pyk2 and Map Kinases, MAPKinase Signaling
<b>!</b>				Pathway, Multiple antiapoptotic pathways from IGF-
				1R signaling lead to BAD phosphphorylation, Nerve
				growth factor pathway (NGF), PDGF Signaling
]				Pathway, Phosphorylation of MEK1 by cdk5/p35
]				down regulates the MAP kinase pathway, Ras
				Signaling Pathway, Signaling Pathway from G-Protein
				Families, T Cell Receptor Signaling Pathway, TPO
3100	20798	NM_012639	V, X, Y	Signaling Pathway, egf, epo, igf-1, il2, il3, il6, insulin,

	(Cen : Enl Acc of . RedSeq ID.: .	Model Gode	Document No. 1935823.1 Pathways
	againe ed inst.		
			Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, BCR, CXCR4, EGF, insulin, Growth Hormone, TPO, and EPO Signaling Pathways, Bioactive Peptide Induced Signaling Pathway, CCR3 signaling in Eosinophils, Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia, Erk1/Erk2 Mapk Signaling pathway, Fc Epsilon Receptor I Signaling in Mast Cells, IGF-1 Signaling Pathway, IL-2, IL-3, and IL-6 signaling pathways, IL-2 Receptor B Protein Interaction Pathway, Influence of Ras and Rho proteins on G1 to S Transition, Inhibition of Cellular Proliferation by Gleevec, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphphorylation, Nerve growth factor pathway (NGF), PDGF Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway, Ras Signaling Pathway, Signaling Pathway
		·	from G-Protein Families, T Cell Receptor Signaling Pathway, egf, epo, igf-1, il2, il3, il6, insulin, interact6-Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, BCR Signaling Pathway, Influence of Ras and Rho proteins on G1 to S Transition, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Rac 1 cell motility signaling pathway, Ras Signaling Pathway, Ras-Independent pathway in NK cell-mediated cytotoxicity, Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration, T Cell Receptor Signaling Pathway, Transcription factor CREB and its extracellular signals, p38 MAPK
2069		C, I, O, P, MM, NNN, TTT, General Core Tox	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Bioactive Peptide Induced
		C, L, DD,	Signaling Pathway Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Bioactive Peptide Induced Signaling Pathway
7906	AA899762	NNN	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, EGF Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, egf Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, EGF Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, egf
	2069 21097 21098 7906	2069 Al103616 21097 M12112 21098 NM_134432 7906 AA899762	2069 AI103616 VV C, I, O, P, MM, NNN, TTT, General Core Tox Markers 21097 M12112 Markers 21098 NM_134432 C, L, DD, NNN 7906 AA899762 NNN

TABLE	2			Attorney Docket 44921-5033-011WO Document No. 1995823.1
869 (D	id ko Grec	CONSONIA ACCO RCISON ID	Good Good Good Good	Pathways
	16604	M37394		Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, EGF Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, egf
3022	10004	W37394	IN, EEE, 000	Apoptotic Signaling in Response to DNA Damage, Caspase Cascade in Apoptosis, D4-GDI Signaling Pathway, Electron -Transfer Reaction in Mitochondria, HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5
3154	11137	NM_012839	D, MM, FFF, TTT	Death Receptors , Role of Mitochondria in Apoptotic Signaling
			TILVV	Apoptotic Signaling in Response to DNA Damage, Caspase Cascade in Apoptosis, D4-GDI Signaling Pathway, Electron -Transfer Reaction in Mitochondria, HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5
3154	11138	NM_012839	T, JJ, KK, LL	Death Receptors , Role of Mitochondria in Apoptotic Signaling
				Apoptotic Signaling in Response to DNA Damage, HIV-I Nef: negative effector of Fas and TNF, IL-2 Receptor B Protein Interaction Pathway, Induction of apoptosis through DR3 and DR4/5 Death Receptors, Inhibition of Cellular Proliferation by Gleevec, Regulation of BAD phosphorylation, Role of Mitochondria in Apoptotic Signaling, p53 Signaling
3245	24897	NM_016993	QQ	Pathway
4149	912	U59184	QQ, UU, General Core Tox Markers	Apoptotic Signaling in Response to DNA Damage, Hypoxia and p53 in the Cardiovascular system, Regulation of BAD phosphorylation, Role of Mitochondria in Apoptotic Signaling, p53 Signaling Pathway
905	22283	AA945172	LL	Arginine and proline metabolism
3581	15683	NM_031011	MM, TTT	Arginine and proline metabolism Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate
1852	16884	AI103758	QQQ	metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
1000	4000-		Core Tox	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine
1890	16885	AI105188	Markers	and isoleucine degradation, beta-Alanine metabolism

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TABLE	9		******	Aftorney Docket 4/1921-5033-0/1000
Mede		<u>:</u>		Document No. 193582.1
		Consonii :		
	@r@c	Accor.	Model	
NO.;;;		ළමැනිලේ ලෙස	COCO : 3 00	Pathways .
				Arginine and proline metabolism, Ascorbate and
				aldarate metabolism, Bile acid biosynthesis,
				Butanoate metabolism, Fatty acid metabolism,
				Glycerolipid metabolism, Glycolysis /
	i			Gluconeogenesis, Histidine metabolism, Lysine
			EEE, LLL,	degradation, Propanoate metabolism, Pyruvate
1				metabolism, Tryptophan metabolism, Valine, leucine
3472	20915	NM_022407	SSS, UUU	and isoleucine degradation, beta-Alanine metabolism
				Arginine and proline metabolism, Ascorbate and
	į			aldarate metabolism, Bile acid biosynthesis,
1	İ			Butanoate metabolism, Fatty acid metabolism,
				Glycerolipid metabolism, Glycolysis /
		ļ		Gluconeogenesis, Histidine metabolism, Lysine
				degradation, Propanoate metabolism, Pyruvate
0070	00004	004704		metabolism, Tryptophan metabolism, Valine, leucine
3678	23884	NM_031731	U	and isoleucine degradation, beta-Alanine metabolism
				Arginine and proline metabolism, Ascorbate and
				aldarate metabolism, Bile acid biosynthesis,
1				Butanoate metabolism, Fatty acid metabolism,
		l		Glycerolipid metabolism, Glycolysis /
Ì		ı		Gluconeogenesis, Histidine metabolism, Lysine
	ļ			degradation, Propanoate metabolism, Pyruvate
1442	12300	AI013333	N	metabolism, Tryptophan metabolism, Valine, leucine
1442	12300	A1013333	14	and isoleucine degradation, beta-Alanine metabolism Arginine and proline metabolism, Ascorbate and
	l			aldarate metabolism, Bile acid biosynthesis,
	l			Butanoate metabolism, Fatty acid metabolism,
				Glycerolipid metabolism, Glycolysis /
i	1			Gluconeogenesis, Histidine metabolism, Lysine
	1	·	•	degradation, Propanoate metabolism, Pyruvate
	ļ			metabolism, Tryptophan metabolism, Valine, leucine
3728	12299	NM 032416	N YY	and isoleucine degradation, beta-Alanine metabolism
0720	12233	14111_002+10	13, 11	Arginine and proline metabolism, Ascorbate and
Ì	i			aldarate metabolism, Bile acid biosynthesis,
Ì		1		Butanoate metabolism, Fatty acid metabolism,
		]		Glycerolipid metabolism, Glycolysis /
	<b>1</b>			Gluconeogenesis, Histidine metabolism, Lysine
				degradation, Propanoate metabolism, Pyruvate
	1	1	M, TT, LLL,	metabolism, Tryptophan metabolism, Valine, leucine
3322	20913	NM_017272	SSS, UUU	and isoleucine degradation, beta-Alanine metabolism
\				Arginine and proline metabolism, Ascorbate and
1				aldarate metabolism, Bile acid biosynthesis,
				Butanoate metabolism, Fatty acid metabolism,
}				Glycerolipid metabolism, Glycolysis /
				Gluconeogenesis, Histidine metabolism, Lysine
1	1		A, B, L, TT,	degradation, Propanoate metabolism, Pyruvate
1	]		DDD, LLL,	metabolism, Tryptophan metabolism, Valine, leucine
3322	20914	NM_017272		and isoleucine degradation, beta-Alanine metabolism

TABLE	2 :	, , , , , , , , , , , , , , , , , , ,	, , , , , , , , , , , , , , , , , , ,	.:. Attornay Doctot 44.227-5033-471WO Document No. 1985828.1
Seq (D No. ;			Model	Paliways .
3082	4573	NM_012570	XX, YY	Arginine and proline metabolism, Catabolic Pathways for Arginine, Histidine, Glutamate, Glutamine, and Proline, D-Glutamine and D-glutamate metabolism, Glutamate metabolism, Nitrogen metabolism, Urea cycle and metabolism of amino groups
3082	4574	NM_012570	GG, OO, DDD	Arginine and proline metabolism, Catabolic Pathways for Arginine, Histidine, Glutamate, Glutamine, and Proline, D-Glutamine and D-glutamate metabolism, Glutamate metabolism, Nitrogen metabolism, Urea cycle and metabolism of amino groups
3283	24693	NM_017134	C, General Alternate	Arginine and proline metabolism, Catabolic Pathways for Arginine, Histidine, Glutamate, Glutamine, and Proline, Urea cycle and metabolism of amino groups Arginine and proline metabolism, D-Arginine and D-
3807	1127	NM_053626	III, JJJ	ornithine metabolism, Glycine, serine and threonine metabolism  Arginine and proline metabolism, Glutamate
3267	20649	NM_017072	L, WW	metabolism, Nitrogen metabolism, Urea cycle and metabolism of amino groups  Arginine and proline metabolism, Glycine, serine and
3233	21396	NM_013198	General Core Tox Markers	threonine metabolism, Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism
3142	16947	NM_012793	N, T, HHH, PPP, QQQ, General Alternate	Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism of amino groups
3142	16948	NM_012793	PPP, QQQ	Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism of amino groups
3191	19391			Arginine and proline metabolism, Hypoxia-Inducible Factor in the Cardiovascular System Arginine and proline metabolism, Hypoxia-Inducible
3191	19392 19393	NM_012998 NM_012998	FF	Factor in the Cardiovascular System Arginine and proline metabolism, Hypoxia-Inducible Factor in the Cardiovascular System
3214	13282	NM_013078	WW, FFF, General Alternate	Arginine and proline metabolism, Urea cycle and metabolism of amino groups
3214	13283	NM_013078	A, B, NN, OO A, B, F, H,	Arginine and proline metabolism, Urea cycle and metabolism of amino groups Arginine and proline metabolism, Urea cycle and
633 3050	4242 25467	AA893325 M93297	X, Y, LLL	metabolism of amino groups  Arginine and proline metabolism, Urea cycle and metabolism of amino groups
3070	4467	NM_012529		Arginine and proline metabolism, Urea cycle and metabolism of amino groups

TABLE	2		4.A	Attorney Docket 44921-5083-011WO Document No. 1985323.1
Seq ID	id ko** Grec ;	Consoni Accor Refsoq ID		Pathways
			A, B, Y, FFF, GGG, HHH, LLL, PPP, QQQ,	
			General Core Tox	
3450	20299	NM_022220	Markers	Ascorbate and aldarate metabolism ATM, BCR, D4-GDI, EGF, and EPO Signaling Pathways, Angiotensin II mediated activation of JNK
				Pathway via Pyk2 dependent signaling, FAS signaling pathway ( CD95 ), Fc Epsilon Receptor I Signaling in Mast Cells, Hypoxia-Inducible Factor in the Cardiovascular System, IGF-1 Signaling Pathway, IL
				2 signaling pathway, IL 6 signaling pathway, Inhibition of Cellular Proliferation by Gleevec, Insulin Signaling Pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling
				Pathway, Nerve growth factor pathway (NGF), PDGF Signaling Pathway, Pertussis toxin-insensitive CCR5 Signaling in Macrophage, Repression of Pain Sensation by the Transcriptional Regulator DREAM, Signal transduction through IL1R, Signaling Pathway from G-Protein Families, T Cell Receptor Signaling
3438	22352	NM 021835	1.11	Pathway, TNF/Stress Related Signaling, TNFR1 Signaling Pathway, TPO Signaling Pathway, TSP-1 Induced Apoptosis in Microvascular Endothelial Cell, The 41BB-dependent immune response, Toll-Like Receptor Pathway, egf, epo, igf-1, il2, il6, insulin, ngf, pdgf, tpo
0.00				ATM Signaling Pathway, Cell Cycle: G1/S Check Point , Cell Cycle: G2/M Checkpoint, Double Stranded RNA Induced Gene Expression, Hypoxia
				and p53 in the Cardiovascular system, Overview of telomerase protein component gene hTert Transcriptional Regulation, RB Tumor Suppressor/Checkpoint Signaling in response to DNA
3576	17377	NM_030989	CC, NN, OO	damage, p53 Signaling Pathway  ATM Signaling Pathway, Cell Cycle: G2/M
3535	351	NM_024127	С	Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway  ATM Signaling Pathway, Cell Cycle: G2/M
3535	353	NM_024127	C, HH, PP, QQ	Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway
3535	354		C, FF, II, PP, NNN	ATM Signaling Pathway, Cell Cycle: G2/M Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway
3846	20939		FFF	ATP Synthesis, Oxidative phosphorylation
3948	15524		V	ATP Synthesis, Oxidative phosphorylation
4002	17203	NM_139099		ATP Synthesis, Oxidative phosphorylation
1828	17400	AI103097	KKK	ATP Synthesis, Oxidative phosphorylation

TABLE	2			Attorney Docket 44921-5183-911770 Document No. 1935323.1
യി മാഹ	Grec	Accor	Madal	
No.:	(D) (Xo.	Rosson ID:	©000	Pathways †
2600	16170	NM 031785	TVUV	ATP Synthesis, Oxidative phosphorylation
3689	16178			
3409	18141	NM_019383	Y, JJ	ATP Synthesis, Oxidative phosphorylation
3409	22727	NM_019383	GG	ATP Synthesis, Oxidative phosphorylation
528	2106	AA892006	SS	ATP Synthesis, Oxidative phosphorylation
528	2107	AA892006	O, P, ZZ, AAA	ATP Synthesis, Oxidative phosphorylation
1498	2108	AI029960	ZZ, AAA	ATP Synthesis, Oxidative phosphorylation
			,,,,,,,,	ATP Synthesis, Oxidative phosphorylation, Purine
3802	20725	NM_053602	Q, R	metabolism
				ATP Synthesis, Oxidative phosphorylation, Purine
3802	20726	NM_053602	LL	metabolism
				Benzoate degradation, Bile acid biosynthesis,
				Butanoate metabolism, Fatty acid biosynthesis (path
ł				2), Fatty acid metabolism, Lysine degradation,
				Propanoate metabolism, Pyruvate metabolism,
				Synthesis and degradation of ketone bodies,
3270	18956	NM_017075	BBB	Tryptophan metabolism
				Benzoate degradation, Bile acid biosynthesis,
		į		Butanoate metabolism, Fatty acid biosynthesis (path
ĺ				2), Fatty acid metabolism, Lysine degradation,
	1		D, U, GG,	Propanoate metabolism, Pyruvate metabolism,
		1	XX, YY,	Synthesis and degradation of ketone bodies,
3270	18957	NM_017075	ввв, ссс	Tryptophan metabolism
				Benzoate degradation, Bile acid biosynthesis,
١.				Butanoate metabolism, Fatty acid biosynthesis (path
				2), Fatty acid metabolism, Lysine degradation,
		ļ	U, FF, XX,	Propanoate metabolism, Pyruvate metabolism,
			ввв, ссс,	Synthesis and degradation of ketone bodies,
3270	18958	NM 017075	RRR, SSS	Tryptophan metabolism
				Benzoate degradation, Butanoate metabolism, Fatty
				acid biosynthesis (path 2), Fatty acid metabolism,
	[			Lysine degradation, Propanoate metabolism,
l				Tryptophan metabolism, Valine, leucine and
3897	21562	NM 078623	s	isoleucine degradation, beta-Alanine metabolism
			A, B, P, U,	
	]	1	ввв, ссс,	Benzoate degradation, Butanoate metabolism, Fatty
			RRR, SSS,	acid biosynthesis (path 2), Fatty acid metabolism,
			General	Lysine degradation, Tryptophan metabolism, Valine,
3667	15175	NM_031682	Alternate	leucine and isoleucine degradation
<del></del>	<del> </del>			Benzoate degradation, Butanoate metabolism, Fatty
1		·		acid biosynthesis (path 2), Fatty acid metabolism,
ł	l			Lysine degradation, Tryptophan metabolism, Valine,
3889	6613	NM_057186	ווא	leucine and isoleucine degradation
	<del></del>			Benzoate degradation, Fatty acid metabolism, Lysine
1897	23596	Al105435	vv	degradation, Tryptophan metabolism
.001			· ·	and a section of the propriet includes the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section

TABLE	2 :		77.1	Aliomay Docket 44921-5999-011VO
		West vone		Document No. 1995323.1
G0 00	GLGC .	Censeni Accor	Model :	
ୟବ ୬ଲୌ ଲେ	100 tags			Pathways
W:	mainae a	MENERAL ITEM		Problems of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
			U, FF, HH,	
			LL, XX,	<u></u>
			BBB, CCC,	Bile acid biosynthesis, Fatty acid biosynthesis (path
			DDD, RRR,	2), Fatty acid metabolism, Valine, leucine and
3058	23698	NM_012489		isoleucine degradation
			U, FF, GG,	Bile acid biosynthesis, Fatty acid biosynthesis (path
2050	00000	1114 040400	HH, LL,	2), Fatty acid metabolism, Valine, leucine and
3058	23699	NM_012489	DDD	isoleucine degradation
	1		LL DDD	Bile acid biosynthesis, Fatty acid metabolism,
4077	420	V00740	U, RRR, SSS	Glycerolipid metabolism, Glycolysis /
4277	420	X90710		Gluconeogenesis, Tyrosine metabolism
3129	10260	NM_012732	T, GG, HH, LL	Bile acid biosynthesis, Glycerolipid metabolism
3129	25563	NM 012732	DD, EE	Bile acid biosynthesis, Glycerolipid metabolism
3129	20000	14141_012732	00, PP,	blie acid biosylltresis, Grycerolipid metabolism
1			QQ, PPP,	Bile acid biosynthesis, Taurine and hypotaurine
2866	1531	D43964	QQQ	metabolism
2000	1001	D40004	444	metabolism
				Bioactive Peptide Induced Signaling Pathway,
				Thrombin signaling and protease-activated receptors,
3519	24838	NM_022924	PPP. QQQ	Transcriptional activation of dbpb from mRNA
			,	Blood group glycolipid biosynthesis - neolact series,
3148	835	NM_012813	ss	Globoside metabolism, Sphingoglycolipid metabolism
		<del></del>		Butanoate metabolism, Fatty acid metabolism, Valine,
3474	2236	NM_022512	ввв, ссс	leucine and isoleucine degradation
				Butanoate metabolism, Glycolysis / Gluconeogenesis,
				Pyruvate metabolism, Shuttle for transfer of acetyl
				groups from mitochondria to the cytosol, Valine,
4287	20426	Z12158	SS, WW	leucine and isoleucine biosynthesis
				Butanoate metabolism, Glycolysis / Gluconeogenesis,
			MM, DDD,	Pyruvate metabolism, Valine, leucine and isoleucine
594	11997	AA892828	111	biosynthesis
			\	Butanoate metabolism, Glycolysis / Gluconeogenesis,
				Pyruvate metabolism, Valine, leucine and isoleucine
594	11998	AA892828	MM, TTT	biosynthesis
				Butanoate metabolism, Glycolysis / Gluconeogenesis,
				Pyruvate metabolism, Valine, leucine and isoleucine
1028	12000	AA957319	MM, TTT	biosynthesis
				Butanoate metabolism, Glycolysis / Gluconeogenesis,
0407	5070	01470447		Pyruvate metabolism, Valine, leucine and isoleucine
2187	5876	AI176117	UU	biosynthesis
			0 11 55	
			G, H, FF,	Dutancete metabolism CDCDD and controls !-!-
				Butanoate metabolism, SREBP and controls lipid
2224	20600	NINA 047000	General	synthesis, Synthesis and degradation of ketone
3321	20600	NM_017268	Alternate	bodies, Valine, leucine and isoleucine degradation

TABLE	2	3		Aliomey Docket 44921-5099-011WO Document No. 1995923.1
 Seg ID	ELEC	Reseat LD Reseat LD		Pathways
			G, H, J, JJ, KK, FFF, KKK, OOO,	Butanoate metabolism, SREBP and controls lipid
3321	20601	NM_017268	General Alternate	synthesis, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
3867	17739	NM_053995	General Alternate	Butanoate metabolism, Synthesis and degradation of ketone bodies
897	2813	AA945052	RRR	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
2079	2811	AI171090	FF, BBB, CCC, RRR, SSS	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
2079	2812	Al171090	BBB, CCC	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
727	22847	AA923982	BBB, CCC	C5-Branched dibasic acid metabolism, Citrate cycle (TCA cycle), Propanoate metabolism, Reductive carboxylate cycle (CO2 fixation)
1360	163	AI010480	X, Y	Carbon fixation, Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism, Reductive carboxylate cycle (CO2 fixation)
1360	164	AI010480	ı	Carbon fixation, Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism, Reductive carboxylate cycle (CO2 fixation)
3476	162	NM_022516	vv	Carbon fixation, Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism, Reductive carboxylate cycle (CO2 fixation)
1870	18277	AI104399	Т, ННН	Carbon fixation, Fructose and mannose metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Glycolysis Pathway, Inositol metabolism
562	820	AA892395	B, PPP, QQQ	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Glycolysis Pathway, Pentose phosphate pathway
4183	818	X02291	HH, SS	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Glycolysis Pathway, Pentose phosphate pathway
3060	7062	NM_012495	·	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway
3060	7063	NM_012495	O, P, PP, QQ, UU, VV	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway

TABLE	2	: 21 :: 21:		Altomay Docket 4X221-5033-01000 Document No. 1935223.1
	id ka Grec	RefSeq ID.	Model	Pathways
			II, VV, PPP, General	Carbon fixation, Fructose and mannose metabolism,
3060	7064	NM_012495	Core Tox Markers	Glycolysis / Gluconeogenesis, Pentose phosphate pathway
3079	16895	NM_012558	T, XX, YY, DDD	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway
3012	1312	M31788	I, J, LLL	Carbon fixation, Glycolysis / Gluconeogenesis, Glycolysis Pathway
3745	5175	NM_053297	O, P, NN, OO, VV, EEE, MMM	Carbon fixation, Glycolysis / Gluconeogenesis, Purine metabolism, Pyruvate metabolism
3494	20802	NM_022592 NM 022592	J, X, BB,	Carbon fixation, Pentose phosphate pathway
3494 3494	20803	NM_022592 NM_022592	CC, HH X	Carbon fixation, Pentose phosphate pathway  Carbon fixation, Pentose phosphate pathway
1265	17353	AI008020	ввв, ссс	Carbon fixation, Pyruvate metabolism, Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3093	18746	NM_012600	888	Carbon fixation, Pyruvate metabolism, Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3093	18747	NM_012600	T, X, Y, BBB, LLL, RRR, SSS,	Carbon fixation, Pyruvate metabolism, Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3093	18749	NM_012600	X, Y, BBB, LLL, RRR, SSS, UUU	Carbon fixation, Pyruvate metabolism, Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3048	291	M88347	JJ	Catabolic Pathways for Methionine, Isoleucine, Threonine and Valin, Glycine, serine and threonine metabolism, Methionine metabolism, Selenoamino acid metabolism
3289	15365	NM_017147	VV, FFF, General Alternate	CCR3 signaling in Eosinophils, Rac 1 cell motility signaling pathway, Rho cell motility signaling pathway
3825	15995	NM_053769	I, J, Q, R C, I, J, R,	CD40L Signaling Pathway, Phosphatidylinositol signaling system, TNFR2 Signaling Pathway CD40L Signaling Pathway, Phosphatidylinositol
3825	15996	NM_053769	LLL	signaling system, TNFR2 Signaling Pathway CD40L Signaling Pathway, Phosphatidylinositol
3825	15997	NM_053769	I, J, R	signaling system, TNFR2 Signaling Pathway Cell Cycle: G1/S Check Point, Cyclins and Cell Cycle Regulation, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Influence of Ras and Rho proteins on G1 to S
1480	2866	AI029058	Z, AA	Transition, WNT Signaling Pathway, p53 Signaling Pathway

TABLE	2			Aliomay Docket 44921-5093-01000 Document No. 1935323.1
(1) (1) (1) (2) (1) (1) (1) (1) (1) (1) (1) (1) (1) (1	id nati	Conson: Acc or Refseq ID:	Modal Coda	Pathways
				Cell Cycle: G1/S Check Point , Cyclins and Cell Cycle
-				Regulation, Inactivation of Gsk3 by AKT causes
				accumulation of b-catenin in Alveolar Macrophages, Influence of Ras and Rho proteins on G1 to S
				Transition, WNT Signaling Pathway, p53 Signaling
2849	25041	D14014	E, HH	Pathway
-	20011	514011		Cell Cycle: G1/S Check Point , TGF beta signaling
4155	871	U66479	вв, сс	pathway
4096	1392	U10188	V	Cell Cycle: G2/M Checkpoint
			General	Cell Cycle: G2/M Checkpoint, Cyclin E Destruction
65	13683	AA799788	Alternate	Pathway, E2F1 Destruction Pathway
	40004		l	Cell Cycle: G2/M Checkpoint, Cyclin E Destruction
187	13684	AA818770	H	Pathway, E2F1 Destruction Pathway
			MM, FFF, TTT,	
			General	Cell Cycle: G2/M Checkpoint, Cyclin E Destruction
2973	13682	L38482	Alternate	Pathway, E2F1 Destruction Pathway
20.0	10002	200 102	, atomato	Cell Cycle: G2/M Checkpoint, Erk1/Erk2 Mapk
				Signaling pathway, Growth Hormone Signaling
				Pathway, Transcription factor CREB and its
3605	17300	NM_031107		extracellular signals
3809	15090	NM_053638		Citrate cycle (TCA cycle)
			KK, WW,	
3809	23305	NM_053638	HHH	Citrate cycle (TCA cycle)
			Q, R, GG, PPP, QQQ,	
			General	Citrate cycle (TCA cycle), Glutathione metabolism,
3635	17427	NM 031510	Alternate	Reductive carboxylate cycle (CO2 fixation)
0000	11 121	1111_001010	ratornato	Citrate cycle (TCA cycle), Glycine, serine and
				threonine metabolism, Glycolysis / Gluconeogenesis,
1578	5697	AI045119	ww .	Pyruvate metabolism
			L, Z, AA,	
			WW, LLL,	Citrate cycle (TCA cycle), Glyoxylate and
			RRR, SSS,	dicarboxylate metabolism, Reductive carboxylate
3557	19992	NM_024398	000	cycle (CO2 fixation)
			\	Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Reductive carboxylate
3557	19993	NM 024398	7 AA GGG	cycle (CO2 fixation)
3337	10000	14141_024030	2, 74, 000	Citrate cycle (TCA cycle), Glyoxylate and
				dicarboxylate metabolism, Reductive carboxylate
3557	19994	NM_024398	ww	cycle (CO2 fixation)
				Citrate cycle (TCA cycle), Glyoxylate and
			T, LL, YY,	dicarboxylate metabolism, Reductive carboxylate
3340	17516	NM_017321	RRR, SSS	cycle (CO2 fixation)
704	47544	A A O C C C C C	VV, General	Citata mula (TOA mala) O 11 m
791	17514	AA925554	Alternate	Citrate cycle (TCA cycle), Oxidative phosphorylation
3921	17512	NM_130428	S, General Alternate	Citrate cycle (TCA cycle), Oxidative phosphorylation
3819	18174	NM_053752		Citrate cycle (TCA cycle), Oxidative priospriorylation  Citrate cycle (TCA cycle), Propanoate metabolism
<del></del>		000102		Chiefe Cycle, 1 Topanoate metabolism

TABLE	3 9			Afternay Docket 44921-5033-0100
I (A) SIGIS	5 43			Document No. 1995323.1
:		Cansania.		
	@r@c	Accor		
Ko.	10 Kg:	RefSeq ID:		Pathways
	10175	050750	L, U, BBB,	0, 1, 704, 1, 0
3819	18175	NM_053752	CCC, RRR	Citrate cycle (TCA cycle), Propanoate metabolism
3248	15621	NM_017005	MM, XX,	Citrate cycle (TCA cycle), Reductive carboxylate
3240	13021	141017005	YY, TTT	cycle (CO2 fixation) Citrate cycle (TCA cycle), Shuttle for transfer of acetyl
3241	15610	NM_016987	7 AA	groups from mitochondria to the cytosol
	1.00.0	10000.	BB, CC,	Citrate cycle (TCA cycle), Shuttle for transfer of acetyl
3241	15612	NM_016987	111,000	groups from mitochondria to the cytosol
			E, J, WW,	
		1	000,	
			General	
. ·	1		Core Tox	
	Ì		Markers,	Citable and (TCA souls). Should for the offer of a sold
3241	15613	NM 016987	General Alternate	Citrate cycle (TCA cycle), Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3241	13013	14141_010967	Allemate	Classic Complement Pathway, Complement Pathway,
4130	15851	U42719	ввв, ссс	Lectin Induced Complement Pathway
			H, S, HH,	
l	1		FFF, GGG,	
ł			General	·
			Core Tox	Complement Pathway, Lectin Induced Complement
3513	24434	NM_022704	Markers	Pathway
	ł			Control of skeletal myogenesis by HDAC &
				calcium/calmodulin-dependent kinase (CaMK), Erk1/Erk2 Mapk Signaling pathway, IGF-1 Signaling
·	İ			Pathway, Multiple antiapoptotic pathways from IGF-
1				1R signaling lead to BAD phosphphorylation,
	j			Regulation of BAD phosphorylation, Skeletal muscle
				hypertrophy is regulated via AKT/mTOR pathway, igf-
3739	25431	NM_052807	D, SS	1
	İ	,		Control of skeletal myogenesis by HDAC &
		•		calcium/calmodulin-dependent kinase (CaMK),
				Erythrocyte Differentiation Pathway, IGF-1 Signaling
			D, G, H,	Pathway, Regulation of BAD phosphorylation, Skeletal muscle hypertrophy is regulated via
2839	21051	D00698	GG, DDD	AKT/mTOR pathway, igf-1
				Control of skeletal myogenesis by HDAC &
				calcium/calmodulin-dependent kinase (CaMK),
			H, S, GGG,	Erythrocyte Differentiation Pathway, IGF-1 Signaling
			PPP, QQQ,	Pathway, Regulation of BAD phosphorylation,
			General	Skeletal muscle hypertrophy is regulated via
2993	21052	M15481	Alternate	AKT/mTOR pathway, igf-1
				Control of skeletal myogenesis by HDAC &
				calcium/calmodulin-dependent kinase (CaMK), Erythrocyte Differentiation Pathway, IGF-1 Signaling
	-32-			Pathway, Regulation of BAD phosphorylation,
			G, H, PPP,	Skeletal muscle hypertrophy is regulated via
2993	21053	M15481	QQQ	AKT/mTOR pathway, igf-1
2993	21053	M15481	QQQ	AKT/mTOR pathway, igf-1

TABLE	2			Aliomey Docket 4X92XI-5033-011XVO Document No. 1935323.1
		Conson!		
Seq (D	@F@C	AGG OT	Model :	
No. ;	ID No. :	AGG OT RESSOG ID :	Code	Pelitweys
				Control of skeletal myogenesis by HDAC &
1		į		calcium/calmodulin-dependent kinase (CaMK),
1		ĺ		Erythrocyte Differentiation Pathway, IGF-1 Signaling
				Pathway, Regulation of BAD phosphorylation,
			G, H, M, S,	Skeletal muscle hypertrophy is regulated via
4190	21054	X06107	GGG	AKT/mTOR pathway, igf-1
			G, J, S,	
			ww, 000,	
	1		PPP, QQQ,	
			General	
			Core Tox	CXCR4 Signaling Pathway, Pertussis toxin-
3444	24321	NM_022177	Markers	insensitive CCR5 Signaling in Macrophage
			A, D, V, BB,	
3741	12577	NM_052981	III, JJJ	Cyclins and Cell Cycle Regulation
0050	0.4770		1	Cysteine metabolism, Glycine, serine and threonine
3856	24778	NM_053962	111	metabolism
2056	24770	NIM DESOCS	C NANA TIT	Cysteine metabolism, Glycine, serine and threonine
3856	24779	NM_053962	MM, FFF,	metabolism Cysteine metabolism, Glycine, serine and threonine
3856	25321	NM 053962	TTT	metabolism
3030	20021	14141_000002		Cysteine metabolism, Glycolysis / Gluconeogenesis,
				Hypoxia-Inducible Factor in the Cardiovascular
			C, U, FF,	System, Propanoate metabolism, Pyruvate
3255	17807	NM_017025		metabolism
				Cysteine metabolism, Methionine metabolism,
3269	18452	NM_017074	L, 00, UU	Nitrogen metabolism, Selenoamino acid metabolism
			L, NN, OO,	
			III, JJJ,	Cysteine metabolism, Methionine metabolism,
3269	18453	NM_017074	000	Nitrogen metabolism, Selenoamino acid metabolism
				Cysteine metabolism, Taurine and hypotaurine
3740	15028	NM_052809	A, B, T, LLL	metabolism
				Cysteine metabolism, Taurine and hypotaurine
3740	25024	NM_052809	A, YY	metabolism
				Cytokine Network, IL 18 Signaling Pathway, Ras-
	4506			Independent pathway in NK cell-mediated
4171	1520	U77777	٧	cytotoxicity, Th1/Th2 Differentiation
				Degradation of the RAR and RXR by the proteasome,
				Nuclear receptors coordinate the activities of
				chromatin remodeling complexes and coactivators to
				facilitate initiation of transcription carcinoma cells,
3638	12996	NIM 024520	C DD	Transcription Regulation by Methyltransferase of CARM1
3036	12990	NM_031528	U, KK	DNA polymerase, Purine metabolism, Pyrimidine
3286	24107	NM_017141	PP OO	metabolism
3155	20885	NM_012842		EGF Signaling Pathway, egf
<del></del>	_0000	012072	**	Lo. Digitaling Latitray, Cgl

TABLE	2			Afformey Docket 4X921-5033-01000  Document No. 1935328.1
: .		CONSONX		
	@F@C	Accor	Model .	
No. :	ID Ko. ,	RefSeq ID	Code : ;	Pathways
				EGF Signaling Pathway, IFN alpha signaling
1				pathway, IFN gamma signaling pathway , IL 2
				signaling pathway, IL 4 signaling pathway, IL-2
				Receptor B Protein Interaction Pathway, PDGF
			_	Signaling Pathway, egf, ifn_alpha, ifn_gamma, il2, il4,
2834	25233	AJ000556	T	il6, interact6-1, pdgf
3462	1914		M, Z, AA	egf, epo, il2, il3, tpo
1586	6697	AI045340	MM, TTT	epo, il2, il3, il6, insulin, interact6-1, ngf, pdgf, tpo
ĺ		1		Erk1/Erk2 Mapk Signaling pathway, IL-2 Receptor B
}				Protein Interaction Pathway, Inhibition of Cellular
				Proliferation by Gleevec, Neuropeptides VIP and
1	1			PACAP inhibit the apoptosis of activated T cells,
		i		Overview of telomerase protein component gene
		NINA 040000	,	hTert Transcriptional Regulation , WNT Signaling
3094	2629	NM_012603	w	Pathway, p38 MAPK Signaling Pathway
				Erk1/Erk2 Mapk Signaling pathway, Nerve growth
		1		factor pathway (NGF), Phosphorylation of MEK1 by
2005	4000	NINA 040040	l.,	cdk5/p35 down regulates the MAP kinase pathway,
3095	1299	NM_012610	V	ngf Erk1/Erk2 Mapk Signaling pathway, PDGF Signaling
				Pathway, Rac 1 cell motility signaling pathway, Role
				of PI3K subunit p85 in regulation of Actin
2578	19287	AI232379	LLL, UUU	Organization and Cell Migration, pdgf
2376	19207	A1232319	LLL, 000	Erythropoietin mediated neuroprotection through NF-
2703	21414	AI235842	W, NN	kB
2703	21717	A1200042	VV, 1414	Erythropoietin mediated neuroprotection through NF-
3262	682	NM 017051	EEE, MMM	kB
0202	-			Erythropoietin mediated neuroprotection through NF-
				kB, Hypoxia and p53 in the Cardiovascular system,
· .	İ			Hypoxia-Inducible Factor in the Cardiovascular
4284	1146	Y09507	ww	System
1309	24249	AI009273	I, J, BB, CC	Fatty acid biosynthesis (path 1)
3343	24247	NM_017332	V	Fatty acid biosynthesis (path 1)
			B, I, J, U,	
			FF, LL, XX,	
2840	18686	D00729	YY	Fatty acid metabolism
2858	3743	D30666	BBB	Fatty acid metabolism
3150	6780	NM_012819		Fatty acid metabolism
3150	6781	NM_012819		Fatty acid metabolism
			A, B, E, I, J,	
			U, FF, LL,	
3335	18687	NM_017306	XX, YY	Fatty acid metabolism
3803	15925	NM_053607	В	Fatty acid metabolism
1				
	45000	05000=	I, J, General	matter and a set by the co
3803	15926	NM_053607	Alternate	Fatty acid metabolism

TABLE	2	., i ka	Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colore	Aliomey Docket 44921-5033-01000 Document No. 1935223.1
		(Centank		Boogrammente nesessasses
Seq ID	@F@C	Acc or	Model	1984
	ID Ko.	Roisog id :		Pathways
			Н, ВВВ,	
1			CCC, RRR,	1
			General	
628	20985	AA893242	Alternate	Fatty acid metabolism
			A, B, BBB,	
			CCC, FFF,	
}			General	
628	20986	AA893242	Alternate	Fatty acid metabolism
			A, FF, JJ,	
			KK, LL,	
			FFF, HHH,	
1			SSS,	
1			General	
1			Core Tox	
			Markers,	
			General	
1566	20983	A1044900	Alternate	Fatty acid metabolism
			U, FF, FFF,	
			HHH, General	·
2001	20084	D00100	1	Eathy said matchalism
2881	20984	D90109	Alternate LL, BBB,	Fatty acid metabolism
3806	13005	NM_053623		Fatty acid metabolism
3000	13003	14141_000020	U, FF, LL,	acty acto metabolism
3345	16148	NM 017340		Fatty acid metabolism
00.0	101.0		J, U, DD,	. any action monacontain
			EE, FF, II,	
3345	16150	NM 017340		Fatty acid metabolism
3234	20854	NM_013200	Z, AA	Fatty acid metabolism, Glycerolipid metabolism
3234	20855	NM_013200	BBB	Fatty acid metabolism, Glycerolipid metabolism
			U, BBB,	Fatty acid metabolism, Glycerolipid metabolism,
			CCC, RRR,	Mitochondrial Carnitine PalmitoyItransferase (CPT)
2932	1977	J05470	SSS	System
				Fatty acid metabolism, Glycerolipid metabolism,
			. 4	Mitochondrial Carnitine Palmitoyltransferase (CPT)
3646	15411	NM_031559		System, Reversal of Insulin Resistance by Leptin
			T, U, X, TT,	Fatty acid metabolism, Propanoate metabolism,
2240	04070	NINA 040000	XX, YY, III,	Valine, leucine and isoleucine degradation, beta-
3240	21078	NM_016986	JJJ, RRR	Alanine metabolism
			U, FF, LL,	
			XX, BBB, CCC, RRR,	
738	20711	AA924267	SSS	Fatty acid metabolism, Tryptophan metabolism
1151	20712	AA997806	FFF	Fatty acid metabolism, Tryptophan metabolism
131	20112	W991000	1, J, U, FF,	i any acid metabolism, myptophian metabolism
2992	20714	M14972	LL, XX, YY	Fatty acid metabolism, Tryptophan metabolism
		17072	U, EE, FF,	any and metabolism, repropriate metabolism
3025	20713	M57718	LL, RRR	Fatty acid metabolism, Tryptophan metabolism
				,

TABLE	2			Attorney Doctet 44921-5033-911WQ
عواقات				Document No. 1935223.1
	elec :	Conson! Accor; Refseq.D	Modal Coda	Palliways
3073	488	NM_012540	A, C, L, GG, HH, DDD	Fatty acid metabolism, Tryptophan metabolism
3073	489	NM_012540		Fatty acid metabolism, Tryptophan metabolism
3073	20705	NM_012540	C, K, L, U, GG, HH, II, DDD, RRR	Fatty acid metabolism, Tryptophan metabolism
3074	20703		C, K, L, M, U, Y, GG, HH, II, RRR, SSS C, K, L, T,	Fatty acid metabolism, Tryptophan metabolism
3074	20704		GG, HH, DDD	Fatty acid metabolism, Tryptophan metabolism
3181	191		GG	Fatty acid metabolism, Tryptophan metabolism
3182	20928	NM_012941	T	Fatty acid metabolism, Tryptophan metabolism
3182	20931	NM_012941	G, H, I, J, FF, General Alternate J, U, DD, FF, LL, XX,	Fatty acid metabolism, Tryptophan metabolism
4192	20715	X07259	QQQ, RRR, SSS	Fatty acid metabolism, Tryptophan metabolism
3128	18730	NM_012730	N, TT	Fatty acid metabolism, Tryptophan metabolism
3294	2967	NM_017158	НН	Fatty acid metabolism, Tryptophan metabolism
3294	2968	NM_017158	MM, TTT	Fatty acid metabolism, Tryptophan metabolism
3294	2969	NM_017158	N, TT	Fatty acid metabolism, Tryptophan metabolism
3294	2970	NM_017158	N, HH, SS	Fatty acid metabolism, Tryptophan metabolism
			N, EEE, HHH, MMM, PPP, QQQ, General	
3411	20716	NM_019623		Fatty acid metabolism, Tryptophan metabolism
3650	15024	NM_031572	GG W, CC, General Core Tox	Fatty acid metabolism, Tryptophan metabolism
3393	1099	NM_019303	Markers EE, MM,	Fatty acid metabolism, Tryptophan metabolism
3643	4010	NM_031543	TTT	Fatty acid metabolism, Tryptophan metabolism
3643	4011	NM_031543	K, O, P, FF, II, NN, OO, QQ, EEE, MMM T, EE, FF,	Fatty acid metabolism, Tryptophan metabolism
3643	4012	NM_031543	MM, EEE, MMM, TTT	Fatty acid metabolism, Tryptophan metabolism
168	12160	AA818412	O, P, X, TT, DDD	Fatty acid metabolism, Tryptophan metabolism

TABLE	2	, .		Aliomay Docket 44921-5033-01100 Document No. 1985328.1
	3.2 .3	CONSIDER.		A Asian and Annual Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Co
ලල ල	Grec.	Acc or	Model	
No.	ID No.:	RefSeq ID	/ <u></u>	Pathways
			K, X, TT,	
			DDD, LLL,	
2935	12156	K00996	RRR, UUU	Fatty acid metabolism, Tryptophan metabolism
			K, L, X, FF,	
0000	40457	1604704	TT, DDD,	Falls and a sale ballons. To also be a sale ballons.
2936	12157	K01721	LLL, UUU	Fatty acid metabolism, Tryptophan metabolism
3013	16305	M33312	E, M, GG JJ, KK, FFF,	Fatty acid metabolism, Tryptophan metabolism
1			HHH, PPP,	
}		İ	QQQ,	
			General	
3116	16306	NM_012692		Fatty acid metabolism, Tryptophan metabolism
31,0	10000	14111_012032	JJ, VV, XX,	atty acid metabolism, myptophan metabolism
			YY, HHH,	
			PPP, QQQ,	
			General	
3117	24707	NM 012693	1	Fatty acid metabolism, Tryptophan metabolism
			T, V, CC,	
,			00, GGG,	
3364	1173	NM_019184	PPP, QQQ	Fatty acid metabolism, Tryptophan metabolism
3364	1174	NM_019184	DD, TT	Fatty acid metabolism, Tryptophan metabolism
			F, T, V, BB,	
1			TT, DDD,	
			FFF, PPP,	
3599	1175		QQQ	Fatty acid metabolism, Tryptophan metabolism
4034	683	NM_147206	М	Fatty acid metabolism, Tryptophan metabolism
			G, H, L, N,	Flavonoids, stilbene and lignin biosynthesis, Methane
3793	19252	NM_053576	НН	metabolism, Phenylalanine metabolism
0700	40050	NA 050530		Flavonoids, stilbene and lignin biosynthesis, Methane
3793	19253	NM_053576	G, H	metabolism, Phenylalanine metabolism
2702	10054	NIA 052576	C 11 1	Flavonoids, stilbene and lignin biosynthesis, Methane
3793 3549	19254 15350	NM_053576 NM_024356	G, H, L	metabolism, Phenylalanine metabolism Folate biosynthesis
4125	368	U38379	XX, YY	Folate biosynthesis
4123	300	030379	^^, 11	r clate biosynthesis
3466	13479	NM 022390	III JUJ KKK	Folate biosynthesis
0100	70470		E, XX, YY,	Toloco biodynaticolo
			III, JJJ,	
			General	
3466	13480	NM 022390	Alternate	Folate biosynthesis
			W, DD, MM,	
			III, JJJ,	
			KKK, NNN,	
3208	14997	NM_013059	TTT	Folate biosynthesis, Glycerolipid metabolism
				Folate biosynthesis, Glyoxylate and dicarboxylate
	1549	J05519	MM, TTT	metabolism, One carbon pool by folate
	20876		N, UUU	Free Radical Induced Apoptosis
3261	20877	NM_017050		Free Radical Induced Apoptosis
			G, H, JJ,	Free Radical Induced Apoptosis, Glutamate
2974	6405	L38615	KK, GGG	metabolism, Glutathione metabolism

TABLE	2			Aliomay Docket 449231-5099-01000 Document No. 1995923.1
Seq (D No	ID Ko. Grec	CONSENS ACCOVED ROSSON	Model Code	Pathways
	,	0.7		Free Radical Induced Apoptosis, Glutamate
2974	6406	L38615	GGG	metabolism, Glutathione metabolism
	<del></del>		MM, TT,	Free Radical Induced Apoptosis, Glutathione
3564	1853	NM_030826	TTT	metabolism
			M, S, DD,	Free Radical Induced Apoptosis, Glutathione
3959	17109	NM_134326	EE, SS, TT	metabolism
				Free Radical Induced Apoptosis, Glutathione
3959	17112	NM_134326		metabolism
ł			E, FF, LLL,	
1		1	RRR, SSS,	
			บบบ,	
	04075	047454	General	
3293	21975	NM_017154		Free Radical Induced Apoptosis, Purine metabolism
	Ì		C, K, T, W,	
			DD, EE,	
	]		KKK, General	
1507	1876	Al030175	Alternate	Fructose and mannose metabolism
1307	1070	A1030173	A, B, BB,	Proctose and mannose metabolism
			CC, HH,	· ·
			OO, FEE,	
			GGG, III,	
ĺ			JJJ, MMM,	
			General	
			Core Tox	
3710	16726	NM_031855	Markers	Fructose and mannose metabolism
0			W, DD, EE, SS, WW,	
			XX, YY,	
			General	[
			Core Tox	
4260	1877	X74593	Markers	Fructose and mannose metabolism
2928	174	J04197	JJ, KK, SS	Fructose and mannose metabolism
			JJ, KK,	
3099	172	NM_012621	WW, YY	Fructose and mannose metabolism
			L, Z, AA, JJ,	
4204	173	X15580	KK, WW	Fructose and mannose metabolism
				Fructose and mannose metabolism, Galactose
				metabolism, Glycerolipid metabolism, Pentose and
2636	13023	AI233740	VV	glucuronate interconversions, Pyruvate metabolism
				Fructose and mannose metabolism, Galactose
				metabolism, Glycolysis / Gluconeogenesis, Pentose
4113	1340	U25651	SS	phosphate pathway

TABLE	3			ACCORNEY DOCKEC 4K927-5093-011WQ
				Document No. 1995:23.1
Seq ID	ELEC :	CONSON ACCON RESESON ID	Model Code	Pathways
		,	А, В,	
			General	
			Core Tox	
			Markers,	
	Ì		General	
3433	19712	NM_021745	Alternate	FXR and LXR Regulation of Cholesterol Metabolism
4099	1639	U11685	W, DD, EE, KKK, NNN, General Alternate	FXR and LXR Regulation of Cholesterol Metabolism
			<u> </u>	Galactose metabolism, Glycolysis / Gluconeogenesis,
1083	1322	AA964628	lw .	Starch and sucrose metabolism
				Galactose metabolism, Glycolysis / Gluconeogenesis,
3218	1321	NM_013098	L	Starch and sucrose metabolism
				Galactose metabolism, Nucleotide sugars
			ввв, ссс,	metabolism, Pentose and glucuronate
2066	17027	Al170679	RRR	interconversions, Starch and sucrose metabolism
220	10157	AA819527	XX, YY	Generation of amyloid b-peptide by PS1
1018	10155	AA956735	V	Generation of amyloid b-peptide by PS1
3363	20256	NM 019163	JJ. KK	Generation of amyloid b-peptide by PS1, HIV-I Nef: negative effector of Fas and TNF, Presenilin action in Notch and Wnt signaling, Proteolysis and Signaling Pathway of Notch, g-Secretase mediated ErbB4 Signaling Pathway
2931	1247	J05181	Q, R, S	Glutamate metabolism, Glutathione metabolism
3334	14003	NM_017305	Q, R, S, X, Y, NN, OO, General	Glutamate metabolism, Glutathione metabolism
3334	14004	NM_017305		Glutamate metabolism, Glutathione metabolism
	44450	NA 047070	II, RR, TT,	Obstance to make the make the make the transfer of
3268 3268	11150	NM_017073		Glutamate metabolism, Nitrogen metabolism
3200	11151	NM_017073	II, LL, TT,	Glutamate metabolism, Nitrogen metabolism
3268	11152	NM_017073	UU, DDD, LLL, UUU	Glutamate metabolism, Nitrogen metabolism
3268	11153	NM 017073	G, K, II, TT, DDD, GGG, LLL	Glutamate metabolism, Nitrogen metabolism
3200	11133	14141_011013	C, UU,	Oldianiale metabolism, Miliogen metabolism
1196 1968	3082 961	AA999172 AI138143	General Alternate	Glutamate metabolism, Purine metabolism Glutathione metabolism
1300	301	A1130143	11	Oldical Hole Helabolistii
3143	960	NM_012796	V, DD, EE, UU, III, JJJ, General Alternate	Glutathione metabolism
3143	1900	NM_012/96	Aitemate	Giutatnione metabolism

TABLE	2		744 A	Altomay Docket 4/1921-5033-011WO Document No. 1935323.1
		Conson's	<u> </u>	westment has reserved
Seq (D	@F@C	Acc or	Model	
No.	id ko.	RefSeq (D)	Code	Pathways
			V, General	
3744	1524	NM_053293		Glutathione metabolism
2667	16781	Al234527	M, GG, TT	Glutathione metabolism
			A, B, GGG, HHH, General	
3620	20862	NM_031154		Glutathione metabolism
3848	15934	NM_053904	w	Glutathione metabolism
00.0	1.000.		X, GG, II,	O TOTAL MINOR OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF T
4242	16780	X62660	XX, YY	Glutathione metabolism
3250	18989	NM_017013	F, K, M, N, GG, HH, TT, DDD, EEE, LLL,	Glutathione metabolism
3296	17686	NM_017165	1 1 11	Glutathione metabolism
0200	17000	11111_017100	G, K, TT,	Oldital mone Thetabolism
3634	18990	NM 031509	SSS	Glutathione metabolism
1423	20817	Al012589	G	Glutathione metabolism
4184	20818	X02904	G	Glutathione metabolism
		<del> </del>	F, PP, QQ,	
2905	21011	H32189	TT, DDD	Glutathione metabolism
2922	21012	J02592	GG, NN, OO, EEE, LLL, MMM	Glutathione metabolism
2322	21012	302332	N, BB, CC,	Gloralitione metabolism
2926	21014	J03914	NN	Glutathione metabolism
		-	F, N, DD, EE, TT,	one damino in one one one
3251	21013	NM_017014	DDD	Glutathione metabolism
3251	21015		F, K, N, TT, DDD	Glutathione metabolism
3250	18988	NM_017013	V, NN, OO	Glutathione metabolism
3962	15017	NM_134349		Glutathione metabolism
2624	624	NA 024500	K, V, NN, TT, DDD,	Chidathia a a sadah alia sa
3634	634	NM_031509		Glutathione metabolism
3634	635	NM_031509	M, NN, TT, DDD, EEE, MMM	Glutathione metabolism
3634	25525	NM 031509	N, V, NN, TT, DDD, EEE, MMM	Glutathione metabolism
3249	1399	NM 017006	G, FF	Glutathione metabolism Glutathione metabolism, Pentose phosphate pathway
J243	1000	14141 017000	J , 1 F	Glutathione metabolism, Pentose prospriate partiway Glutathione metabolism, Styrene degradation,
1996	17812	Al169075	PPP, QQQ	Tyrosine metabolism
2843	1306	D10262	GG	Glycerolipid metabolism

TABLE	<u> 2</u>			Altomey Docket 44:221-50:33-011WO Document No. 1935:223.1
രഹത്ര	@L@C	Consonia Accor	Model	
Mor was	ID Ko.			Pathways
			B, F, G, NN,	
İ			00, GGG,	
ļ			LLL,	
	1	I	General	
;	1		Core Tox	
2995	2505	M16235	Markers	Glycerolipid metabolism
			ннн,	
			General	
			Core Tox	
			Markers,	
			General	
3554	20380	NM_024381	Alternate	Glycerolipid metabolism
1166	14149	AA998172	GG	Glycerolipid metabolism
3763	6774	NM_053410	CC	Glycerolipid metabolism
			ввв, ссс,	
1205	3512	AB006607	RRR	Glycerolipid metabolism
	1		BBB, RRR,	
1205	3513	AB006607	SSS	Glycerolipid metabolism
			L, BBB,	
3764	14621	NM_053437	ccc	Glycerolipid metabolism
1				Glycerolipid metabolism, Glycolysis /
	00400			Gluconeogenesis, Pentose and glucuronate
3580	23109	NM_031000	G, H	interconversions
2270	20.425	NIN 040000		Glycerolipid metabolism, Phospholipid degradation,
3370	20435	NM_019202	UU NN, EEE,	Prostaglandin and leukotriene metabolism Glycerolipid metabolism, Phospholipid degradation,
4207	1893	X51529	MMM	Prostaglandin and leukotriene metabolism
4207	1093	751529	O, P, EEE,	Glycerolipid metabolism, Visceral Fat Deposits and
3091	18385	NM_012598	MMM	the Metabolic Syndrome
3031	10303	1414_012330	O, P, X, Y,	the Metabolic Syndrome
624	1552	AA893219	ww	Glycine, serine and threonine metabolism
1384	21040	AI011734	K, L	Glycine, serine and threonine metabolism
	1		F, N, O, P,	
			X, Y, EEE,	1
3273	1550	NM 017084		Glycine, serine and threonine metabolism
			F, O, P, X,	
			GGG, LLL,	
3273	1551	NM_017084	บบบ	Glycine, serine and threonine metabolism
3561	21038	NM_024484	TT	Glycine, serine and threonine metabolism
3561	21039	NM_024484	K, QQ, TT	Glycine, serine and threonine metabolism
3194	24718	NM_013003	EE, JJ, KK	Glycine, serine and threonine metabolism
3658	21586		G	Glycine, serine and threonine metabolism
3232	16448	NM_013197	M, T	Glycine, serine and threonine metabolism
			C, NN, OO,	Glycine, serine and threonine metabolism, Methionine
1233	1995	AF038870	DDD	metabolism

TABLE	2	• • •	. <del></del>	Altorney Docket 44921-5093-01000 Document No. 1935323.1
		Censent .		
Seg (D	Grec Grec		Model	Pathmana
No. :::	In Ko	RefSeq (D		Pathways
			X, Y, FFF,	
		j	GGG, General	
			Core Tox	
			Markers,	
			General	
2018	4091	AI169417	Alternate	Glycolysis / Gluconeogenesis, Glycolysis Pathway
2437	4092	AI228723	K, DDD	Glycolysis / Gluconeogenesis, Glycolysis Pathway
			S, GGG,	
2552	4093	AI232001	LLL	Glycolysis / Gluconeogenesis, Glycolysis Pathway
			JJ, KK,	
3743	4090	NM_053290	GGG, HHH	Glycolysis / Gluconeogenesis, Glycolysis Pathway
3743	25499	NM_053290	G, H, X, Y	Glycolysis / Gluconeogenesis, Glycolysis Pathway
2076	19407	NIM 012554	C H VV	Glycolysis / Gluconeogenesis, Glycolysis Pathway,
3076	19407	NM_012554	G, H, VV	Phenylalanine, tyrosine and tryptophan biosynthesis Glycolysis / Gluconeogenesis, Histidine metabolism,
3714	24644	NM 031972	GG	Phenylalanine metabolism, Tyrosine metabolism
37.14	27077	1411-001372		Glycolysis / Gluconeogenesis, Phenylalanine,
1497	1114	AI029917	NNN	tyrosine and tryptophan biosynthesis
11111				Glycosaminoglycan degradation, Porphyrin and
				chlorophyll metabolism, Starch and sucrose
3252	17815	NM_017015	NNN	metabolism
			O, VV, EEE,	
3412	574	NM_019905	MMM	Glyoxylate and dicarboxylate metabolism
			A, B, M,	
			OOO, UUU, General	
			Core Tox	
2558	573	AI232087	Markers	Glyoxylate and dicarboxylate metabolism
	0.0		War Noro	Glyoxylate and dicarboxylate metabolism, Pyruvate
592	22537	AA892799	s	metabolism
				Glyoxylate and dicarboxylate metabolism, Pyruvate
592	22538	AA892799	М	metabolism
				Glyoxylate and dicarboxylate metabolism, Pyruvate
2557	22542	AI232066	QQ, XX, YY	
	0.77.0			Growth Hormone Signaling Pathway, Insulin
3266	24719	NM_017071	RR	Signaling Pathway, insulin Growth Hormone Signaling Pathway, Presenilin
				action in Notch and Wnt signaling, WNT Signaling
3110	24427	NM 012669	£ 41	Pathway
13110	24421	14141_012009	K, GG, OO,	1 auway
			General	
3027	70	M58308	Alternate	Histidine metabolism, Nitrogen metabolism
3791	9267	NM_053567	OO, PP, TT	Histidine metabolism, One carbon pool by folate
3088	15097	NM_012588	Z	Hypoxia and p53 in the Cardiovascular system
3088	15098	NM_012588		Hypoxia and p53 in the Cardiovascular system
			K, S, GG,	Hypoxia and p53 in the Cardiovascular system, Sterol
3247	1698	NM_017000	HH, GGG	biosynthesis
2600	2746	A1225204	7 ^^	Hypoxia and p53 in the Cardiovascular system, WNT
2688	2746	Al235291	Z, AA	Signaling Pathway

TABLE	2			Attorney Docket 44921-5033-911WO Document No. 1935323.1
- 4-	i	Consant :		
Seqid	GFGC.		Model.	
	D No.	Rossog ID		Pathways
				Hypoxia and p53 in the Cardiovascular system, WNT
3804	20243	NM 053615	vv	Signaling Pathway
				Hypoxia-Inducible Factor in the Cardiovascular
4101	1424	U14746	w	System
				IL 4 signaling pathway, Selective expression of
	ļ			chemokine receptors during T-cell polarization,
3937	656	NM_133380	Υ	Th1/Th2 Differentiation, il4
	İ			IL 5 Signaling Pathway, Msp/Ron Receptor Signaling
İ				Pathway, Signal transduction through IL1R, interact6-
3636	24710	NM_031512	w	1
		<del></del>		
			DD, EE, SS,	·
3253	6598	NM_017020	ww, uuu	IL 6 signaling pathway, il6, interact6-1
			I, J, MM,	
3534	21238	NM_024125	TTT	IL 6 signaling pathway, il6, interact6-1
			MM, TTT,	
			General	
3534	21239	NM_024125	Alternate	IL 6 signaling pathway, il6, interact6-1
3278	4391	NM_017101	11	IL-2 Receptor B Protein Interaction Pathway
3278	4392	NM_017101	XX, YY	IL-2 Receptor B Protein Interaction Pathway
			A, D, E, V,	
	ļ		W, BB, NN,	
			EEE, III,	Inactivation of Gsk3 by AKT causes accumulation of b
3309	20529	NM_017208	JJJ, MMM	catenin in Alveolar Macrophages
				Inactivation of Gsk3 by AKT causes accumulation of b
				catenin in Alveolar Macrophages, Presenilin action in
3422	21336	NM_021266	บบบ	Notch and Wnt signaling, WNT Signaling Pathway
				Inactivation of Gsk3 by AKT causes accumulation of b
				catenin in Alveolar Macrophages, Presenilin action in
1790	19373	AI102044	LL, NNN	Notch and Wnt signaling, WNT Signaling Pathway
3443	243	NM_021989	EE	Inhibition of Matrix Metalloproteinases
				Inhibition of Matrix Metalloproteinases, p53 Signaling
1814	17234	AI102741	RR	Pathway
0500	47000		General	Inositol metabolism, Propanoate metabolism, Valine,
3592	17269	NM_031057		leucine and isoleucine degradation
4026	9096	NM_145771	RRR	Inositol phosphate metabolism
2050	4500	1114 050000	II, General	In a State to a section of the Plane
3852	4588	NM_053923	Alternate	Inositol phosphate metabolism
				Inositol phosphate metabolism, Phosphatidylinositol
3523	19669	NINA 000044	77	signaling system, Skeletal muscle hypertrophy is
3523	19009	NM_022944	ZZ U, GG, HH,	regulated via AKT/mTOR pathway
			BBB, CCC,	Inocital phocphoto matchaliam Dhaanhatidulinasital
409	23336	AA859981	RRR	Inositol phosphate metabolism, Phosphatidylinositol
709	2000	LAND39901	C, I, J, TT,	signaling system, Streptomycin biosynthesis Inositol phosphate metabolism, Phosphatidylinositol
3723	18640	NM 032057	000	
794	21821	AA925664	LL	signaling system, Streptomycin biosynthesis Integrin Signaling Pathway
3360	20863		D	Integrin Signaling Pathway Integrin Signaling Pathway
3067	15740		LL	Methane metabolism, Tryptophan metabolism
3067	15740		EEE, MMM	Methane metabolism, Tryptophan metabolism
3001	13741	TAIN_0 12320	LLL, IVIIVIIVI	menane metavolism, rryptophan metavolism

TABLE	2	<del></del>	4	. Altomay Docket 44921-5033-011WO
· .	,	W-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1	S	Document No. 1935328.1
രവ രോ	@L@@	Consoni Accor:	Model:	a de
	(D) K(3.	RefSeq ID	Coolo	Pathways A
0000		54000 J 45 _. .		Methionine metabolism, Selenoamino acid
203	576	AA819118	C, YY	metabolism
F				Methionine metabolism, Selenoamino acid
3307	20779	NM_017201	I, J, HH	metabolism
			F, L, T, RR,	
			SS, WW,	Methionine metabolism, Selenoamino acid
4205	575	X15734	SSS, UUU	metabolism
2620	20449	NIM 021520	W, II, EEE, MMM	Msp/Ron Receptor Signaling Pathway, Pertussis toxin
3639	20448	NM_031530	INIMINI	insensitive CCR5 Signaling in Macrophage Msp/Ron Receptor Signaling Pathway, Pertussis toxin
3639	20449	NM_031530	w II oo	insensitive CCR5 Signaling in Macrophage
2193	6782	AI176170	FFF	mTOR Signaling Pathway
3220	15295	NM_013102		mTOR Signaling Pathway
3220	15296	NM_013102	O, P, HH	mTOR Signaling Pathway
3081	17237	NM_012562		N-Glycan degradation
1161	16625	AA998062	A, B, N	N-Glycans biosynthesis
3670	21575		V, FF	N-Glycans biosynthesis
3211	19335	NM_013067		N-Glycans biosynthesis
3572	15186	NM_030861	DD, EE FF, TT,	N-Glycans biosynthesis
3572	15187	NM_030861	NNN	N-Glycans biosynthesis
3372	13107	1411_030001	DD, EE,	N-Glycans biosynthesis
3572	15188	NM_030861		N-Glycans biosynthesis
2857	2005	D29646		Nicotinate and nicotinamide metabolism
			BB, CC,	
204	6018	AA819140	PPP, QQQ	Nitrogen metabolism
			A, B, S, X,	
			Y, GGG, HHH,	
ļ			General	
			Core Tox	
3389	6017	NM_019292		Nitrogen metabolism
3388	15057		JJ	Nitrogen metabolism
			00,	
			General	
			Core Tox	
3390	24883	NM_019293	Markers	Nitrogen metabolism
			E C 10/10/	Nucleotide sugars metabolism, Pentose and
3625	18597	NM 031325	E, S, WW, DDD	glucuronate interconversions, Starch and sucrose metabolism
3023	10031	14141_031323	O, P, NN,	metabolism
·			00, VV,	
			EEE, III,	
			JJJ, MMM,	
			General	
3490	12606	NM_022547	Alternate	One carbon pool by folate
2880	1414	D89514	VV	One carbon pool by folate, Purine metabolism
420	4000			Overview of telomerase RNA component gene hTerc
438	4339	AA875121	UU	Transcriptional Regulation

TABLE	2	264	2	Attenney Docket 44921-5033-01WO
		(conson)		Document No. 1935323.1
SeqiD	രു രര	AGE OF 1	ගැලෙලා 🦸	
			Godo é	Pathmana
		RefSeq (D)		Pathways
3204	20535	NM_013049		OX40 Signaling Pathway
1266	22056	A1008066	F	Oxidative phosphorylation
3308	14696	NM_017202	LL	Oxidative phosphorylation
3771	21866	NM_053472	V, RR, UU	Oxidative phosphorylation
3795	21424	NM_053586	XX, YY	Oxidative phosphorylation
4029	1448	NM_145783	U	Oxidative phosphorylation
3147	20605	NM_012812	BB, CC	Oxidative phosphorylation
1872	23574	AI104520	LL	Oxidative phosphorylation
4257	23576	X72757	HH, LL	Oxidative phosphorylation
20	16901	AA799479	FF	Oxidative phosphorylation, Ubiquinone biosynthesis
2090	4428	AI171362	CCC	Oxidative phosphorylation, Ubiquinone biosynthesis
2471	3099	AI229680	RRR	Oxidative phosphorylation, Ubiquinone biosynthesis
3375	20938	NM_019223	V, EE	Oxidative phosphorylation, Ubiquinone biosynthesis
			KK, GGG,	
			ннн,	
			General	
22	15654	AA799501	Alternate	Oxidative phosphorylation, Ubiquinone biosynthesis
			N, PPP,	
2479	17672	A1230074	aga	Oxidative phosphorylation, Ubiquinone biosynthesis
3187	20943	NM 012985	MM, TTT	Oxidative phosphorylation, Ubiquinone biosynthesis
4198	15653	X14210	CC, II	Oxidative phosphorylation, Ubiquinone biosynthesis
1676	4437	A1070308	Q, R	Oxidative phosphorylation, Ubiquinone biosynthesis
10.0	1101	7 1107 0000	Q, R, EEE,	
10	1600	AA686470	MMM	p38 MAPK Signaling Pathway
3463	11454	NM 022381	VV	p53 Signaling Pathway
0.100	11404	14111_022001	<del>                                     </del>	poo oignamig r attitoy
			VV, General	
3463	11455	NM_022381	Alternate	p53 Signaling Pathway
3403	11400	14141_022301	Alternate	poo oigilaling Fattway
İ .			B, L, III, JJJ,	
			000, QQQ,	
			General	Dantath and and CaA binavallagia. Divinishing
0074	044	D00704	Core Tox	Pantothenate and CoA biosynthesis, Pyrimidine
2871	811	D63704	Markers	metabolism, beta-Alanine metabolism
			000, PPP,	
			QQQ,	
			General	
			Core Tox	Pantothenate and CoA biosynthesis, Pyrimidine
2871	812	D63704	Markers	metabolism, beta-Alanine metabolism
				Pantothenate and CoA biosynthesis, Pyrimidine
3056	1508	M97662	М	metabolism, beta-Alanine metabolism
3692	16039		J, FF	Pentose phosphate pathway
416	17742	AA866302	HH, WW	Phenylalanine metabolism, Tyrosine metabolism
			L, S, EE,	
3314	17740	NM_017233		Phenylalanine metabolism, Tyrosine metabolism
			WW, LLL,	
			RRR, SSS,	
3098	6055	NM_012619	บบบ	Phenylalanine, tyrosine and tryptophan biosynthesis
2269	14977	Al177386	JJ, KK	Phosphatidylinositol signaling system

TABLE	2		5 - 4.4 1	Altorney Docket 44921-5053-011WO Document No. 1955123.1
	elec 	(531) 531) Acc or RefSeq (10	Model Code	Palliways
3197	11904	NM_013016	E, BB, PP, EEE, III,	Phosphatidylinositol signaling system
3356	14971	NM 019140		Phosphatidylinositol signaling system
3330	14371	14141_013140	JJ, KK,	i nospitatioyinositoi sigitating system
			General	
3356	14973	NM 019140	Alternate	Phosphatidylinositol signaling system
3356	14974		T	Phosphatidylinositol signaling system
			B, W, BB, CC, DD, EE, JJ, NN, OO, PP, HHH, III, KKK, NNN, General Core Tox Markers,	
3866	16809	NM 053990	General Alternate	Phosphatidylinositol signaling system
1928	1841	Al113289	O, P, Q, R, V, DD, NN, OO, PP, QQ, III, JJJ, General Alternate DD, ZZ,	Phosphatidylinositol signaling system
3016	1843	M33962	AAA, III, JJJ, KKK	Phosphatidylinositol signaling system
3016	1844	M33962	E, DD, ZZ, AAA, III, JJJ I, J, Y, FF,	Phosphatidylinositol signaling system
3029	1973	M60103	KKK, LLL, OOO, RRR, SSS, General Core Tox Markers, General Alternate	Phosphatidylinositol signaling system
2271	18095	Al177482	S	Phosphatidylinositol signaling system
			C, I, L, W, XX, YY, LLL, OOO, General	Phospholipase C d1 in phospholipid associated cell
3030	64	M60655	Alternate	signaling
3075	23868	NM_012551	A, BB, CC, NNN	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway

TABLE	2			Afformay Docket 4/1921-5019-011WO Document No. 1935323.1
Seq ID No.	GLGC D No.	Consent Acc or Reference	Code :	Pathways
3075	23869	NM_012551	A, BB, CC, NNN	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway
3075	23871	NM_012551	w	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway Phosphorylation of MEK1 by cdk5/p35 down
3075	23872	NM_012551	A, 00, NNN	regulates the MAP kinase pathway
2353	16081	AI179610	B, E, Q, PP, EEE, MMM E, OO, PP,	Porphyrin and chlorophyll metabolism
3085	16080	NM_012580		Porphyrin and chlorophyll metabolism
			L, CC, DD, EE, III, JJJ, KKK, OOO, General Core Tox Markers, General	
3171	18564	NM_012899	Alternate E, General	Porphyrin and chlorophyll metabolism
393	14138	AA859700	Alternate	Porphyrin and chlorophyll metabolism
393	14139	AA859700	E, III, JJJ, NNN, General Alternate	Porphyrin and chlorophyll metabolism
3541	1161	NM_024153	D	Porphyrin and chlorophyll metabolism
1359	16521	AI010470	FF BB, CC, NN, SSS,	Porphyrin and chlorophyll metabolism
3072 3072	16519 16520	NM_012532 NM_012532	UUU BB, CC	Porphyrin and chlorophyll metabolism  Porphyrin and chlorophyll metabolism
2872	1125	D82071	000	Prostaglandin and leukotriene metabolism
338	13523	AA858552	NN, 00	Prostaglandin and leukotriene metabolism
4084	13520			Prostaglandin and leukotriene metabolism
260	18673 3256		DDD H, K, LLL, SSS, VUU	Proteasome Proteasome
3123	4002		KKK	Proteasome
3123	4003	NM_012708	I, J, KKK	Proteasome
3323	15141	NM_017278	A, D, GGG, PPP, QQQ	Proteasome
3324	5747	NM_017279	D, General Alternate	Proteasome
3324	5748		X, Y	Proteasome
2224	E740		D, LL, YY, GGG, PPP,	Drotonoono
3324 3325	5749 3987	NM_017279 NM_017280	QQQ GGG HHH	Proteasome Proteasome
0020	2201	111VI_V1/200	<del>555, [                                     </del>	· rotousonie

TABLE	<u> </u>	•		Afformey Docket 44921-5033-011440
				Document No. 1925323.1
		GOUPEUN?		
කුලේ බ	RETOR!	AGE OF	Model :	Pathways
NO.	אסאו שוו	RefSeq (D)		reunweys .
l .			A, BBB,	
2226	4 4 4 7	NM_017281	CCC, GGG,	Dratagama
3326 3327	1447 3253	NM 017282		Proteasome Proteasome
3327	3233	14141_017202	TT, GGG,	Floteasome
3327	3254	NM_017282		Proteasome
3329	8956	NM 017284		Proteasome
3329	8957	NM_017284		Proteasome
			G, H, X, Y,	
3660	20940	NM_031629		Proteasome
3660	20942	NM_031629	UUU	Proteasome
3875	22849	NM_057099		Proteasome
			B, G, H,	
3875	25253	NM_057099		Proteasome
3906	25252	NM_080767	O, P, HH	Proteasome
			X, Y, RR,	
3797	20842	NM_053590		Proteasome
0000	0000	500004	A, B, RR,	Dt
2860	9029	D30804	WW, SSS	Proteasome
2867	9135	D45247	N, RRR S, GGG,	Proteasome
3328	15535	NM_017283		Proteasome
3328	15538	NM_017283		Proteasome
0020	10000	1111_011200	G, H, PPP,	i rotodorino
3330	12523	NM 017285	QQQ	Proteasome
			G, H, S, X,	
			Y, GGG,	
3330	12524	NM_017285	PPP, QQQ	Proteasome
			K, X, Y,	
3781	18401	NM_053532	บบบ	Proteasome
			G, H, K, X,	
0000	oroc:	D00004	Y, LLL,	D., 4
2860	25281	D30804	SSS, UUU	Proteasome
]			CHKDD	
2867	9134	D45247	G, H, K, BB, CC, GGG	Proteasome
57	14250	AA799729	W	Purine metabolism
2629	16709	Al233602	PP, QQ	Purine metabolism
3169	16708	NM 012895	UU, WW	Purine metabolism
3547	10980		Z, AA	Purine metabolism
3574	17050	NM_030986	UU	Purine metabolism
4288	442	Z22867	Z, AA	Purine metabolism
			A, B, M,	
			FFF, HHH,	
			KKK, NNN,	
		,	000,	
			General	
10004	4040	1457507	Core Tox	Duning weakshallows
3024	1246	M57507	Markers	Purine metabolism
3687	14184	NM_031776	V, UU	Purine metabolism

TABLE	2			ZAXIemey Dockei 44921-5033-011VVO Document No. 1955323.1
Seq (D	erec		Model .	
No.	(D K)@.;	Re(\$99 (D	Code : 4	Pathways
3687	14185	NM_031776		Purine metabolism
3033	13547	M63983	EE	Purine metabolism
3039	997	M80550	RR	Purine metabolism
			JJ, KK, NN, OO, EEE,	
2251	14384	Al177096	1	Purine metabolism
2927	1869	J03959		Purine metabolism
2927	1870	J03959	M	Purine metabolism
3824	1868	NM_053768		Purine metabolism
3219	24	NM_013101	Z, AA, RRR, SSS	Purine metabolism
			O, P, General	
3701	11170	NM_031833	Alternate	Purine metabolism, Pyrimidine metabolism
				Purine metabolism, Pyrimidine metabolism, RNA
3854	15857	NM_053948	ZZ, AAA	polymerase
				Purine metabolism, Pyrimidine metabolism, RNA
2616	5778	AI233246	G, H	polymerase
0000	45050	AUA 004005		Purine metabolism, Pyrimidine metabolism, RNA
3630 .	15359	NM_031335	ZZ, AAA	polymerase
595	17332	AA892829	K, ZZ, AAA	Purine metabolism, Selenoamino acid metabolism, Sulfur metabolism
3657	24234	NM_031614	G, H, Q, II	Pyrimidine metabolism
			Q, HH, ZZ,	
3657	24235	NM_031614		Pyrimidine metabolism
838	24262	AA943116	X, Y, UUU	Pyrimidine metabolism
3239	20826		C, HH	Pyrimidine metabolism
3798	20896	NM_053592	U, NNN A, B, M, HH,	Pyrimidine metabolism
			SS, UU, III, JJJ, KKK, OOO, General Core Tox	
1430	1409	Al012802	Markers	Pyruvate metabolism
1600	24374	Al045973	E	Rac 1 cell motility signaling pathway
				Rac 1 cell motility signaling pathway, Ras Signaling
3726	21809	NM_032067	ZZ, AAA	Pathway
3726	21810	NM_032067	ZZ, AAA	Rac 1 cell motility signaling pathway, Ras Signaling Pathway
785	22843	AA925473	vv	Ras Signaling Pathway, Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration, p38 MAPK Signaling Pathway
2403	22845	Al227887	к	Ras Signaling Pathway, Role of Pl3K subunit p85 in regulation of Actin Organization and Cell Migration, p38 MAPK Signaling Pathway
3259	21580	NM_017041	ZZ, AAA	Regulation of ck1/cdk5 by type 1 glutamate receptors

TABLE	2		. N	Afterney Docket 44921-5099-01000 Document No. 1995323.1
		(Consent		200000000000000000000000000000000000000
<b>Seq ID</b>	නවු ව	Acc or	Model	
	D Ko.	RefSeq (D	Codo	Paliways :
				Regulation of ck1/cdk5 by type 1 glutamate receptors,
3637	9369	NM 031527	E	Regulation of elF2
				Regulation of ck1/cdk5 by type 1 glutamate receptors,
3637	9370	NM_031527	RR, SS	Regulation of eIF2
3414	18713	NM_020075		Regulation of eIF2
3414	18715	NM_020075		Regulation of eIF2
			ZZ, AAA,	
3655	14295	NM_031599		Regulation of eIF2
			II, General	
4097	1928	U10357	Alternate	Regulation of elF4e and p70 S6 Kinase
			_	Regulation of eIF4e and p70 S6 Kinase, mTOR
2002	23152	AI169170	S	Signaling Pathway
3358	17304	NM_019144		Riboflavin metabolism
3242	24649	NM_016988	GG, HH	Riboflavin metabolism
				Role of nicotinic acetylcholine receptors in the
3359	20373	NM_019145		regulation of apoptosis
53	2040	AA799700	MM, TTT	Selenoamino acid metabolism
			G, H, II, JJ,	
1			KK, DDD,	
		ļ	FFF, HHH,	
2005	17101	047400	General	Skeletal muscle hypertrophy is regulated via
3295	17104	NM_017160		AKT/mTOR pathway, mTOR Signaling Pathway
			H, II,	Chalatal associate by mandromby, in an avolated sign
2005	47405	NINA 047460	General	Skeletal muscle hypertrophy is regulated via
3295	17105	NM_017160	Alternate	AKT/mTOR pathway, mTOR Signaling Pathway
3295	17107	NM_017160	lvv vv	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, mTOR Signaling Pathway
4055	18356	R47042	XX, YY	Small Leucine-rich Proteoglycan (SLRP) molecules
2853	179	D17809	GG, WW	Sphingoglycolipid metabolism
894	17471	AA944965	LL	Sphingoglycolipid metabolism
2984	4254	M12450	M, S, NNN	Sphingoglycolipid metabolism
2304	7207	11112400	FFF,	opiningogryconpid metabonom
Ì			General	
2062	15393	AI170663	Alternate	SREBP and controls lipid synthesis
87	4832	AA800190	ZZ, AAA	Starch and sucrose metabolism
1304	4833	Al009178	E	Starch and sucrose metabolism
	.000		B, I, J, V,	otaron and degrees metabolism
			GGG, 000,	
			General	
			Core Tox	
3457	10509	NM_022268		Starch and sucrose metabolism
			I, FF,	
			General	
3457	25814	NM_022268		Starch and sucrose metabolism
			GGG, 000,	
			General	
			Core Tox	
3633	24645	NM_031502	Markers	Starch and sucrose metabolism
2054	11585	Al170502	PP, QQ, YY	Starch and sucrose metabolism

TABLE	2 -	·		Aliomey Docket 44921-5093-011WO Document No. 1995323.1
		CONSON!		alicest Alice
Seq (D	ଜ୍ୟୁ ଜ୍ୟୁ	Accor	Model Recta	
			ලිලුල්ල :	Padhways
3226	650	NM_013134		Sterol biosynthesis
3226	651	NM_013134		Sterol biosynthesis
3226	652	NM_013134	Q, R G, WW,	Sterol biosynthesis
			General	
3885	8592	NM_057137	Alternate	Sterol biosynthesis
3284	16681	NM 017136	A, B	Sterol biosynthesis, Terpenoid biosynthesis
3204	10001	14141_017130	SS, KKK,	Steror biosynthesis, Terperiola biosynthesis
			000,	
1			General	
3378	16449	NM_019238		Sterol biosynthesis, Terpenoid biosynthesis
			C, I, J, FF,	
			000,	
			General	
3378	16450	NM_019238	Alternate	Sterol biosynthesis, Terpenoid biosynthesis
1217	1058	AF003835	B, XX, YY	Sterol biosynthesis, Terpenoid biosynthesis
2740	7691	Al236611	Υ	Sterol biosynthesis, Terpenoid biosynthesis
			I, J, N, T,	
			General	
3707	15069	NM_031840		Sterol biosynthesis, Terpenoid biosynthesis
3707	15070		I, T	Sterol biosynthesis, Terpenoid biosynthesis
3707	25460		I, J, T	Sterol biosynthesis, Terpenoid biosynthesis
3302	23961	NM_017181	PPP, QQQ	Styrene degradation, Tyrosine metabolism
			A, G, II, GGG, PPP,	
			QQQ,	1
			General	
3679	24810	NM 031732	Alternate	Sulfur metabolism
00.0	2-1010	11111_001702	A, B, G, S,	Cultar metabolism
			VV, GGG,	
		,	PPP, QQQ,	
			General	
			Core Tox	
			Markers,	
			General	
3679	24811	NM_031732	Alternate	Sulfur metabolism
			G, I, J,	
			000, PPP,	
			QQQ,	
			General	
			Core Tox	
			Markers, General	
3613	14970	NM_031127	Alternate	Sulfur metabolism
	4748	NM_031834		Sulfur metabolism
	4749		Y	Sulfur metabolism
<del></del> -	., .,	001004	<u></u>	T Cytotoxic Cell Surface Molecules, T Helper Cell
742	17116	AA924339	X, Y	Surface Molecules
				T Cytotoxic Cell Surface Molecules, T Helper Cell
3111	17117	NM_012673	κ	Surface Molecules
<u></u>				· · · · · · · · · · · · · · · · · · ·

TABLE	2	+		Aliomey Dealer 44921-5033-01140 Decument No. 1986323.1
രവരാ	Grec.	Consenz Cor or	Model	17.500 24.500 M
MO	MD No.	Refseq (D)		Pathways
			A, B, JJ,	
			ннн,	
1	Ì		General	
3434	19824	NM_021750	Alternate	Taurine and hypotaurine metabolism
			B, I, J, JJ,	
			ннн,	
2404	40005	004750	General	
3434	19825	NM_021750	Alternate	Taurine and hypotaurine metabolism
			F, N, S, CC,	·
			II, NN, OO,	
		]	PP, QQ, TT,	
			DDD, EEE,	
			LLL, MMM,	
l		ŀ	SSS, UUU,	
			General	
3156	17541	NM_012844		Tetrachloroethene degradation
3367	15242	NM_019191		TGF beta signaling pathway, tgf-beta
3648 3648	16163 16164	NM_031563 NM_031563	RR, VV	Transcriptional activation of dbpb from mRNA Transcriptional activation of dbpb from mRNA
3648	16165		D	Transcriptional activation of dbpb from mRNA
10040	10100	14141_001000	C, E, DD,	Transcriptional activation of copp from mixty
			ss, ww,	
901	402	AA945143	KKK, NNN	Tryptophan metabolism
3415	20493	NM_020076	W	Tryptophan metabolism
			B, G, M,	``
			GG, HH,	
			NN, OO,	
	,		FFF, GGG, III, JJJ,	
			General	
]			Core Tox	·
4158	794	U68168	Markers	Tryptophan metabolism
			A, B, FF,	
			ввв, ссс,	TSP-1 Induced Apoptosis in Microvascular
3647	18315	NM_031561	RRR, SSS	Endothelial Cell
			A, B, II,	Top 44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
2647	10246	NINA 024504	BBB, CCC,	TSP-1 Induced Apoptosis in Microvascular
3647	18316	NM_031561	RRR BBB, HHH,	Endothelial Cell TSP-1 Induced Apoptosis in Microvascular
3647	18318	NM_031561	RRR	Endothelial Cell
	.55.5	001001		TSP-1 Induced Apoptosis in Microvascular
3647	18319	NM_031561	ввв, ссс	Endothelial Cell
3071		NM_012531	M	Tyrosine metabolism
3071	11116	NM_012531	М	Tyrosine metabolism
			F, V, Z, AA,	•
			XX, YY,	·
3000	4440	NINA 040500	General	Voline louging and instruction described
3090	4449	NM_012592	Alternate	Valine, leucine and isoleucine degradation

TABLE	2		g. a.	Aliomay Docket 44921-5033-01100 Document No. 1935323.1
	elec B Ko. 4	Constant Acc or Refect ID	Model Code :	Palliways
2000	4450	NM_012592	A, B, V, BB, CC, II, OOO, General Alternate	Valine, leucine and isoleucine degradation
3090	4450	NIVI_012392	Alternate	valifie, ledcifie and isoledcifie degradation
		}	VV, General	
3090	4451	NM_012592	Alternate	Valine, leucine and isoleucine degradation
3090	4452	NM_012592	VV, General Alternate	Valine, leucine and isoleucine degradation
			G, General	
1459	21950	AI013861	Alternate	Valine, leucine and isoleucine degradation
1990	5232	AI168942	ww	Valine, leucine and isoleucine degradation
2925	17284	J02827	VV, XX, YY, EEE, MMM	Valine, leucine and isoleucine degradation
3369	18573	NM 019201	A, B, KK, HHH	WNT Signaling Pathway

TABLE 2	3.8				Attorney Docket 4492/1-6058-0/1WO
6 8 9 9	ON EG) [D]	्री ऑब्येंडो (देव्ह	三宝宝	man Homologous own/GenerName: Human Homologous/Sequence Gruster/IIIII	
923	1707	AA945698	00	15 kDa selenoprotein, 15-kDa selenoprotein	15 kDa selenoprotein, 15-kDa selenoprotein
3891	15408	NM_057197	M, U, FF, 2, 4-dienoyl XX, YY, BBB, reductase 1, CCC mitochondria	2, 4-dienoyl CoA reductase 1, mitochondrial	2, 4-dienoyl CoA reductase 1, mitochondrial
3891	15409	U, U NM_057197 SSS	J, U, FF, VV, reductase 1, SSS	2, 4-dienoyl CoA reductase 1, mitochondrial	2, 4-dienoyl CoA reductase 1, mitochondrial
				2, 4-dienoyl CoA reductase 2, peroxisomal, 2-4-	2, 4-dienoyl CoA reductase 1, mitochondrial, 2, 4-dienoyl CoA reductase 2, peroxisomal, 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal, Mus musculus,
914	22604	AA945578	U, FF, KK, XX, RRR	dienoyl-Coenzyme A reductase 2, peroxisomal	Similar to hypothetical protein MGC4172, clone MGC:18716 IMAGE:4219994, mRNA, complete cds, carbonyl reductase 2, peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase, peroxisomal trans-2-enoyl-CoA reductase.
				2, 4-dienoyl CoA reductase 2,	2, 4-dienoyl CoA reductase 1, mitochondrial, 2, 4-dienoyl CoA reductase 2,
1234	22602	AF044574	U, FF, BBB, CCC, RRR, SSS	peroxisoriiai, 2-4- dienoyl-Coenzyme A reductase 2, peroxisomal	peroxisomal, 2-4-dienoyi-Coenzyme A reductase 2, peroxisomal, Mus musculus, Similar to hypothetical protein MGC4172, clone MGC:18716 IMAGE:4219994, mRNA, complete cds, carbonyl reductase 2, peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase, peroxisomal trans-2-enoyl-CoA reductase.
				2, 4-dienoyl CoA reductase 2, peroxisomal, 2-4-	2, 4-dienoyl CoA reductase 1, mitochondrial, 2, 4-dienoyl CoA reductase 2, peroxisomal, 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal, Mus musculus
1234	22603	AF044574	U, FF, LL, BBB, CCC, RRR, SSS	dienoyl-Coenzyme A reductase 2, peroxisomal	Similar to hypothetical protein MGC4172, clone MGC:18716 IMAGE:4219994, mRNA, complete cds, carbonyl reductase 2, peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase, peroxisomal trans-2-enoyl-CoA reductase

TABU F	33				### Attorney Docket 4492/1-5038-011W0
) (200 (100)	60.00 10 No.	ල්බෙන්න ර්මේග් යිවෙනිමු (D)	Model Godo	delicoder Knownicene Name K	い おいかまか Homologous Sequences Glüster Intle
3226	650	NM_013134	ō	3-hydroxy-3- methylglutaryl- Coenzyme A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase, Mus musculus, Similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase, clone MGC:25828 IMAGE:4166540, mRNA, complete cds, SREBP CLEAVAGE-ACTIVATING PROTEIN
3226		NM_013134	ō	3-hydroxy-3- methylglutaryl- Coenzyme A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase, Mus musculus, Similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase, clone MGC:25828 IMAGE:4166540, mRNA, complete cds, SREBP CLEAVAGE-ACTIVATING PROTEIN
3226	652	NM_013134	Q, R	3-hydroxy-3- methylglutaryl- Coenzyme A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase, Mus musculus, Similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase, clone MGC:25828 IMAGE:4166540, mRNA, complete cds, SREBP CLEAVAGE-ACTIVATING PROTEIN
3321	20600	NM_017268	G, H, FF, JJ, KK, FFF, General Alternate	3-hydroxy-3- methylglutaryl- Coenzyme A synthase 1, 3- JJ, hydroxy-3- methylglutaryl- Coenzyme A synthase 1 (soluble)	3-hydroxy-3-methyiglutaryl-Coenzyme A synthase 1 (soluble), 3-hydroxy-3- methyiglutaryl-Coenzyme A synthase 2, pre B-cell leukemia transcription factor 1
3321	20601	G, H, J, KK, FFF KKK, OC General NM_017268 Alternate	3, 6	3-hydroxy-3- methylglutaryl- Coenzyme A synthase 1, 3- hydroxy-3- methylglutaryl- Coenzyme A synthase 1 (soluble)	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble), 3-hydroxy-3- methylglutaryl-Coenzyme A synthase 2, pre B-cell leukemia transcription factor 1

PCT/US03/03194 10/501933

Anomay Docket 44921-5033-61W6	Human Homologous	3-hydroxyanthranilate 3, 4-dioxygenase						3-phosphoglycerate dehydrogenase, EST, Moderately similar to SERA MOUSE D-3-	PHOSPHOGLYCERALE DEHYDROGENASE [M.musculus], ESTS, Weakly similar to 3-phosphoglycerate dehydrogenase [Rattus norvegicus] [R.norvegicus], Mus musculus	adult male testis cDNA, RIKEN full-length enriched library, clone:4930404C15:3-phosphoglycerate dehydrogenase, full insert sequence, glyoxylate	reductase/hydroxypyruvate reductase, phosphoglycerate dehydrogenase		4-hydroxyphenylpyruvate dioxygenase, 4-hydroxyphenylpyruvic acid dioxygenase
	Auman Homologou Known Gene Name	3-hydroxyanthranilate 3, 4-dioxygenase	3- monooxgenase/trypto phan 5-	monooxgenase activation protein,	gamma polypeptide, tyrosine 3-	monooxygenase/trypt ophan 5-	monooxygenase activation protein,	gamma polypeptide	3-phosphoglycerate	dehydrogenase, phosphoglycerate	dehydrogenase	4- hydroxyphenylpyruvat	e dioxygenase, 4- hydroxyphenylpyruvic acid dioxygenase
	Model Gode						R, PPP,	מממ					нн, ww
		<u>₩</u>		·							9		
	Reference Reference Reference	NM_020076						NW 019376			NM 031620		17742 AA866302
ေ	ම <u>ැලි</u> ම	20493						13580			21586		17742
	නිලේ [ම්	3415						340/			3658		416

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ම ල මු	ි මැල ම	Cemeenik Aee or Roiseq (D	Model Gode -		Human Homologous Known Gene Namen Homen Human Jogous Scapence Cluster Mile
3314	17740	NM_017233	L, S, EE, TT,	4- hydroxyphenylpyruvat e dioxygenase, 4- hydroxyphenylpyruvic acid dioxygenase	4-hydroxyphenylpyruvate dioxygenase, 4-hydroxyphenylpyruvic acid dioxygenase
				-4- IIMP	
2880	1414	D89514	>	cyclohydrolase 5-hydroxytryptamine (serotonin) receptor	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
3087	20313	NM_012585	D, E Z, AA, MM,	0	5-hydroxytryptamine (serotonin) receptor 1A
3556	22282	NM 024394 WW,		3A 5-hydroxytryptamine (serotonin) receptor 6	5-hydroxytryptamine (serotonin) receptor 3A 5-hydroxytryotamine (serotonin) receptor 6
2928		J04197	JJ, KK, SS		
3099	172	NM_012621	JJ, KK, WW,	6-phosphofructo-2- kinase/fructose-2, 6- biphosphatase 1	
4204	173	X15580	L, Z, AA, JJ, KK, WW	6-phosphofructo-2- kinase/fructose-2, 6- biphosphatase 1	

																								_
Altomey Dockel 44924-5039-01W0	umani Homologous nowni Genet Name   Humani Homologous Sequence (cluster III II)					Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone	lacyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase). acetyl-Coenzyme A	acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)				•			Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone	MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A		acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)					dehydrogenase, long acetyl-Coenzyme A dehydrogenase, long-chain, acyl-Coenzyme A dehydrogenase,	long chain
	HumaniHomologous Known Gene Name	acetyl-Coenzyme A acyltransferase	(peroxisomal 3-	thiolase), acetyl-	Coenzyme A	acyltransferase 1	oxoacvi-Coenzyme A	thiolase)	acetyl-Coenzyme A	acyltransferase	(peroxisomal 3-	oxoacyl-Coenzyme A	thiolase), acetyl-	Coenzyme A	acyltransferase 1	(peroxisomal 3-	oxoacyl-Coenzyme A	thiolase)	acetyl-Coenzyme A	dehydrogenase, long-	chain, acyl-	Coenzyme A	dehydrogenase, long	chain
	Modell Gode				U, FF, HH,	ഹ്	RRR. SSS.										U, FF, GG,	HH, LL, DDD						O, KKK
(ASD) SERIAL	Collection Age of the Refsee To		٠		٠			NM_012489										NM_012489					070070	NM_012819 U,
33	errec To No							23698										23699						6/80
TABUES F	ි. මු		<del>.</del>					3058								-		3058						3150

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် တို့ <u>ဓ</u>	erec To No.	ල්බාවෙක්ය  Aee ලේ  RetSeq ID	Modell Godo		Human Homologous Known Gene Name Human Homologous Sequence Cluster intie
				acetyl-Coenzyme A dehydrogenase, long- chain, acyl-	
3150	6781	NM 012819	£	Coenzyme A dehydrogenase, long chain	Coenzyme A dehydrogenase, long acetyl-Coenzyme A dehydrogenase, long-chain, acyl-Coenzyme A dehydrogenase, chain
				acetyl-Coenzyme A dehydrogenase,	
				medium chain, acyl-	CIBICARA MANCAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARKA ARAMARA ARAMARKA ARAMARKA ARAMARKA AR
		·		dehydrogenase, C-4 F	ESTS, Pigniy similar to ACYL-COA DEHYDROGENASE, MEDIOM-CHAIN SPECIFIC PRECURSOR [M.musculus], acetyl-Coenzyme A dehydrogenase, medium chain, acyl-
3240	21078	NM_016986	JJJ, RRR	to C-12 straight chain	Coenzyme A dehydrogenase, C-4 to C-12 straight chain
				phatase 2,	ESTs, Weakly similar to A33395 acid phosphatase (EC 3.1.3.2) precursor - rat
3242	24649	NM_016988	GG, HH	lysosomal	[R.norvegicus], acid phosphatase 2, lysosomal, acid phosphatase, testicular
			L, Z, AA, WW, LLL,		
3557	19992	NM_024398		aconitase 2, mitochondrial	aconitase 2, mitochondrial
3557	19993	NM_024398	NM_024398 Z, AA, GGG		aconitase 2, mitochondrial
3557	19994	NM_024398	ww	aconitase 2, mitochondrial	aconitase 2, mitochondrial
3175	24431	24431 NM_012912 W,	w, =	activating transcription factor 3	ESTs, Weakly similar to A39382 liver regeneration factor LRF1 - rat [R.norvegicus], ctivating transcription ESTs, Weakly similar to A54025 transcription factor ATF3 [H.sapiens], activating actor 3
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ි. ලිල් ම	A GLGG ID No.	ලේඛණිකි?     හිලේ ලේ   ශින්පිලේ (ම		Human Homologous Known Gene Namer	
3547	10980	NM_024349	Z, AA	adenylate kinase 1	RIKEN cDNA 0610011D08 gene, adenylate kinase 1
3574	17050	9860E0_MN	ΩΩ	adenylate kinase 2	Homo sapiens cDNA FLJ30976 fis, clone HHDPC2000055, weakly similar to ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3), Mus musculus AK5 mRNA for adenylate kinase isozyme 5, complete cds, adenylate kinase 2
1850	3764	AI103651	ပ	0	ADP-ribosylarginine hydrolase, ESTs, Weakly similar to ADP-RIBOSYLARGININE HYDROLASE [M.musculus]
					ADP-ribosylation factor 4-like, ADP-ribosylation factor-like 7, ADP-ribosylation-like 4, ESTs, Weakly similar to ADP-ribosylation-like 4 IMus musculus IM.musculus Mus
					musculus, Similar to ADP-ribosylation-like 4, clone MGC:5774 IMAGE:3599701,
000	0,0,0	0000		 م'	mRNA, complete cds, RIKEN cDNA 1110036H21 gene, epithelial protein lost in
2200	24013	ININI 018100	Alternate	ribosylation-like 4	neoplasm beta
			C, I, L, W. XX, YY, LLL,		
			,000	adrenergic receptor,	
			General	alpha 1b, adrenergic,	
3030	64	M60655	Alternate	alpha-1B-, receptor	
				adrenergic receptor,	
				σ	Mus musculus histamine H4 receptor mRNA, complete cds, adrenergic, alpha-1D-,
3560	1835	NM_024483	HH	alpha-1D-, receptor	receptor
				alanine-glyoxylate	
				aminotransferase,	
				alanine-glyoxylate	•
			,	aminotransferase	
·-				(oxalosis I;	
				hyperoxaluria I;	
				glycolicaciduria;	
	0000	1000			alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I;
1944	24803	AI13/065	MM, VV, 111	aminotransterase)	hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)

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Doctor 449						otransferas	erase)								otransferas	erase)								otransferas arase)
- Altomesy						oxvlate amir	aminotransf								oxylate amir	aminotransf								oxylate amir aminotransf
	Ser mae					alanine-alv	e-pyruvate								alanine-gly	e-pyruvate							,	alanine-gly e-ovruvate
	ogows Sequence ©wste					ansferase.	iduria; serin								ansferase,	iduria; serin								'ansferase, iduria: serin
						late aminotr	l; glycolicac								late aminoti	l; glycolicac							•	late aminoti I: glvcolicac
	HumaniHomo					anine-qivoxv	hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase								anine-glyoxy	hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)								alanine-glyoxylate aminotransferase,alanine-glyoxylate aminotran hyperoxaluria I: glycolicaciduria: serine-oyruvate aminotransferase`
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	iumani Homologous inowni Genei Namer	lanine-glyoxylate minotransferase,	lanine-glyoxylate minotransferase	(oxalosis I;	hyperoxaluria I;	glycolicaciduria; serine-pyruvate	aminotransferase)	lanine-glyoxylate	minotransferase,	lanine-glyoxylate	minotransferase	oxalosis I;	hyperoxaluria I;	glycolicaciduria;	erine-pyruvatı	minotransferase)	lanine-glyoxylate	minotransferase,	lanine-glyoxylate	minotransferase	(oxalosis I;	hyperoxaluria I;	giycolicaciduria;	erine-pyruvate minotransferase)
	) (Code)	<u> </u>	<u> </u>	<u> </u>	<u>E</u> _	ő		छ	Ö	<u>a</u>	<u></u>	<u>=</u>	<u>.c</u>		X, Y, MM, s	TTT	Ø	Ö	w	Ö	<u>=</u>		<u>.</u>	BBB, se
	Moet					MM, PP	RR,								≻ <u>×</u>	. 'SS						!	Z (	SS, BBB,
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				alanine-glyoxylate aminotransferase,	
				alanine-glyoxylate	
				(oxalosis I;	
				hyperoxaluria I;	
				glycolicaciduria;	
0	0000	0.000	MM, RR, SS,	serine-pyruvate	alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I;
200	24800	03060 MN		aminotransferase)	hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)
				alanine-glyoxylate	
				aminotransferase,	
				alanine-glyoxylate	
				aminotransferase	
				(oxalosis I;	
				hyperoxaluria I;	
				glycolicaciduria;	
				serine-pyruvate	alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I;
3263	24801	NM_030656	MM, VV, TTT	aminotransferase)	hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)
				alanyl-tRNA	
3429	23424	NM_021680	E	synthetase	alanyl-tRNA synthetase
					ESTs, Moderately similar to ALBU_RAT Serum albumin precursor (Contains:
412	17110	AA860062	Z, AA	albumin, albumin 1	Neurotensin-related peptide (NRP)] [R.norvegicus], albumin, albumin 1
					ESTs, Moderately similar to ALBU_RAT Serum albumin precursor [Contains:
412	17111	AA860062	S, SS		Neurotensin-related peptide (NRP)] [R.norvegicus], albumin, albumin 1
				albumin, albumin 1,	
				glutathione	ESTs, Moderately similar to ALBU_RAT Serum albumin precursor [Contains:
3929	1/109	NM_134326	EE, SS, TT	peroxidase 1	Neurotensin-related peptide (NRP)] [R.norvegicus], albumin, albumin 1

Microsoft Cheral Comment No. 1995-678-678-678-678-678-678-678-678-678-678	ESTs, Moderately similar to ALBU_RAT Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)] [R.norvegicus], ESTs, Weakly similar to GSHC_RAT Glutathione peroxidase (GSHPX-1) (Cellular glutathione peroxidase) [R.norvegicus], albumin, albumin 1, glutathione peroxidase 1, glutathione peroxidase 2 (gastrointestinal)	alcohol dehydrogenase 4 (class II), pi polypeptide	aldehyde dehydrogenase 1 family, member A1, aldehyde dehydrogenase 8 family, member A1, clone aldehyde family IMAGE:4234742, mRNA, partial cds, aldehyde dehydrogenase family aldehyde dehydrogenase family 1, subfamily A1	aldehyde dehydrogenase 2 ESTs, Moderately similar to DHAM_RAT ALDEHYDE DEHYDROGENASE, family (mitochondrial), MITOCHONDRIAL PRECURSOR (ALDH CLASS 2) (ALDH1) (ALDH-E2) aldehyde fR.norvegicus], RIKEN cDNA 2410004H02 gene, aldehyde dehydrogenase 1 family, member B1, aldehyde dehydrogenase 2 family (mitochondrial), aldehyde mitochondrial
	albumin, albumin 1, glutathione peroxidase 1	alcohol dehydrogenase 4 (class II), pi polypeptide	aldehyde dehydrogenase 1 family, member A1, aldehyde dehydrogenase family 1, subfamily A1	aldehyde dehydrogenase 2 family (mitochondrial), aldehyde dehydrogenase 2, mitochondrial
Model Gode	S, HH	alcohol dehydrogen (class II), pi U, RRR, SSS polypeptide	F, U, LL, TT, BBB, CCC, EEE, LLL, MMM, RRR, SSS, UUU	z
Consent	NM_134326	X90710	NM_022407	12300 Al013333
E 3 CONDING	17112	420	20915	
TABLES See @	3959	4277	3472	1442

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3728	12299	NM_032416	, У,	aldehyde dehydrogenase 2 family (mitochondrial), aldehyde dehydrogenase 2, mitochondrial	aldehyde dehydrogenase 2 ESTs, Moderately similar to DHAM_RAT ALDEHYDE DEHYDROGENASE, family (mitochondrial), MITOCHONDRIAL PRECURSOR (ALDH CLASS 2) (ALDH1) (ALDH-E2) aldehyde [R.norvegicus], RIKEN cDNA 2410004H02 gene, aldehyde dehydrogenase 1 family, member B1, aldehyde dehydrogenase 2 family (mitochondrial), aldehyde dehydrogenase 2, mitochondrial
3678	23884	NM_031731	ח	aldehyde dehydrogenase 3 family, member A2, aldehyde dehydrogenase family 3, subfamily A2	aldehyde dehydrogenase 3 family, member A2, aldehyde dehydrogenase family dehydrogenase 3 family, member A2, aldehyde dehydrogenase family 3, subfamily 3, subfamily A2 A2, expressed sequence AI848594
1852	16884	Al103758	000	aldehyde dehydrogenase 9 family, member A1, aldehyde dehydrogenase 9, subfamily A1	Mus musculus, Similar to aldehyde dehydrogenase 4 family, member A1, clone IMAGE:5102023, mRNA, partial cds, RIKEN cDNA 1110038105 gene, aldehyde dehydrogenase 4 family, member A1, aldehyde dehydrogenase 9 family, member A1, aldehyde dehydrogenase 9, subfamily A1
1890		16885 Al105188	PP, General Core Tox Markers	aldehyde dehydrogenase 9 family, member A1, aldehyde dehydrogenase 9, subfamily A1	Mus musculus, Similar to aldehyde dehydrogenase 4 family, member A1, clone IMAGE:5102023, mRNA, partial cds, RIKEN cDNA 1110038105 gene, aldehyde dehydrogenase 4 family, member A1, aldehyde dehydrogenase 9 family, member A1, aldehyde dehydrogenase 9 family, member A1, aldehyde dehydrogenase 9, subfamily A1

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	(1) No.	ලෙකවෙකා?  ක්ෂේ ගැ  ශ්ණීමල් (D	Hw Model Gode K	Human Homologous Known Gene Namer	imani Homologous swn Gener Namer Human Ho <mark>molog</mark> ous Sequence (dusteratitie
4026	9606	NM_145771	RRR	aldehyde reductase (aldose reductase) like 6, aldehyde reductase (aldose reductase)-like 6	aldehyde reductase (aldose reductase) like 6, aldehyde reductase (aldose reductase)- like 6
3060	7062	NM_012495		aldolase 1, A isoform, aldolase A, fructose- bisphosphate	EST, Moderately similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], EST, Weakly similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], ESTs, Highly similar to 139435 fructose-bisphosphate aldolase [H.sapiens], ESTs, Moderately similar to aldolase A [M.musculus], ESTs, Weakly similar to ALFA_HUMAN FRUCTOSE-aldolase 1, A isoform, BISPHOSPHATE ALDOLASE A [H.sapiens], Mus musculus, clone MGC:25455 aldolase A, fructose-bisphosphate A isoform, aldolase 3, C isoform, aldolase A, fructose-bisphosphate
3060	. 2063	NM_012495	0, P, PP, QQ, UU, W	isoform, uctose-	EST, Moderately similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], EST, Weakly similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], ESTs, Highly similar to 139435 fructose-bisphosphate aldolase [H.sapiens], ESTs, Moderately similar to aldolase A [M.musculus], ESTs, Weakly similar to ALFA_HUMAN FRUCTOSE-aldolase 1, A isoform, BISPHOSPHATE ALDOLASE A [H.sapiens], Mus musculus, clone MGC:25455 aldolase A, fructose-limAGE:4241025, mRNA, complete cds, RIKEN cDNA 4933425L11 gene, aldolase 1, A isoform, aldolase 3, C isoform, aldolase A, fructose-bisphosphate
3060	7064	NM_012495	II, VV, PPP, General Core	aldolase 1, A isoform, aldolase A, fructose- bisphosphate	EST, Moderately similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], EST, Weakly similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], ESTs, Highly similar to 139435 fructose-bisphosphate aldolase [H.sapiens], ESTs, Moderately similar to aldolase A [M.musculus], ESTs, Weakly similar to ALFA_HUMAN FRUCTOSE-to aldolase A [M.musculus], ESTs, Weakly similar to ALFA_HUMAN FRUCTOSE-to aldolase A [M.sapiens], Mus musculus, clone MGC:25455 and A fructose-limage and aldolase A [M.sapiens], Riken CDNA 4933425L11 gene, aldolase 1, sphosphate

Aitomey Docket 4492A-5059-01W0	Tuman Homologous กับman Homologous กัดองงก (Gene Name ) Human Homologous Sequence (Gluster IIII)ใช้	m, Mus musculus, clone MGC:25455 IMAGE:4241025, mRNA, complete cds, aldolase 1, A isoform, aldolase 3, C isoform, aldolase B, fructose-bisphosphate		Alg5, S. cerevisiae, homolog of	Mus musculus, clone MGC:30545 IMAGE:5044495, mRNA, complete cds, RIKEN ry cDNA 2600015J22 gene, allograft inflammatory factor 1, expressed sequence Al607846	in, RIKEN cDNA 1700013L23 gene, WAP, FS, Ig, KU, and NTR-containing protein, alpha 1 microglobulin/bikunin, alpha-1-microglobulin/bikunin precursor, complement component 8, gamma polypeptide, serine protease inhibitor, Kunitz type 2	-	
	Human Homologous Known Gene Name	aldolase 2, B isoform, aldolase B, fructose- bisphosphate	aldolase 2, B isoform aldolase B, fructose- bisphosphate	Alg5, S. cerevisiae, homolog of	allograft inflammatory factor 1	alpha 1 microglobulin/bikunin alpha-1- microglobulin/bikunin precursor	alpha 1 microglobulin/bikunin alpha-1- microglobulin/bikunin precursor	alpha 1 microglobulin/bikunin alpha-1- microglobulin/bikunin precursor
	Checkler (Code	В, РРР, QQQ	HH, SS	a S Z	> ×	NNN SS	Z	חחח
	Ceneral Age or Referent	AA892395	X02291	AA998062	NM 017196	1	NM 012901	NM_012901
ଜ	alec Diver	. 820	818	16625	16269	7897	7898	7899
		562	4183	1161	3305	3172	3172	3172

	38				
See 10	erec Idno	ල්කෙන්කැකි කිලේකේ ි  RefSegillම	Medal Geels	Human Homologous Known Gener Name	Human Homologous   Known Gene Name
3059	23942	NM_012493	General Alternate	alpha fetoprotein, alpha-fetoprotein	ESTs, Weakly similar to FETA_RAT Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-fetoprotein) [R.norvegicus], alpha fetoprotein, alpha-fetoprotein
3152	20587	NM_012826	0, P, W	alpha-2-glycoprotein 1, zinc	UL16 binding protein 1, UL16 binding protein 2, alpha-2-glycoprotein 1, zinc
3170	16274	NM_012898 M, S, SS,	=	sha-2-HS-	alpha-2-HS-glycoprotein
3170	16275	NM_012898	S, FF, HH, SS, NNN	pha-2-HS- ycoprotein	alpha-2-HS-glycoprotein
3057	22512	NM_012488	BB, NN, EEE, MMM	alpha-2-macroglobulin	ESTs, Highly similar to A2MG_RAT ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) [R.norvegicus], ESTs, Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR [M.musculus], alpha-2-macroglobulin, pregnancy-zone protein
3057	22513	NM_012488	A, E, W, BB, UU, EEE, MMM	alpha-2-macroglobulin	ESTS, Highly similar to A2MG_RAT ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) [R.norvegicus], ESTS, Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR [M.musculus], alpha-2-macroglobulin, pregnancy-zone protein
3057	22514	NM_012488	BB, NN, UU	alpha-2-macroglobulin	ESTs, Highly similar to A2MG_RAT ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) [R.norvegicus], ESTs, Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR [M.musculus], alpha-2-macroglobulin murinoglobulin 1, pregnancy-zone protein
3057	22515	NM_012488	E, W, BB, NN, OO, EEE, III, JJJ, KKK, MMM	alpha-2-macroglobulin	ESTs, Highly similar to A2MG_RAT ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) [R.norvegicus], ESTs, Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR [M.musculus], alpha-2-macroglobulin, murinoglobulin 1, pregnancy-zone protein
3081	17237	NM_012562 XX, YY		alpha-L-fucosidase, fucosidase, alpha-L- 1, tissue	

TABL	VENE 3				Atterney, Doctret 14:92/1-5088-01W/0
00 00 00	elec Tono Tono	රෙකවෙනි. Accor Re(පිදෝ [මු	Model Gode	Human Homologous Known Genel Name	
3149	15032	NM 012816	> ×	alpha-methylacyl-CoA racemase	alpha-methylacyl-CoA alpha-methylacyl-CoA racemase, cDNA sequence AF397014, chromosome 7 open racemase
				amelogenin, amelogenin (X chromosome,	
4052	1937	R46934	НН	amelogenesis imperfecta 1)	
				amiloride binding	EST, Moderately similar to amiloride binding protein 1 [Rattus norvegicus] [R.norvegicus], EST, Weakly similar to amiloride binding protein 1 [Rattus norvegicus]
				protein 1 (amine oxidase (copper-	[R.norvegicus], EST, Weakly similar to amiloride binding protein [Rattus norvegicus]   IR.norvegicus], ESTs. Moderately similar to AOC3 MOUSE MEMBRANE COPPER
·				containing)), amiloride bindina	AMINE OXIDASE [M.musculus], ESTs, Weakly similar to AOC3 MOUSE MEMBRANE COPPER AMINE OXIDASE [M.musculus]. RIKEN cDNA 1600015110 gene, amiloride
				protein 1 (amine	binding protein 1 (amine oxidase (copper-containing)), amiloride binding protein 1
3521	16184	NM 022935	Z, AA	oxidase, copper- containing)	(amine oxidase, copper-containing), amine oxidase, copper containing 3, androgen- responsive protein pSv-2
		1		amine oxidase,	
				copper containing 3,	
				amine oxidase,	
				(vascular adhesion	
4163	25083	U72632	RR	protein 1)	
			L, CC, DD,		
			KKK, 000,		
			General Core		
			Tox Markers,	:	
			General	aminolevulinate, delta	
3171	18564	NM_012899 Alternate	Alternate	l, dehydratase	aminolevulinate, delta-, dehydratase

	<b>3</b> 3				Afterney Docket 44921-5085-01WO
	erec Id No	Consent Récor Réseq (D:			1.00
				aminolevulinate, delta-	
				, synthase 1,	aminolevulinate, delta-, synthase 1, aminolevulinic acid synthase 1, aminolevulinic
				aminolevulinic acid	acid synthase 2, erythroid, serine palmitoyltransferase, long chain base subunit 1,
1384	21040	AI011734	K, L	synthase 1	serine palmitoyltransferase, long chain base subunit 2
				aminolevulinate, delta	
				, synthase 1,	aminolevulinate, delta-, synthase 1, aminolevulinic acid synthase 1, aminolevulinic
				aminolevulinic acid	acid synthase 2, erythroid, serine palmitoyltransferase, long chain base subunit 1,
3561	21038	NM_024484	F	synthase 1	serine palmitoyltransferase, long chain base subunit 2
				aminolevulinate, delta-	
				, synthase 1,	aminolevulinate, delta-, synthase 1, aminolevulinic acid synthase 1, aminolevulinic
				aminolevulinic acid	acid synthase 2, erythroid, serine palmitoyltransferase, long chain base subunit 1,
3561	21039	NM 024484	К, ФФ, П	synthase 1	serine palmitoyltransferase, long chain base subunit 2
				amino-terminal	
3373	2078	NM_019220	S, V	enhancer of split	amino-terminal enhancer of split
			General	amino-terminal	
3373	2079	NM_019220	_	enhancer of split	amino-terminal enhancer of split
			.000 '999	amylase 1, salivary,	ESTs, Moderately similar to AMYP_HUMAN ALPHA-AMYLASE, PANCREATIC
				amylase, alpha 1A;	PRECURSOR [H.sapiens], amylase 1, salivary, amylase 2, pancreatic, amylase,
3633	24645	NM_031502	Tox Markers	salivary	alpha 1A; salivary, amylase, alpha 2A; pancreatic
				amyloid beta (A4)	
				precursor protein	ESTs, Highly similar to 139451 amyloid-beta protein [H.sapiens], ESTs, Weakly similar
				(protease nexin-II,	to S23094 beta-amyloid protein precursor - rat [R.norvegicus], amyloid beta (A4)
220	10157	AA819527	XX, Y≺	Alzheimer disease)	precursor protein (protease nexin-II, Alzheimer disease)
				amyloid beta (A4)	
				precursor protein	ESTs, Highly similar to 139451 amyloid-beta protein [H.sapiens], ESTs, Weakly similar
				(protease nexin-II,	to S23094 beta-amyloid protein precursor - rat [R.norvegicus], amyloid beta (A4)
1018	10155	AA956735	>	Alzheimer disease)	precursor protein (protease nexin-II, Alzheimer disease)

		3		THE PROCEEDINGS IN THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF TH
(190 (No.	centents lace or Refreq ID	Modell Gode	Human Komologous Knovni Gene Name	tuman Komologous known Gene Name   HumantHomologous Sequence Gusterittte
11260	X77934	ww	amyloid beta (A4) precursor-like protein 2	amyloid beta (A4) ESTs, Weakly similar to 2019243A amyloid precursor-like protein 2 [Rattus norvegicus] precursor-like protein [R.norvegicus], ESTs, Weakly similar to EPPI_MOUSE Eppin precursor [M.musculus], amyloid beta (A4) precursor-like protein 1, amyloid beta (A4) precursor-like protein 2
8182	NM_017170	GG, LL, MM, CCC, GGG, RRR, TTT	amyloid P component, serum, aerum amyloid P-component	EST, Weakly similar to S11473 serum amyloid P-component - rat [R.norvegicus], EST, myloid P component, Weakly similar to SAMP MOUSE SERUM AMYLOID P-COMPONENT PRECURSOR erum, serum [M.musculus], ESTs, Weakly similar to SAMP_HUMAN SERUM AMYLOID P-myloid P-component   COMPONENT PRECURSOR [H.sapiens], amyloid P component, serum
21097	M12112	C, I, O, P, MM, NNN, TTT, General Core Tox Markers	angiotensinogen, angiotensinogen (serine (or cysteine) proteinase inhibitor, ciade A (alpha-1 antiproteinase, antitrypsin), member 8)	angiotensinogen, angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8)
21098 7197	C, L, DD, NM 134432 NNN NM 012904 O, P, VV	C, L, DD,	angiotensinogen, angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8)	angiotensinogen, angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8)

TABUE 8	3.9				
ි ද ගුම		Censent Aee or Resse D	Model Gode		uman Homologous nown Cenelvame Human Homologous Sequence Chister Title
					EST, Moderately similar to 0806162C protein COI [M.musculus], EST, Moderately
					similar to 810024C cytochrome oxidase i [H.sapiens], EST, Weakty similar to 0806162C protein COI [M.musculus], ESTs, Highly similar to hydroxyacid oxidase 3
				annexin A2,	(medium-chain) [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to
				hydroxyacid oxidase	hydroxyacid oxidase   0806162C protein COI [M.musculus], ESTs, Moderately similar to 810024C
				(glycolate oxidase) 3,	cytochrome oxidase I [H.sapiens], ESTs, Weakly similar to 0806162C protein COI
			O, W, EEE,	hydroxyacid oxidase 3	[M.musculus], annexin A2, annexin A9, hydroxyacid oxidase (glycolate oxidase) 3,
3412	574	NM_019905   MMM	MMM	(medium-chain)	hydroxyacid oxidase 1, liver
					ESTs, Moderately similar to ANX4 MOUSE ANNEXIN IV [M.musculus], ESTs, Weakly
					similar to ZAP 36/annexin IV [Rattus norvegicus] [R.norvegicus], Mus musculus,
					Similar to annexin A8, clone MGC:13875 IMAGE:4013266, mRNA, complete cds,
2699	8440	AI235611	⊢	annexin A4	annexin A13, annexin A4, annexin A8
					ESTs, Moderately similar to ANX4 MOUSE ANNEXIN IV [M.musculus], ESTs, Weakly
					similar to ZAP 36/annexin IV [Rattus norvegicus] [R.norvegicus], Mus musculus,
					Similar to annexin A8, clone MGC:13875 IMAGE:4013266, mRNA, complete cds,
- 1		NM_024155   O,	О, Р	annexin A4	annexin A13, annexin A4, annexin A8
3920	21391	NM_130416	Х, Ү	annexin A7	annexin A11, annexin A13, annexin A7
				anti-oxidant protein 2	
				(non-selenium	
				glutathione	
				peroxidase, acidic	ESTs, Moderately similar to AOP2 MOUSE ANTIOXIDANT PROTEIN 2 [M.musculus],
				calcium-independent	ESTs, Moderately similar to AOP2_HUMAN ANTIOXIDANT PROTEIN 2 (H.sapiens),
			G, H, L, N,	phospholipase A2),	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-
3793	19252	NM_053576	王	peroxiredoxin 5	independent phospholipase A2), peroxiredoxin 5

	<b>3</b> 3				
	ELEC PONO.	Genernk Aee or Rasseg ID	Medel Geeb	Human Homologous Kinown Gene Name	Human Homologous   Human Homologous Sequence Gluster Title:
				anti-oxidant protein 2 (non-selenium	
				glutathione	
				peroxidase, acidic calcium-independent	ESTS, Moderately similar to AOP2 MOUSE ANTIOXIDANT PROTEIN 2 [M.musculus], ESTs. Moderately similar to AOP2 HUMAN ANTIOXIDANT PROTEIN 2 [H.saoiens].
			:	phospholipase A2),	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-
3793	19253	NM_053576	В	peroxiredoxin 5	independent phospholipase A2), peroxiredoxin 5
				anti-oxidant protein 2	
				(non-selenium	
				glutathione	
				peroxidase, acidic	ESTs, Moderately similar to AOP2 MOUSE ANTIOXIDANT PROTEIN 2 [M.musculus],
				calcium-independent	ESTs, Moderately similar to AOP2_HUMAN ANTIOXIDANT PROTEIN 2 [H.sapiens],
				phospholipase A2),	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-
3793	19254	NM_053576	G, H, L	peroxiredoxin 5	independent phospholipase A2), peroxiredoxin 5
				APEX nuclease	-
				(multifunctional DNA	
				repair enzyme),	
				apurinic/apyrimidinic	APEX nuclease (multifunctional DNA repair enzyme), Mus musculus ape2 mRNA for
3537	20801	NM_024148	FFF, QQQ	endonuclease	AP endonuclease 2, complete cds, apurinic/apyrimidinic endonuclease
					ESTs, Weakly similar to apolipoprotein A-I [Rattus norvegicus] [R.norvegicus],
2979	427	M00001	၁၁၁	apolipoprotein A-I	apolipoprotein A-I
3132	5318	NM_012737	PP, QQ	apolipoprotein A-IV	apolipoprotein A-IV, desmoplakin (DPI, DPII)
3132	18236	NM_012737	۸	apolipoprotein A-1V	apolipoprotein A-IV, desmoplakin (DPI, DPII)
3132	5317	NM_012737	BBB, CCC	apolipoprotein A-IV	
					EST, Moderately similar to LPHUC1 apolipoprotein C-I precursor [H.sapiens], RIKEN
3151	23670	NM_012824		apolipoprotein C-I	cDNA 4932417P04 gene, apolipoprotein C-1, apolipoprotein Cl
3061	17785	NM 012501	Μ, <	apolipoprotein C-III	apolipoprotein C-III, apolipoprotein CIII
3061	17787	NM 012501	S, DD, EE, HH. XX. YY	apolipoprotein C-III	apolipoprotein C-III. apolipoprotein CIII

@ G		Γ	Т	Г				Т		T	$\neg$					_		Γ				_				<u></u>		
		apolipoprotein E	aquaporin 8						arginase 1, liver, arginase, liver		arginine vasopressin receptor 1B					arginine vasopressin, arginine vasopressin (neurophysin II, antidiuretic hormone,	diabetes insipidus, neurohypophyseal)			argininosuccinate synthetase, argininosuccinate synthetase 1, expressed sequence	AA408052	AAAA III Gaaa aa ah ah ah ah ah ah ah ah ah ah ah	ARR'S actin-related protein 3 nomolog (yeast), EST, Weakly Similar to ARR'S TOWAN	ACTIN-LIKE PROTEIN SIN SAPIENSI, EST, Weakly Similar to ATKI actin, Skeletal	muscle - rat [R.norvegicus], ESTs, Moderately similar to ARP3_HUMAN ACTIN-LIKE	PROTEIN 3 [H.sapiens], ESTs, Weakly similar to ATHU actin alpha 1, skeletal muscle	[H.sapiens], Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955, actin-related	protein 3-beta, hypothetical protein FLJ12785, mitochondrial ribosomal protein L47
	HumaniHomologous Known Genei Name	apolipoprotein E	aquaporin 8				aquaporin 9	arginase 1, liver,	arginase, liver	arginine vasopressin	receptor 1B	arginine vasopressin,	arginine vasopressin	(neurophysin II,	antidiuretic hormone,	diabetes insipidus,	neurohypophyseal)	argininosuccinate	synthetase,	argininosuccinate	synthetase 1			ARP3 actin-related	protein 3 homolog	(yeast), actin-related	protein 3 homolog	(yeast)
	(1) (1)			о В	<u> (</u>	o y															888							
	ම් ම		노	S, U, X	EE, DDD,	LLL, 000,	ý ∑	General	Alternate								₹				, Β Υ							O, W, HHH
	88	8	8 KKK	<u>ن</u>	Ш:	7 8		ပ	₹	-:	z						2 Z,				ပ							힉
	<u>ලට දින්නේ ගින</u> මටමට දින්නේ ග සම්බන්නේ සමාන්න්	NM_138828	NM_019158				NM 022960		NM_017134		AF064541						NM_016992				X12459							AI230743
8	ा.''' जा.ल्ट © No.	6400	21090				15755		24693		145						24869				20597							23013
3 ETTEN		3983	3362				3528	Γ	3283		1238					_	3244				4194							2503

	5.8°.				Atterney Docket (1924-5038-0100)
68 (19	euge Ib No.	Consent Ace or ReSeq (D	Modeli Gode	Human Homologous Known GeneName	Human Homologous    Knovn CeneName   Human Homologous Sequence © uster Mile
3303	24670	NM_017189	١	asialoglycoprotein receptor 2	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 6, C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 7, C-type lectin related f, RIKEN cDNA 1810029C22 gene, asialoglycoprotein receptor 2
4093	1583	U07201	E, GG, III, JJJ	asparagine synthetase	
3241	15610	NM_016987	Z, AA	ATP citrate lyase	ATP citrate lyase, EST, Moderately similar to SUCA_MOUSE SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITOCHONDRIAL PRECURSOR (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) [M.musculus], expressed sequence AW538652, succinate-CoA ligase, GDP-forming, alpha subunit
3241	15612	NM_016987	BB, 6	ATP citrate lyase	ATP citrate lyase, EST, Moderately similar to SUCA_MOUSE SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITOCHONDRIAL PRECURSOR (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) [M.musculus], expressed sequence AW538652, succinate-CoA ligase, GDP-forming, alpha subunit
3241	15613	NM_016987	E, J, ww, OOO, General Core Tox Markers, General Alternate	ATP citrate lyase	ATP citrate lyase, EST, Moderately similar to SUCA_MOUSE SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITOCHONDRIAL PRECURSOR (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) [M.musculus], expressed sequence AW538652, succinate-CoA ligase, GDP-forming, alpha subunit
,	2000	NIM OFSERS	0		ATP synthase, H+ transporting, mitochondrial F0 complex subunit F, ATP synthase,
2005		ZUOSCU_MIN	z, x	complex, subunit F6	H+ transporting, mitochondrial F0 complex, subunit F6

Altomay Docket 44921-5008-01170	Human Homologous Sequence Gustermide	ATP synthase, H+ transporting, mitochondrial F0 complex subunit F, ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit, RIKEN cDNA 2410043G19 gene, expressed sequence AV000645		ATPase, Class II, type 9A, EST, Highly similar to AT2A_HUMAN POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IIA [H.sapiens], ESTS, Moderately similar to AT2A_HUMAN POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IIA [H.sapiens], ESTS, Weakly similar to AT2A_HUMAN POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IIA [H.sapiens], Homo sapiens mRNA; cDNA DKFZp58610624 (from clone DKFZp58610624)
	KinowniGenelName	ATP synthase, H+ transporting, mitochondrial F0 complex subunit F, ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATPase, Class II, type 9A, ATPase, class II, type 9A
	Modeli Gode	. 11	>	RRR	PP, QQ	, χ Χ,
	General Legion Refeeq 10 =	NM_053602	NM_133556	NM_139099	NM_017290	7.687.0
্ৰিন্ত	(euge (b) (v)	20726	15524	17203	12350	1359
	Seo [D	3802	3948	4002	3331	4173

	ाइ ३ ः				(人) (100 may Docket 4492/1-5038-9/1/7/0) (100 may Docket 4492/1-5038-9/1/7/0)
	elec D No.	Consent Accor Roßeg (D	Wodel Gode	Rumani Homologous Knowni Gene Name	umani Homologous Jown Gene Name   HumaniHomologous Sequence (Gluster Mile)
				ATPase, H+/K+	
			····	exchanging, alpha polypeptide, ATPase.	
2923	1577	302649	۵	H+/K+ transporting, alpha polypeptide	
				ATPase, Na+/K+	ATPase, Na+/K+ transporting, alpha 1 polypeptide, ATPase, Na+/K+ transporting,
3062	15675	NM_012504 H, DD,	H, DD, EE	alpha 1	alpha 4 polypeptide, Mus musculus, Similar to ATPase, Na+/K+ transporting, alpha 1a.1 polypeptide, clone IMAGE:3599053, mRNA, partial cds
					ATPase, Na+/K+ transporting, alpha 1 polypeptide, ATPase, Na+/K+ transporting,
3062	15677	NM_012504	NM_012504 N, RR, WW	transporting, alpha 1 polypeptide	alpha 4 polypeptide, Mus musculus, Similar to ATPase, Na+/K+ transporting, alpha 1a.1 polypeptide, clone IMAGE:3599053, mRNA, partial cds
					ATPase, Na+/K+ transporting, beta 3 polypeptide, ESTs, Highly similar to
3176	18119	NM_012913_VV	W	transporting, peta 3 polypeptide	ATING_HOMAN SOUIDM/POTASSIOM-TRANSPORTING ATPASE BETA-3 CHAIN [H.sapiens], expressed sequence AI664000
				ATP-binding cassette,	
				sub-family B (MDR/TAP), member	sub-family B ATP-binding cassette, sub-family B (MDR/TAP), member 4, ESTs, Highly similar to (MDR/TAP), member MDR3 HUMAN MULTIDRUG RESISTANCE PROTEIN 3 fH.sapiens]. ESTs. Weakly
				1A, ATP-binding	similar to B54774 ATP binding cassette transporter ABC2 - human [M.musculus], Mus
				nily	musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library,
3115	3115 24453	NM_012690	٨	b (MDR/1AP), member 4	cione:2810428N17:A1P-binding cassette, sub-family B (MDR/TAP), member 10, full insert sequence

Sode Known Genel Name: HumantHomologous/Sequence eluster Title:	ATP-binding cassette, sub-family B (MDR/TAP), member 2, ESTs, Highly similar to binding cassette, sub-family B (MDR/TAP), member 2, ESTs, Highly similar to binding cassette, sub-S13426 multidrug resistance protein homolog - rat [R.norvegicus], transporter 1, ATP-family B (MDR/TAP)	ATP-binding cassette, sub-family B (MDR/TAP), member 3, ATP-binding cassette, 3, transporter 2, ATP-binding cassette, sub-family B (MDR/TAP), member 3, ATP-binding cassette, binding cassette, sub-family B (MDR/TAP), member 9, transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	e, ATP-binding cassette, sub-family C (CFTR/MRP), member 2, ATP-binding cassette, sub-family C (CFTR/MRP), member 4, expressed sequence AI173996	e, ATP-binding cassette, sub-family C (CFTR/MRP), member 6
Known Genel Name	ATP-binding cassette, sub-family B (MDR/TAP), member 2, transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	ATP-binding cassette, sub-family B (MDR/TAP), member 3, transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	VV, FFF, GGG, III, JJJ, ATP-binding cassette, KKK, OOO, sub-family C General Core (CFTR/MRP), Tox Markers member 6
Model Gods	=	ΩΩ		VV, FFF, GGG, III, JJJ, KKK, OOO, General Core Tox Markers
Consent Resor Resseq (D	X67523	X63854	NN, UU, NM_012833_KKK, NNN	VV, FFF, GGG, III, JJ, KKK, OOO, General Core 15700 NM_031013 Tox Markers
E 3	1037	515	373	15700
TABLE 3 Seq. (C)	4223	4245	3153	3582

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Sed De.	erec In No.	ලෙකළකාය  යුලේ මැිි  යිමෙලේ [Dි	्रिक्ता हर्जा	ode   Known Cene Name	HumaniHomologous/Sequence:@lusteratitide:
1244	25211	AF087839	sss, uuu	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9, ESTs, Weakly similar to T42751 sulfonylurea receptor 2 - rat [R.norvegicus], Homo sapiens cDNA FLJ31957 fis, clone NT2RP7007381, highly similar to Sulfonylurea receptor 2A, Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330439B14:ATP-binding cassette, sub-family C (CFTR/MRP), member 9, full insert sequence
3201	730	NM_013040	E, Z, AA,	ATP-binding cassette, sub-family C (CFTR/MRP), RR member 9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9, ESTs, Weakly similar to ATP-binding cassette, T42751 sulfonylurea receptor 2 - rat [R.norvegicus], Homo sapiens cDNA FLJ31957 fis, clone NT2RP7007381, highly similar to Sulfonylurea receptor 2A, Mus musculus adult (CFTR/MRP), male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330439B14:ATP-member 9 full insert sequence
3145	21729	NM_012804	WW, RRR, SSS	ATP-binding cassette, sub-family D (ALD), member 3	ATP-binding cassette, sub-family D (ALD), member 3, ATP-binding cassette, sub-family D (ALD), member 4, ESTs, Weakly similar to A35723 70K peroxisomal membrane protein - rat [R.norvegicus]
3145	21730	NM_012804	K, U, FF	ATP-binding cassette, sub-family D (ALD), member 3	ATP-binding cassette, ATP-binding cassette, sub-family D (ALD), member 3, ATP-binding cassette, subsub-family D (ALD), family D (ALD), member 4, ESTs, Weakly similar to A35723 70K peroxisomal member 3
				esis	BAI1-associated protein 2, ESTs, Weakly similar to brain-specific angiogenesis inhibitor 1-associated protein 2 [Mus musculus] [M.musculus], Mus musculus, Similar to KIAA0429 gene product, clone IMAGE:2811240, mRNA, partial cds, RIKEN cDNA
2309	.	A1178652	RR		1300006M19 gene, brain-specific angiogenesis inhibitor 1-associated protein 2, hypothetical protein FLJ22582, insulin receptor tyrosine kinase substrate
3139	11938	NM_012783	X, Y, EE	basigin, basigin (OK iblood group)	ESTs, Weakly similar to A46506 leukocyte activation antigen M6 [H.sapiens], Mus musculus, Similar to spindle pole body protein, clone IMAGE:5324982, mRNA, partial cds, basigin, basigin (OK blood group), spindle pole body protein
3245	24897	NM_016993	gg	B-cell CLL/lymphoma 2, B-cell leukemia/lymphoma 2	

	3.8				October 14921-6068-011WO
ි. මුගු ඔ	@ @ @ @ @ W	Kenenk Regor Reseq (D	Medal Gede	25.52	Iman Homologous Sovn Gene Name : Human Homologous Sequence (Ruster III/16)
2968	ō.	- 26268	N, BB, CC, DD, HH, III, JJJ, KKK, NNN, General	_ 🛦 🖰 🖰	B-cell translocation gene 1, anti-proliferative, Homo sapiens cDNA FLJ30547 fis, clone BRAWH2001439, transducer of ERBB2, 1, transducer of ERBB2, 2, transducer of
2968	20		BB, CC, DD, LL, UU, III, JJJ, KKK, NNN, General Alternate	B-cell translocation gene 1, anti- proliferative	B-cell translocation gene 1, anti-proliferative, Homo sapiens cDNA FLJ30547 fis, clone BRAWH2001439, transducer of ERBB2, 1, transducer of ERBB2, 2, transducer of ErbB-2.1
3319	15299	NM_017259	W, II, KKK, OOO, General Core Tox Markers	B-cell translocation gene 2, anti- proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 4, BTG family, member 2, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]
3319		NM_017259	W, II	B-cell translocation gene 2, anti- proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 4, BTG family, member 2, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]
3319	15301	NM_017259	A, B, W, II	B-cell translocation gene 2, anti- proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 4, BTG family, member 2, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]
4149	912	U59184	QQ, UU, General Core Tox Markers	BCL2-associated X protein, Bcl2-associated X protein	
3064	7427	NM_012515	O, P, NN, OO, VV, EEE, MMM	benzodiazapine receptor (peripheral), benzodiazepine receptor, peripheral	ESTs, Weakly similar to 138724 mitochondrial benzodiazepine receptor [H.sapiens], benzodiazapine receptor (peripheral),

	ිමු ම				Altornay Docket 44921-5069-01100
නිලේ ම	eleg Dina	Gensenix   Ase or =   RefSeq (D=	Model Gode	Human Homologous Known Gene Name	1bmain/Homologous  ທັດວັນທີ່ເຮັດຄຣິName   Human Homologous Sequence (dioster Titili)
3252	17815	NM_017015 NNN	NNN	beta-glucuronidase, glucuronidase, beta	ESTs, Highly similar to A26581 beta-glucuronidase [H.sapiens], SMA3, beta-glucuronidase structural, glucuronidase, beta
_				bile acid Coenzyme A: amino acid N-	
				acyltransferase	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [Heanjane] Mus musculus Similar to hile acid Coopying A: aming acid N
				choloyltransferase),	acyltransferase (glycine N-choloyltransferase), clone MGC:19156 IMAGE:4220620,
				bile acid-Coenzyme A:	bile acid-Coenzyme A: mRNA, complete cds, bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-
			00, PP, QQ,	amino acid N-	choloyltransferase), bile acid-Coenzyme A. amino acid N-acyltransferase, expressed
5866	1531	D43964	РРР, ООО	acyltransferase	sequence Al118337
		<del></del>			ESTs, Highly similar to BMP2_RAT Bone morphogenetic protein 2 precursor (BMP-2)
					GROWTH/DIFFERENTIATION FACTOR 3 PRECURSOR [M.musculus], bone
				bone morphogenetic	morphogenetic protein 2, growth differentiation factor 5 (cartilage-derived
88	22504	AA944827	Q, R	protein 2	morphogenetic protein-1), nodal
			I, J, U, FF,	brain.acyl-CoA	
3235	397	NM 013214	888	hydrolase	
			BBB, CCC,	brain acyl-CoA	
3235	20851	NM_013214	RRR, SSS	hydrolase	
				brain acyl-CoA	
4136	396	U49694	NNN	hydrolase	

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(S)	୍ଟୋଡ୍ର ଆହାନ୍ଧତ	ලෙක්වෙක්දූ Xee ලැ RefSeq ID ැ	Model Gode		HumaniHomologous KnowniGene Names HumaniHomologous Sequence @uster™ile
				branched chain keto	
				acid dehydrogenase	
				(maple syrup urine	
	· 	<del></del>		disease), branched	
			, ××, ××,	dehydrogenase E1,	
2925	17284	J02827	EEE, MMM	alpha polypeptide	
				branched chain keto	
<del></del>				acid dehydrogenase	
				E1, beta polypeptide	
			· — .	(maple syrup urine	EST, Highly similar to ODBB_RAT 2-OXOISOVALERATE DEHYDROGENASE BETA
				disease), branched	SUBUNIT, MITOCHONDRIAL PRECURSOR (BRANCHED-CHAIN ALPHA-KETO
				chain Ketoacio	ACID DEHYDROGENASE COMPONENT BETA CHAIN (E1)) (BCKDH E1-BETA)
1990	5232	A1168942	ww	denydrogenase E1,	[K.norvegicus], branched chain keto acid dehydrogenase E1, beta polypeptide (maple   svriin urine disease), hranched chain ketoacid dehydrogenase E1, heta polyneotide
				brevican, chondroitin	
				sulfate proteoglycan	
4123	433	U37142	RR	BEHAB/brevican	
2969	1632	L27487	99	calcitonin receptor-like calcitonin receptor-like	calcitonin receptor-like
				calcium/calmodulin-	
				dependent protein kinase) II	
				beta,	
				calcium/calmodulin-	
3430	17976	NM 021739	<u>z</u> \	dependent protein kinase II. beta	

TANSILE 3	39	A THE STREET OF THE STREET			Attorney Docket 4492/1-6038-0/WO
Seq. 10	GLGG. ID No:	(ट्यान्हामार Ace or Rassog (D	Model Gode	Humani He Kaowin Ge	Humani Homologous   Humani Homologous Sequence Ouster mile
				calmodulin 1,	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase,
				calmodulin 1	delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3,
2744	10101	034060	c	(phosphorylase	calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence
	18181	8081 CO MIN		Kinase, deita)	Al3Z/UZ/, expressed sequence ALUZ4UUU, troponin C, tast skeletal
				calmodulin 1,	RIKEN cDNA 2310068022 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase,
			,	Calmodulin I	delta), calmodulin z, calmodulin z (phosphorylase kinase, delta), calmodulin 3,
3711	25802	NM 031969	ה ה ה ה	(phosphorylase	calmodulin-like 3, centrin 1, centrin, Er-hand protein, 1, expressed sequence
		200100	ייייי יאויאוואו	ningae, della	Aloziozi, expressed sequence Alozagou, iloponini C, iasi skeletal
				calmodulin 2,	KIKEIN CUINA 2310068022 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase,
			•	calmodulin 2	delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3,
				(phosphorylase	calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence
3342	20809	NM_017326	¥	kinase, delta)	Al327027, expressed sequence AL024000, troponin C, fast skeletal
				calmodulin 3,	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase,
				calmodulin 3	delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3,
				(phosphorylase	calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence
88	15476	AA944426	ZZ, AAA	kinase, delta)	Al327027, expressed sequence AL024000, troponin C, fast skeletal
				calmodulin 3,	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase,
				calmodulin 3	delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3,
				(phosphorylase	calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence
3066	20518	NM_012518	œ	kinase, delta)	Al327027, expressed sequence AL024000, troponin C, fast skeletal
					ESTs, Weakly similar to CAN1_MOUSE CALPAIN 1, LARGE [CATALYTIC] SUBUNIT
			[1	_	(CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE) [M.musculus],
3360	20863	NM_019152	۵	(mu/l) large subunit	calpain 1, calpain 11, small optic lobes homolog (Drosophila)
3281	21538	NM 017116	<u>a</u>	calpain 2, calpain 2, (m/II) large subunit	RIKEN cDNA 2600002E23 gene. calbain 12. calbain 2. calbain 2. (m/ll) large subunit
					EST, Moderately similar to CAN3 MOUSE CALPAIN P94, LARGE [M.musculus].
					ESTs, Highly similar to A56218 calpain [H.sapiens], RIKEN cDNA 2310005G05 gene,
					calpain 3, calpain 3, (p94), calpain 9 (nCL-4), expressed sequence Al323605,
4176	1084	U89514	ΠΩ	calpain 9 (nCL-4)	programmed cell death 6

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ි ලිකි ම	GLGC DNo.	genzenik Agelor Refiseg (D	Modal ଜିବ୍ୟ	Kuman Homologous Known Genei Name	umaniylomologous  nown GeneiName   Humaniylomologous Sequence Gluster IIItle
593	17080	AA892814	Σ	calpain, small subunit	EST, Moderately similar to CAN3 MOUSE CALPAIN P94, LARGE [M.musculus], ESTs, Weakly similar to A55143 calpain (EC 3.4.22.17) light chain - rat (fragment) [R.norvegicus], Mus musculus, Similar to grancalcin, EF-hand calcium binding protein, calpain, small subunit clone MGC:29240 IMAGE:5044040, mRNA, complete cds, RIKEN cDNA 2310005G05 gene, calpain 3, calpain, small subunit 1, expressed sequence Al323605, sorcin
4141	17078	U53859	Σ	calpain, small subunit 1	EST, Moderately similar to CAN3 MOUSE CALPAIN P94, LARGE [M.musculus], ESTs, Weakly similar to A55143 calpain (EC 3.4.22.17) light chain - rat (fragment) [R.norvegicus], Mus musculus, Similar to grancalcin, EF-hand calcium binding protein, calpain, small subunit clone MGC:29240 IMAGE:5044040, mRNA, complete cds, RIKEN cDNA 2310005G05 gene, calpain 3, calpain, small subunit 1, expressed sequence Al323605, sorcin
4141	17079	U53859	Σ	calpain, small subunit	EST, Moderately similar to CAN3 MOUSE CALPAIN P94, LARGE [M.musculus], ESTs, Weakly similar to A55143 calpain (EC 3.4.22.17) light chain - rat (fragment) [R.norvegicus], Mus musculus, Similar to grancalcin, EF-hand calcium binding protein, calpain, small subunit clone MGC:29240 IMAGE:5044040, mRNA, complete cds, RIKEN cDNA 2310005G05 gene, calpain 3, calpain, small subunit 1, expressed sequence Al323605, sorcin
3401	23491	NM_019359	С, Е, DD, JJ, ММ, ННН, ТТТ	calponin 3, acidic	ESTs, Moderately similar to CALPONIN H1, SMOOTH MUSCLE [M.musculus], calponin 2, calponin 3, acidic
					ESTs, Highly similar to CAQS MOUSE CALSEQUESTRIN, SKELETAL MUSCLE ISOFORM PRECURSOR [M.musculus], ESTs, Moderately similar to CAQC_RAT CALSEQUESTRIN, CARDIAC MUSCLE ISOFORM PRECURSOR [R.norvegicus], calsequestrin 1, calsequestrin 1 (fast-twitch, skeletal muscle), calsequestrin 2,
1583	169	AI045171	Щ	(cardiac muscle)	calsequestrin 2 (cardiac muscle)

Attorney bocket (1927-5028-01W0)    Comment No. 1985323.1   Chuman Homologous   Chuman Homologous Sequence Glusterititie	carboxyl carboxyl carboxyl LL (brain)	2 2 5	U, LL, BBB, carnitine O-SSS octanoyltransferase	U, FF, BBB, carnitine O-7 CCC, RRR octanoyltransferase carnitine O-octanoyltransferase	carnitine palmitoyltransferase 1, liver, carnitine palmitoyltransferase I, MITOCHONDRIAL LIVER ISOFORM [M.musculus], carnitine palmitoyltransferase 1, liver	carnitine palmitoyltransferase 1, muscle, carnitine
A Human Human Human (Human)	carboxyles carboxyles (brain)		L, 888, , RRR,	m.	carnitine palmitoyltr 1, liver, c palmitoyltr	carnitine palmitoyltr 1, muscle
4. Consent	0 NM_133295 LL	AA998857	NM_031987	NM_031987	1 NM_031559 J	
TABLE 3.	3933 20880	1188 3062	3722 20554	3722 20555	3646 15411	

Human Homologous Known Cene Name:- Human Homologous Sequence ©
sarnitine balmitoyltransferase 1, muscle carnitine palmitoyltransferase 1, muscle
carnitine palmitoyltransferase 2, carnitine palmitoyltransferase II carnitine palmitoyltransferase 2, carnitine palmitoyltransferase II
ESTs, Weakly similar to casein kinase [M.musculus], RIKEN cDNA 2610208K14 gene, RIKEN cDNA 3300002K07 gene, casein kinase 1, alpha 1, casein kinase 1, delta
ESTs, Weakly similar to casein kinase [M.musculus], RIKEN cDNA 2610208K14 gene, RIKEN cDNA 3300002K07 gene, casein kinase 1, alpha 1, casein kinase 1, delta
П
catalase, catalase 1 catalase, catalase 1
RIKEN cDNA 6330414C15 gene, catechol-O-methyltransferase
RIKEN cDNA 6330414C15 gene. catechol-O-methyltransferase
·
RIKEN cDNA 4921537117 gene, cathepsin C

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Attorney Docket 44921-5038-0100 of the month of the most second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the s	RIKEN cDNA 4921537117 gene, cathepsin C	ESTs, Weakly similar to CATL MOUSE CATHEPSIN L PRECURSOR [M.musculus], RIKEN cDNA 4930486L24 gene, cathepsin L, expressed sequence AA408230	ESTs, Weakly similar to CATL MOUSE CATHEPSIN L PRECURSOR [M.musculus], RIKEN cDNA 4930486L24 gene, cathepsin L, expressed sequence AA408230	CCAAT/enhancer binding protein (C/EBP), beta	CCAAT/enhancer binding protein (C/EBP), beta	CCAAT/enhancer binding protein (C/EBP), delta
お、差別は、常にてり、こ	Z O	cathepsin L	cathepsin L	CCAAT/enhancer binding protein (C/EBP), beta	CCAAT/enhancer binding protein (C/EBP), beta	CCAAT/enhancer binding protein (C/EBP), delta
Wandel Pendia	LL, FFF, GGG, OOO, RRR, SSS, UUU, General Core Tox Markers, General Alternate	C, D, W, BB, CC, FF, KKK, NNN, OOO, General Core Tox Markers, General Alternate	C, Q, W, MM, 000, TTT	I, J, MM, TTT	MM, TTT, General Alternate	D, GG, HH
Gensenk Reeor Dassenin	WM 017097	A176595	NM_013156	NM_024125	MM, TTI General NM_024125 Alternate	NM_013154  D, GG, HH
13 8 13 16 16 16 16 16 16 16 16 16 16 16 16 16	2150	3431	3430	21238	21239	21681
UZABIL Seq.	3276	2218	3229	3534	3534	3228

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Occument No. 1995323.1	Godo:   Kinowin GeneliName:   Human Homologous Sequence Gluster inttle	CD164 antigen, CD164 antigen, sialomucin, pro-oncosis receptor inducing membrane injury gene					CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1, scavenger receptor class B1					CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)					CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)					CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)
	S Hum	CD16 injury					CD36	<del>                                     </del>	Φ			_	$\overline{}$	e)				(0	Θ			CD36
	Human Homologou Known Gene Name	CD164 antigen, CD164 antigen, sialomucin	CD36 antigen (collagen type I	receptor,	thrombospondin	receptor)-like 1,	scavenger receptor class B1	CD36 antigen, CD36	antigen (collagen type	I receptor,	thrombospondin	receptor)	CD36 antigen, CD36	antigen (collagen type	I receptor,	A, B, II, BBB, thrombospondin	receptor)	CD36 antigen, CD36	antigen (collagen type	I receptor,	thrombospondin	receptor)
	ලංගු									H.	_	SSS				I, BBB,	RR				_	
	Model	T, XX, YY, PPP, QQQ					Ŏ			A, B, FF	BBB, CCC,	RRR, 8	,			A, B,	CCC,				BBB, TH	RRR
100 E00 P	Sewerna Age of A Refere (10	NM_031812					NM 031541 NN, 00					NM_031561			_		NM_031561					NM_031561
88	erec To No.	17941					16048					18315					18316					18318
REDIEVA	ි ලින් 10	3693					3642					3647					3647					3647

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Adjorney Docket 44.924-5068-011W0	Viman Homologous เกิดพาก Gene Name Humani Homologous Seguence Gluster illitie		CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	CD38 antigen, CD38 antigen (p45)		CD47 antigen (Rh-related antigen, integrin-associated signal transducer), RIKEN cDNA 1700026J12 gene, integrin-associated protein		CD47 antigen (Rh-related antigen, integrin-associated signal transducer), RIKEN cDNA 1700026J12 gene, integrin-associated protein	CD53 antigen, ESTs, Weakly similar to A39574 leukocyte antigen OX-44 - rat [R.norvegicus], ESTs, Weakly similar to CD53 MOUSE LEUKOCYTE SURFACE ANTIGEN CD53 [M.musculus], RIKEN cDNA 2610042G18 gene, RIKEN cDNA 9030418M05 gene, solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34 kDa), member 17, tetraspan transmembrane 4 super family.	transmembrane 4 superfamily member 7
	25 25	CD36 antigen, CD36 antigen (collagen type I receptor,	thrombospondin receptor)	CD38 antigen, CD38 antigen (p45)	CD47 antigen (Rh-related antigen, integrin-associated signal transducer),	integrin-associated protein	CD47 antigen (Rh- related antigen, integrin-associated signal transducer).	integrin-associated protein		CD53 antigen
	Model Gode		ввв, ссс	NN, 00, VV		၁၁၁		BBB, CCC		0, P
	consent laceori Rasog 10		NM_031561	D29646		NM_019195		NM_019195		NM_012523
38.3	elec Ido No		18319	2002		22062		22063		16214
TABLES	- - - - - - - - - - - - - - - - - - -		3647	2857		3368		3368		3068

	ි ලිදි				Altomey Docket 4492/1-5028-0/1WO Document No. 1935328.1
	GLEG ID No.	ලබෙන්නේ. Aee හැ. RefSeg (D)	Model Gode		Human Homologous Known Gene Name: Human Homologous Sequence (cluster IIII)
				CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30,	
147	2830	AA818025	χ̈́	EL32 and G344), CD59a antigen	
				CD59 antigen p18-20 (antigen identified by monoclonal antibodies	
147	2831	AA818025	<u>,</u> X, ≺	16.3A5, EJ16, EJ30, EL32 and G344), CD59a antigen	
					CD63 antigen (melanoma 1 antigen), Cd63 antigen, EST, Weakly similar to CD63 MOUSE CD63 ANTIGEN [M.musculus], ESTs, Weakly similar to CD63_RAT CD63
				CD63 antigen	antigen (AD1 antigen) [K.norvegicus], Mus musculus, clone MGC:36554 IMAGE:4954874, mRNA, complete cds, RIKEN cDNA 1300010A20 gene, expressed
1153	1437	AA997844	. >	(melanoma 1 antigen), Cd63 antigen	(melanoma 1 antigen), sequence C75951, expressed sequence C80071, transmembrane 4 superfamily Cd63 antigen
					CD63 antigen (melanoma 1 antigen), Cd63 antigen, EST, Weakly similar to CD63 MOUSE CD63 ANTIGEN [M.musculus], ESTs, Weakly similar to CD63_RAT CD63
				CD63 antigen	antigen (AD1 antigen) [R.norvegicus], Mus musculus, clone MGC:36554 IMAGE:4954874, mRNA, complete cds, RIKEN cDNA 1300010A20 gene, expressed
4236	1435	X61654	О, Р	(melanoma 1 antigen), Cd63 antigen	(melanoma 1 antigen), sequence C75951, expressed sequence C80071, transmembrane 4 superfamily Cd63 antigen member 2

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0 0 0	96 190 190 190 190 190 190 190 190 190 190	General Accor Reson	Mödelfésas.	Human Homologous Known Gene Name	umani Hormologous  novvni Genei Namei≓ Humani Homologous Sequénce (Gluster IIII)
				CDC42 binding	CDC42 binding protein kinase beta (DMPK-like), DNA segment, Chr X, Immunex 40,
				protein kinase beta	expressed, ESTs, Highly similar to Cdc42-binding protein kinase beta [Rattus
				(DMPK-like), Cdc42	norvegicus] [R.norvegicus], ESTs, Weakly similar to Cdc42-binding protein kinase
				ding protein kinase	beta [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 1190006F07 gene, dystrophia
3805	1178	NM_053620	PP, QQ	beta	myotonica kinase, B15
				CDC5 cell division	
				cycle 5-like (S.	
					cell division cycle 5-like (S. pombe), myeloblastosis oncogene-like 1, myeloblastosis
				cycle 5-like (S.	oncogene-like 2, v-myb myeloblastosis viral oncogene homolog (avian), v-myb
1216	2016	AF000578	РРР, ааа	pombe)	myeloblastosis viral oncogene homolog (avian)-like 2
				CEA-related cell	
				adhesion molecule 1,	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein),
				carcinoembryonic	carcinoembryonic antigen-related cell adhesion molecule 5, carcinoembryonic antigen-
				antigen-related cell	related cell adhesion molecule 6 (non-specific cross reacting antigen),
				adhesion molecule 1	carcinoembryonic antigen-related cell adhesion molecule 8, pregnancy specific beta-1-
3683	13185	NM_031755	GG, RR	(biliary glycoprotein)	glycoprotein 2, pregnancy specific beta-1-glycoprotein 4
				CEA-related cell	
				adhesion molecule 1,	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein),
				carcinoembryonic	carcinoembryonic antigen-related cell adhesion molecule 5, carcinoembryonic antigen-
				antigen-related cell	related cell adhesion molecule 6 (non-specific cross reacting antigen),
				adhesion molecule 1	carcinoembryonic antigen-related cell adhesion molecule 8, pregnancy specific beta-1-
3683	13186	NM_031755	L, RR	(biliary glycoprotein)	glycoprotein 2, pregnancy specific beta-1-glycoprotein 4
				CEA-related cell	
				adhesion molecule 1,	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein),
				carcinoembryonic	carcinoembryonic antigen-related cell adhesion molecule 5, carcinoembryonic antigen-
				antigen-related cell	related cell adhesion molecule 6 (non-specific cross reacting antigen),
				adhesion molecule 1	carcinoembryonic antigen-related cell adhesion molecule 8, pregnancy specific beta-1-
3683	13187	NM_031755	GG, OO	(biliary glycoprotein)	glycoprotein 2, pregnancy specific beta-1-glycoprotein 4

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Sec. 10.	erec One	Genefink Resor ^{es} Reßeg (D	्राज्यवा <u>ट</u> ुट्य	Human Homologous Known Gene Name	mologowsi Sequencei Gluster i III
					ESTs, Highly similar to A41222 ubiquitinprotein ligase [H.sapiens], ESTs, Weakly similar to UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD
					[M.musculus], RIKEN cDNA 2610301N02 gene, cell division cycle 34, expressed
65	13683	AA799788	General Alternate	cell division cycle 34	sequence Al327276, ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae), ubiquitin-conjugating enzyme E2C
					ESTs, Highly similar to A41222 ubiquitinprotein ligase [H.sapiens], ESTs, Weakly
					similar to UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD
					[M.musculus], KIKEN CDNA 2610301N02 gene, cell division cycle 34, expressed
187	13684	0.0848770			sequence Al32/2/6, ubiquitin-conjugating enzyme E2B, RAD6 homology (S.
ò	13004	A4010770	<u> </u>	ceil division cycle 34	cerevisiae), uoiquiin-conjugaiing enzyme Ezc
					ESTs, Highly similar to A41222 ubiquitinprotein ligase [H.sapiens], ESTs, Weakly similar to UBC2 HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD
			MM, FFF,		[M.musculus], RIKEN cDNA 2610301N02 gene, cell division cycle 34, expressed
			TTT, General		sequence Al327276, ubiquitin-conjugating enzyme E2B, RAD6 homology (S.
2973	13682	L38482	Alternate	cell division cycle 34	cerevisiae), ubiquitin-conjugating enzyme E2C
				cell division cycle 42	
				Gran binding protein,	
					KIKEN CUNA 4930544G11 gene, KIKEN CUNA 583040UA04 gene, cell division cycle
	0,000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		omolog (S.	42 (GTP binding protein, 25kD), plysia ras-related homolog A2, ras homolog 9.
8	22843	AA925473	۸۸	cerevisiae)	(KhoC), ras homolog A2, ras homolog gene family, member C
				cell division cycle 42	
				(GTP binding protein,	
					RIKEN cDNA 4930544G11 gene, RIKEN cDNA 5830400A04 gene, cell division cycle
				cycle 42 homolog (S.	42 (GTP binding protein, 25kD), plysia ras-related homolog A2, ras homolog 9
2403	22845	AI227887	ᅩ	cerevisiae)	(RhoC), ras homolog A2, ras homolog gene family, member C

	ees				Occument No. 1995/2018
8 8 9	eleç Dine	leemeema Aee off RefSeg ID	Model Godo	Human Homologous Known Gene Name	Vumanikomologous Vumanikomologous Vnowni Genenikame i Krumanikomologousi Seguence Gluster viitue
					DNA segment, Chr 3, ERATO Doi 555, expressed, EST, Highly similar to FA8 HUMAN COAGULATION FACTOR VIII PRECURSOR [H.sapiens], ESTs,
					Weakly similar to CERU MOUSE CERULOPLASMIN PRECURSOR [M.musculus], ESTs. Weakly similar to CERU RAT CERUI OPI ASMIN PRECURSOR
	·			ceruloplasmin,	(FERROXIDASE) [R.norvegicus], ESTs, Weakly similar to KUHU ferroxidase
					[H.sapiens], ceruloplasmin, ceruloplasmin (ferroxidase), coagulation factor VIII,
1359	16521	AI010470	FF	(ferroxidase)	procoagulant component (hemophilia A)
					DNA segment, Chr 3, ERATO Doi 555, expressed, EST, Highly similar to
					FA8_HUMAN COAGULATION FACTOR VIII PRECURSOR [H.sapiens], ESTs,
					Weakly similar to CERU MOUSE CERULOPLASMIN PRECURSOR [M.musculus],
					ESTs, Weakly similar to CERU_RAT CERULOPLASMIN PRECURSOR
				ceruloplasmin,	FERROXIDASE) [R.norvegicus], ESTs, Weakly similar to KUHU ferroxidase
			BB, CC, NN,	ceruloplasmin	[H.sapiens], ceruloplasmin, ceruloplasmin (ferroxidase), coagulation factor VIII,
3072	16519	NM_012532	SSS, UUU	(ferroxidase)	procoagulant component (hemophilia A)
					DNA segment, Chr 3, ERATO Doi 555, expressed, EST, Highly similar to
					FA8_HUMAN COAGULATION FACTOR VIII PRECURSOR [H.sapiens], ESTs,
<del></del>					Weakly similar to CERU MOUSE CERULOPLASMIN PRECURSOR [M.musculus],
					EST's, Weakly similar to CERU_RAT CERULOPLASMIN PRECURSOR
				ceruloplasmin,	(FERROXIDASE) [R.norvegicus], ESTs, Weakly similar to KUHU ferroxidase
				ceruloplasmin	[H.sapiens], ceruloplasmin, ceruloplasmin (ferroxidase), coagulation factor VIII,
3072	16520	16520 · NM 012532	BB, CC	(ferroxidase)	procoagulant component (hemophilia A)
				chloride channel, nucleotide-sensitive,	
3676	19048	NM_031719	RR, SS	1A	chloride channel, nucleotide-sensitive, 1A
				cholecystokinin B	
4266	447	X79208	RR	receptor	cholecystokinin B receptor
					Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library,
	_				clone:3110043M12:choline kinase, full insert sequence, choline kinase, hypothetical
2843	1306	D10262	99	choline kinase	protein FLJ10761

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8 9 9	<u>ැල</u> මැලි මැරි	<u>                                     </u>	Model Gode	Ruman Homologous Knovni Genei Namer	
	*				EST, Weakly similar to KICE MOUSE CHOLINE/ETHANOLAMINE KINASE [M.musculus], ESTs, Weakly similar to KICE_RAT Choline/ethanolamine kinase [Includes: Choline kinase (CK); Ethanolamine kinase (EK)] [R.norvegicus], Homo sapiens. Similar to hypothetical protein FLJ10761, clone MGC:19512 IMAGE:4329734.
1205	3512	AB006607	BBB, CCC, RRR	choline kinase-like	mRNA, complete cds, RIKEN cDNA 4930555L11 gene, choline kinase-like, ethanolamine kinase, expressed sequence Al197444
					EST, Weakly similar to KICE MOUSE CHOLINE/ETHANOLAMINE KINASE [M.musculus], ESTs, Weakly similar to KICE_RAT Choline/ethanolamine kinase [Includes: Choline kinase (CK); Ethanolamine kinase (EK)] [R.norvegicus], Homo
			BBB. RRR.		sapiens, Similar to hypothetical protein FLJ10761, clone MGC:19512 IMAGE:4329734, mRNA. complete cds. RIKEN cDNA 49305551 11 oene. choline kinase-like
1205	3513	AB006607	SSS	choline kinase-like	ethanolamine kinase, expressed sequence Al197444
				cholinergic receptor, muscarlnic 3,	
3069	24433	NM_012527	PP, QQ	cholinergic receptor, muscarinic 3, cardiac	cholinergic receptor, muscarinic 3, cholinergic receptor, muscarinic 3, cardiac, cholinergic receptor, muscarinic 5
				cholinergic receptor, nicotinic, gamma	
3359	20373	NM_019145	D, Z, AA	polypeptide	cholinergic receptor, nicotinic, gamma polypeptide
					ESTs, Weakly similar to claudin 1 [Rattus norvegicus] [R.norvegicus], Homo sapiens, clone MGC:23949 IMAGE:4243903, mRNA, complete cds, Mus musculus claudin 19
- 1		_	go	claudin 1	mRNA, complete cds, claudin 1, claudin 18
3672	20404	NM_031700	К, НН, ТТ	claudin 3	claudin 3
				coagulation factor II,	
3519	24838	NM_022924 PPP,	PPP, QQQ	(thrombin)	coagulation factor II, coagulation factor II (thrombin)

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Human Homologous Known Genes Name	coagulation factor IX, coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B)	coagulation factor X	coagulation factor X	coated vesicle membrane protein	coatomer protein complex, subunit beta, coatomer protein complex, subunit beta 1
Model Gode	N, WW, UUU	VV, FFF, GGG, General Alternate	S, GG, W, PPP, QQQ	cc, ww	n
Reforms	M26247	NM_017143	NM_017143	NM_031722	NM_080781
53. 00.00 00.00 00.00	25430		10504	12052	19831
	3006	3287	3287	3677	3907

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Sed (D	OLGC OLGC ONO.	<u>කොහොදින</u>     යුරෙහිලේ (D	्रम् शब्दा दुरुदेव	Kiriman Homologous Kirown Genei Namer	uman Homologous nown Genen Namen Human Homologous Sequence Gluster Title
3289	15365	NM 017147	VV, FFF, General Alternate	cofilin 1 (non-muscle),	cofilin 1 (non-muscle), cofilin 1 (non-muscle), cofilin 1, non-muscle, cofilin 2 (muscle), cofilin 2, muscle, cofilin 1, non-muscle expressed sequence AW987265
2855	16610	D28557	2Q, eneral	1	Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610205119:Y box protein 1, full insert sequence, Mus musculus Y-box binding protein (oxyR) mRNA, partial cds, cold shock domain protein A
					EST, Weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to CA11_HUMAN COLLAGEN
					ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], F-box only protein Mus musculus. Similar to RIKEN cDNA 1700051112 gene. clone MGC:28741
				collagen, type I,	IMAGE:4481590, mRNA, complete cds, collagen, type IV, alpha 3 (Goodpasture antigen), expressed sequence AW742721, procollagen, type I, alpha 1, procollagen,
3007	15571	M27207	Ξ,	alpha 1, procollagen, type I, alpha 1	pha 1, procollagen, type IV, alpha 1, procollagen, type IV, alpha 4, procollagen, type IV, alpha 5, pe 1, alpha 1 procollagen, type VI, alpha 1, putative emu1
505	21674	AA891828	SSS	collagen, type I, alpha 2, procollagen, type I, alpha 2	collagen, type I, F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, alpha 2, procollagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over type I, alpha 2 expressed gene 1, retinoblastoma binding protein 1
2160	21676	AI175101	IIII SSS	collagen, type I, alpha 2, procollagen, type I	ollagen, type I, F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, pha 2, procollagen, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over per lapha 2, prostate tumor over per lapha 2, prostate tumor over lapha 2, prostate tumor over lapha 2, prostate tumor over lapha 2, processed gene 1, retinoblastoma binding protein 1
3754	6155	NM_053356	I	collagen, type I, alpha 2, procollagen, type I, alpha 2	collagen, type I, F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, alpha 2, procollagen, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over type I, alpha 2
3754	6156	NM_053356	Σ	collagen, type I, alpha 2, procollagen, type I, alpha 2	bilagen, type I, F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, pha 2, procollagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over pe I, alpha 2 expressed gene 1, retinoblastoma binding protein 1

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Seq. 10	erec To No.	eමොහොය Aeeේේ Rekseg (D	Wodel Gode	Human Homologous Knowni Gene Name	Numan (Homologous) Knowni Gene Name)   Human Homologous Sequence (cluster iiitle:
3754	6157	NM 053356	တ	collagen, type I, alpha 2, procollagen, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1
					EST, Highly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Moderately similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to CA13 MOUSE COLLAGEN
					ALPHA 1(III) CHAIN PRECURSOR [M.musculus], EST, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], ESTs,
				collagen, type III, alpha 1 (Ehlers-	Weakly similar to CA13 MOUSE COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to S41067 collagen alpha 1(III) chain - rat
				Danlos syndrome type IV, autosomal	Danlos syndrome type [R.norvegicus], Mus musculus, Similar to putative protein phosphatase 1 nuclear IV, autosomal targeting subunit, clone IMAGE:3157989, mRNA, partial cds, RIKEN cDNA
				dominant),	2010011D20 gene, cleavage and polyadenylation specific factor 6, 68kD subunit,
3001	16427	M21354	M, ==		congentified, apria 2, congent, type III, alpha 1 autosomal dominant), procollagen, type III, alpha 1
					EST, Highly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]. EST. Moderately similar to CA13_HUMAN COLLAGEN ALPHA 1(III)
					CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to CA13 MOUSE COLLAGEN AT PHA 1/11) CHAIN PRECURSOR [M.m.iscripted FST Meakly similar to
					CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], ESTs,
				collagen, type III,	Weakly similar to CA13 MOUSE COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
				Danlos syndrome type	Danlos syndrome type [R.norvegicus], Mus musculus, Similar to putative protein phosphatase 1 nuclear
		_		IV, autosomal	targeting subunit, clone IMAGE:3157989, mRNA, partial cds, RIKEN cDNA
					2010011D20 gene, cleavage and polyadenylation specific factor 6, 68kD subunit,
4254	16426	X70369	M, 11	alpha 1	conagen type v, apria z, conagen, type III, alpha 1 (Enliers-Danios syndrome type IV, autosomal dominant), procollagen, type III, alpha 1

TABLES	88				
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					EST, Weakly similar to CGHU1V collagen alpha 1(V) chain precursor [H.sapiens], Homo sapiens cDNA FLJ30442 fis, clone BRACE2009212, Homo sapiens proline-rich
					acidic protein mRNA, complete cds, Mus musculus, clone IMAGE:3490511, mRNA, partial cds, collagen, type V, alpha 1, collagen, type XI, alpha 1, endoplasmic
				collagen, type V,	reticulum chaperone SIL1, homolog of yeast, hypothetical protein MGC2705,
	1			agen,	procollagen, type V, alpha 1, procollagen, type V, alpha 3, procollagen, type XI,
3970	25237	NM 134452	NNN		alpha 1
				collagen, type X,	ESTs, Highly similar to 1917150A collagen:SUBUNIT=alpha1:ISOTYPE=VIII [Rattus
				alpha 1(Schmid	norvegicus] [R.norvegicus], ESTs, Moderately similar to CA18 MOUSE COLLAGEN
				metaphyseal	ALPHA 1(VIII) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to CGHU1D
				chondrodysplasia),	collagen alpha 1(X) chain precursor [H.sapiens], RIKEN cDNA 1810033K05 gene,
				procollagen, type X,	collagen, type VIII, alpha 1, collagen, type X, alpha 1(Schmid metaphyseal
4079	9687	S79214	G, H	alpha 1	chondrodysplasia), procollagen, type VIII, alpha 1, procollagen, type X, alpha 1
					ESTs, Weakly similar to DPY1 MOUSE DIHYDROPYRIMIDINASE RELATED
				collapsin response	PROTEIN-1 [M.musculus], Ellis van Creveld syndrome, collapsin response mediator
4138	1960	U52102	FF	mediator protein 1	protein 1
				complement	
				component 1, q	
				subcomponent	
3382	15259	NM_019259	Alternate	binding protein	complement component 1, q subcomponent binding protein
				complement	
				component 1, q	
				subcomponent, beta	
3383	21443	NM_019262	NN	polypeptide	
					EST, Weakly similar to CO3_RAT COMPLEMENT C3 PRECURSOR [CONTAINS: C3A
					ANAPHITLA I UXINJ [R.noivegicus], complement component 3, complement
3246	1958	NM 016994 L.	L, S, HH	component 3	component 4 (Within H-2S), complement component 4A, complement component 4B, expressed sequence Al663842, hemolytic complement

TABLES	ଞ୍ଜ				Alticaney Docket (44921-5033-6117) Alticaney Docket (44921-5033-6117)
, , , , , , ,	elec Id No.	Centeni Ace or Rafseq D	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	Human Homologous Known Gener Name	Homologous GeneiName HumaniHomologousiSequencei@usterviilia
			E H U	**************************************	EST, Weakly similar to CO3_RAT COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN] [R.norvegicus], complement component 3, complement
4212	1959	X52477	SS, TTT	component 3	component 4 (Within H-43), complement component 4A, complement component 4B, expressed sequence Al663842, hemolytic complement
				complement component 4 (within H	
4130	15851	U42719	BBB, CCC	2S), complement component 4B	complement component 4 (within H-2S). complement component 4A
				complement	
				component 4 binding	
				protein, beta,	
			E, I, J, BB,	complement	-
			JJ, EEE,	component 4 binding	
			GGG, III, JJJ,	GGG, III, JJJ, protein, pseudogene	
4290	1561	Z50052	MMM, SSS	-	complement component 4 binding protein, beta
				complement	ESTs, Moderately similar to NBHUC4 C4b-binding protein alpha chain precursor
					[H.sapiens], complement component (3d/Epstein Barr virus) receptor 2, complement
				protein, complement	component 4 binding protein, complement component 4 binding protein, alpha,
					complement receptor 2, decay-accelarating factor, expressed sequence Al195242,
3065	563	NM_012516	BB, JJ, KK	protein, alpha	zona pellucida 3 receptor
				complement	
				component 5 receptor	
				1 (C5a ligand),	
				complement	ESTs, Weakly similar to GPRY_MOUSE PROBABLE G PROTEIN-COUPLED
				component 5,	RECEPTOR GPR34 [M.musculus], complement component 5 receptor 1 (C5a ligand),
1203   926	926	AB003042	о, <b>Р</b> , W	receptor 1	complement component 5, receptor 1

	ខ្មោ				Attorney Doctret 44921-5038-01000
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					EST, Weakly similar to T14158 neurexin IV - mouse [M.musculus], EST, Weakly similar to T31083 paranodin - rat [R.norvegicus], ESTs, Weakly similar to T14158
1215	954	AF000114	0	contactin associated protein 1	neurexin IV - mouse [M.musculus], ESTs, Weakly similar to T31083 paranodin - rat [R.norvegicus], contactin associated protein 1
				coronin, actin binding	
	-				ESTs, Moderately similar to CO1B_RAT Coronin 1B (Coronin 2) [R.norvegicus],
3374	15347	NM_019222	P, T	actin-binding protein,	coronin o, coronin, actin binding protein 1B, coronin, actin binding protein 1C, coronin, actin binding protein, 1C, hypothetical protein DKF2o7621166
				coronin, actin binding	
					ESTs, Moderately similar to CO1B_RAT Coronin 1B (Coronin 2) [R.norvegicus],
7,000	16340	184 040000		in-binding protein,	coronin 6, coronin, actin binding protein 1B, coronin, actin binding protein 1C,
3	13348	222810 MINI	≤	18	coronin, actin binding protein, 1C, hypothetical protein DKFZp762l166
			DD. KKK.	C-reactive protein, pentraxin-related C-	
		- 1.	NNN, PPP,	reactive protein,	C-reactive protein, petaxin related. Homo sapiens. Similar to C-reactive protein.
3275	6013	NM_017096		petaxin related	pentraxin-related, clone MGC:22631 IMAGE:4766715, mRNA, complete cds
3070	4467	NM_012529 ZZ, AAA	ZZ, AAA	creatine kinase, brain	
			A, B, KK,	C-terminal binding	C-terminal binding protein 1, Homo sapiens mRNA; cDNA DKFZp434B0914 (from
3369	18573	NM_019201	HHH	protein 1	clone DKFZp434B0914); partial cds
_				cyclic AMP	
				phosphoprotein, 19	
			-	kD, cyclic AMP	
9				phosphoprotein, 19	
1808	2057	AI102579	nnn	кDа	cyclic AMP phosphoprotein, 19 kD, cyclic AMP phosphoprotein, 19 kDa
				cyclin D1, cyclin D1	
1480	2866	AI029058	z, AA	(PRAD1: parathyroid adenomatosis 1)	EST,Moderately similar to JC2342 cyclin D1 - rat [R.norvegicus],cyclin D1,cyclin D1 (PRAD1: parathyroid adenomatosis 1)

MARLES	E3				Auguney Doeket 44921-5033-01WO
- 68 89 90	elec Bono	Ceneral Lecor Mal Reseate	Medal Gode	Human Homologous Known Gener Name	Human Homologous   Known Gener Name   Human Homologous Sequence @uster Title:
2849	25041	D14014		cyclin D1, cyclin D1 (PRAD1: parathyroid adenomatosis 1)	EST, Moderately similar to JC2342 cyclin D1 - rat [R.norvegicus], cyclin D1, cyclin D1 (PRAD1: parathyroid adenomatosis 1)
3178	20755	NM_012923	F, R, II, W, General Alternate	cyclin G, cyclin G1	ESTs, Weakly similar to CGG1_RAT Cyclin G1 (Cyclin G) [R.norvegicus], cyclin G, cyclin G2, cyclin 1
3178	20757	NM_012923	F, II, FFF, General Core Tox Markers	cyclin G, cyclin G1	ESTs, Weakly similar to CGG1_RAT Cyclin G1 (Cyclin G) [R.norvegicus], cyclin G, cyclin G2, cyclin I
3741	12577	NM 052981	A, D, V, BB,	cyclin H	cyclin H
3048	291	M88347	ſΥ	cystathionine beta- synthase, cystathionine-beta- synthase	cystathionine-beta-synthase, expressed sequence AU040765, serine dehydratase, serine dehydratase,
1287	2853	AI008888	B, O, BB, CC, GG, NN, OO		cystatin B, cystatin B (stefin B)
1287	2854	A1008888	0	cystatin B, cystatin B (stefin B)	cystatin B, cystatin B (stefin B)
2743	2855	AI236707	EEE, MMM	cystatin B, cystatin B (stefin B)	cystatin B, cystatin B (stefin B)
				cystatin C, cystatin C (amyloid angiopathy	ESTs, Moderately similar to CYTC MOUSE CYSTATIN C PRECURSOR [M.musculus], ESTs, Weakly similar to CYTC MOUSE CYSTATIN C PRECURSOR [M.musculus], RIKEN cDNA 1110017E11 gene, RIKEN cDNA 9230101F08 gene, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C, cystatin C
2527	2527 24326	AI231292	×, ×		o (anitylolo arigiopairiy arid cerebrar nemormage), cystatin D, cystatin S, cystatin SA, cystatin SN

Alternacy, Document No. 1993-01W0 Document No. 1993223.1 KumaniHomologous Sequence Gluster III 10	cysteine and glycine- rich protein 2, cysteine-rich protein 2 RIKEN cDNA 0610010123 gene, cysteine-rich protein 2, thymus LIM protein	cysteine and glycine- rich protein 2, cysteine-rich protein 2 RIKEN cDNA 0610010123 gene, cysteine-rich protein 2, thymus LIM protein	cysteine dioxygenase 1, cytosolic, cysteine dioxygenase, type l	cysteine dioxygenase 1, cytosolic, cysteine dioxygenase, type l	cytochrome c oxidase EST, Weakly similar to COX4_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE subunit IV isoform 1, IV PRECURSO [H.sapiens], ESTs, Moderately similar to COX4_HUMAN cytochrome c oxidase, CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSO [H.sapiens], cytochrome subunit IVa coxidase subunit IV isoform 1, cytochrome c oxidase, subunit IVa	cytochrome c oxidase subunit IV isoform 2, cytochrome c oxidase, subunit IVb
Humen Homologous Known Gene Name   Hu	cysteine and glycine- rich protein 2, cysteine-rich protein 2	cysteine and glycine- rich protein 2, cysteine-rich protein 2	cysteine dioxygenase 1, cytosolic, cysteine dioxygenase, type l	cysteine dioxygenase 1, cytosolic, cysteine dioxygenase, type l	cytochrome c oxidase subunit IV isoform 1, cytochrome c oxidase, subunit IVa	cytochrome c oxidase subunit IV isoform 2, cytochrome c oxidase, subunit IVb
Model Gode	E, GG, HH, GGG	General Alternate	A, B, T, LLL	Α, ΥΥ	רר	UU
Consent Les en l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination l'Assentination	D17512	U44948	NM_052809	NM_052809	NM_017202	NM_053472 V, RR,
33 8 6 6 6 6 8	2515	19543	15028	25024	14696	21866
MABLES Seq eq D	2852	4131	3740	3740	3308	3771

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30 10 10 10 10 10 10 10 10 10 10 10 10 10	GLGG: ID No	Consent	March Gaza	Human Romologous	The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon
		<u> </u>		9 0	堰
				subunit Vla	
				polypeptide 1,	
				cytochrome c oxidase,	
				subunit VI a,	
1872	23574	AI104520	LL	polypeptide 1	
				cytochrome c oxidase	
				subunit VIa	
		****		polypeptide 1,	
				cytochrome c oxidase,	
				subunit VI a,	
4257	23576	X72757	HH, LL	polypeptide 1	
				cytochrome c oxidase	
				subunit VIa	EST, Moderately similar to COXD_RAT Cytochrome c oxidase polypeptide VIa-heart,
	_			polypeptide 2,	mitochondrial precursor (COXVIAH) [R.norvegicus], ESTs, Weakly similar to COXD
				cytochrome c oxidase,	ytochrome c oxidase, MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE VIA·HEART PRECURSOR
				subunit VI a,	[M.musculus], cytochrome c oxidase subunit VIa polypeptide 2, cytochrome c oxidase,
3147	20905	NM_012812	BB, CC	polypeptide 2	subunit VI a, polypeptide 2
				cytochrome c,	
			D, MM, FFF,	cytochrome c,	
3154	11137	NM_012839	Ш	somatic	
				cytochrome c,	
				cytochrome c,	
3154	11138	NM_012839 T, JJ, KK,	T, JJ, KK, LL	somatic	

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<i>-5056-011WO</i> o. 199 <i>6322</i> 8.1		subfamily l			subfamily I			subfamily I			- Mimoghin	Subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective in the subjective i
omey Doekst 44221-5059-61W • • • Doeument No. 1995323		rtochrome P450,			ytochrome P450,			ytochrome P450,			dochrome DAEO	y too in online in 450,
William N. Attom	man Homologous/Sequence! @luster Intle	cytochrome P450, 1a1, aromatic compound inducible, cytochrome P450, subfamily l	(aromatic compound-inducible), polypeptide 1		cytochrome P450, 1a1, aromatic compound inducible, cytochrome P450, subfamily (aromatic compound-inducible), polypeptide 1			cytochrome P450, 1a2, aromatic compound inducible, cytochrome P450, subfamily l (aromatic compound-inducible), polypeptide 2			subfamily I (aromatic compound-inducible) cytochrome D450 1s2 aromatic compound inducible cytochrome D450 subfamily I	(aromatic compound-inducible), polypeptide 2
		cytochrome F	(aromatic con		cytochrome F			cytochrome F (aromatic cor			a emorphoops	(aromatic cor
	អ្វីបញ្ជាក់ អ្វីបញ្ជាក់ ស្រាល់ស្រាល់ Gene Name	4 D 6	polypeptide 1 cytochrome P450,	1a1, aromatic compound inducible, cytochrome P450,	ic e),	cytochrome P450, 1a2, aromatic compound inducible		<u>~</u>	cytochrome P450, 1a2, aromatic	compound inducible, cytochrome P450,	subfamily I (aromatic	polypeptide 2
	ුවුමෙ ලාලෙඟු	99	нн, оро		С, L, GG, НН		C, K, L, U,	GG, HH, II, DDD, RRR			U, Y, GG, HH = RRR	: !
	Consent Recor Ressq D		NM_012540		NM_012540			NM_012540				NM 012541
E3	elec One		488		489			20705				20703
TABLE 8			3073		3073			3073				3074

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17ABUE 3 See BUGG 1000 1000 1000 1000 1000 1000 1000 1	CEMBERN   NA O12541   NM O12940   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31543   NM O31544   (EE, MM, TTT (B, NN, OO, III, NN, OO, III)	HumaniHomologous Mamoninami Homologous Sytochrome P450, 142, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), sollypeptide 2 cytochrome P450, subfamily I (dioxin-inducible), sollypeptide 1 (dioxin-inducible), sollypeptide 1 (dioxin-inducible), sollypeptide 1 (dioxin-inducible), sollypeptide 1 (dioxin-inducible), sollypeptide 1 (dioxin-inducible), sollypeptide 2 (ethanol ducible, cytochrome P450, set, ethanol ducible, cytochrome P450, subfamily IIE (ethanol-inducible)	Municipies of the many cytochrome P450, 1b1, benz[alanthracene inducible, cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary ridantile) (dioxin-inducible), polypeptide 1 (glaucoma 3, primary cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol inducible), polypeptide 1 (glaucoma 3, primary cytochrome P450, 1b1, benz[alanthracene inducible, cytochrome P450, 2e1, ethanol inducible), polypeptide 1 (glaucoma 3, primary cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol inducible, cytochrome P450, 2e1, ethanol	
3643 4011	NM_031543	MMM LLL	(ethanol-inducible)	

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	Alumani Homologous Knowin Genel Namer Human Homologousi Sequence Gluster Mile							cytochrome P450, 51, cytochrome P450, 51 (lanosterol 14-alpha-demethylase)				cytochrome P450 51. cytochrome P450 51 (Janosterol 14-alpha-demethylase)							cytochrome P450, 8b1, sterol 12 alpha-hydrolase, cytochrome P450, subfamily VIIIB	(sterol 12-alpha-hydroxylase), polypeptide 1
	Human Homologous Known Gene Name,	cytochrome P450, 2e1, ethanol	inducible, cytochrome P450, subfamily IIE	(ethanol-inducible)	cytochrome P450,	51, cytochrome	r450, 31 (ialiosterol 14-alpha-	demethylase)	cytochrome P450,	51, cytochrome	P450, 51 (lanosterol	14-alpha- demethvlase)	cytochrome P450,	8b1, sterol 12 alpha-	hydrolase,	cytochrome P450,	subfamily VIIIB (sterol	12-alpha-	hydroxylase),	polypeptide 1
	Modeli Godo		T, EE, FF, MM, EEE,	MMM, TTT				T			G, H, C,	۲۲, General Alternate								NM_031241 JJ, KK, HHH
	Consent			NM_031543				NM_012941				NM 012941								NM_031241
3.8	OLGG ID No.			4012				20928				20931								12313
	ි ල ලුල් ( <u>ව</u>			3643				3182				3182							,	3622

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88	SELEC SELEC	General Recor		HumaniHomologous	Umaniffomologous
, (a)	ID No.	යිස්පිදෝ [ම	Model Gode	Known Gene Name	Humanifiomologous Seguence Gluster III III
				cytochrome P450,	EST, Moderately similar to 165981 fatty acid omega-hydroxylase [H.sapiens], Mus
				subfamily IV B,	musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837,
			U, FF, LL,	polypeptide 1,	mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone
			XX, 88B,	cytochrome P450,	MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene,
			CCC, RRR,	subfamily IVB,	cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11,
738	20711	AA924267	SSS	polypeptide 1	expressed sequence Al314743
				cytochrome P450,	EST, Moderately similar to 165981 fatty acid omega-hydroxylase [H.sapiens], Mus
				subfamily IV B,	musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837,
				polypeptide 1,	mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone
				cytochrome P450,	MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene,
				subfamily IVB,	cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11,
1151	20712	AA997806	FFF	polypeptide 1	expressed sequence AI314743
				cytochrome P450,	EST, Moderately similar to 165981 fatty acid omega-hydroxylase [H.sapiens], Mus
				subfamily IV B,	musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837,
				polypeptide 1,	mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone
		_		cytochrome P450,	MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene,
			, J, U, FF,	subfamily IVB,	cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11,
2992	20714	M14972	LL, XX, YY	polypeptide 1	expressed sequence Al314743
				cytochrome P450,	EST, Moderately similar to 165981 fatty acid omega-hydroxylase [H.sapiens], Mus
				subfamily IV B,	musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837,
				polypeptide 1,	mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone
				cytochrome P450,	MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene,
			U, EE, FF,	subfamily IVB,	cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11,
3025	3025   20713	M57718	LL, RRR	polypeptide 1	expressed sequence Al314743

	33				KANOOMAN DOGKGY 4492A-5028-01/WO ************************************
 	GLGG GLGG GDND	<u>Gentenik</u>   Aee er   RefSeq (D	Model Gode		man Romologous Jown GeneriName   Human:Homologous/Sequence (Sluster Mile)
				chrome P450,	EST, Moderately similar to 165981 fatty acid omega-hydroxylase [H.sapiens], Mus
				Ivpeptide 1.	msNA. complete cds. Mus musculus. Similar to cytochrome P450, 4a10, clone
			J, U, DD, FF,	50,	MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene,
			LL, XX, QQQ, subfamily IVB,		cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11,
4192	20715	X07259	RRR, SSS	polypeptide 1	expressed sequence Al314743
					EST, Moderately similar to PTE2_HUMAN PEROXISOMAL ACYL-COENZYME A
					THIOESTER HYDROLASE 2 (PEROXISOMAL LONG-CHAIN ACYL-COA
					THIOESTERASE 2) (ZAP128) [H.sapiens], ESTs, Weakly similar to MTE1_RAT Acyl
					coenzyme A thioester hydrolase, mitochondrial precursor (Very-long-chain acyl-CoA
					thioesterase) (MTE-I) [R.norvegicus], ESTs, Weakly similar to PTE2_HUMAN
					PEROXISOMAL ACYL-COENZYME A THIOESTER HYDROLASE 2 (PEROXISOMAL
				cytosolic acyl-CoA	LONG-CHAIN ACYL-COA THIOESTERASE 2) (ZAP128) [H.sapiens], Homo sapiens
				thioesterase 1,	cDNA FLJ31235 fis, clone KIDNE2004681, moderately similar to Mus musculus
				mitochondrial acyl-	peroxisomal long chain acyl-CoA thioesterase lb (Pte1b) gene, Mus musculus, Similar
				CoA thioesterase 1,	to bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choloyltransferase),
				peroxisomal long-	clone MGC:19156 IMAGE:4220620, mRNA, complete cds, cytosolic acyl-CoA
	•			chain acyl-coA	thioesterase 1, mitochondrial acyl-CoA thioesterase 1, peroxisomal long-chain acyl-coA
3994	1858	NM_138907	FF, LL	thioesterase	thioesterase
					EST, Moderately similar to PTE2_HUMAN PEROXISOMAL ACYL-COENZYME A
					THIOESTER HYDROLASE 2 (PEROXISOMAL LONG-CHAIN ACYL-COA
	····				THIOESTERASE 2) (ZAP128) [H.sapiens], ESTs, Weakly similar to PTE2_HUMAN
			A.C. 44/64	cytosolic acyl-CoA	PEROXISOMAL ACYL-COENZYME A THIOESTER HYDROLASE 2 (PEROXISOMAL
				thioesterase 1,	LONG-CHAIN ACYL-COA THIOESTERASE 2) (ZAP128) [H.sapiens], Homo sapiens
			-	peroxisomal long-	cDNA FLJ31235 fis, clone KIDNE2004681, moderately similar to Mus musculus
				chain acyl-coA	peroxisomal long chain acyl-CoA thioesterase Ib (Pte1b) gene, cytosolic acyl-CoA
3623	1857	NM_031315	FF, LL	thioesterase	thioesterase 1, peroxisomal long-chain acyl-coA thioesterase
	_			D-dopachrome	D-dopachrome tautomerase, EST, Moderately similar to DOPD_HUMAN D-
3536	17226	NM_024131 Q, R, Y	Q, R, Y	tautomerase	DOPACHROME TAUTOMERASE [H.sapiens]

	38				Attorney Doctot (4924-6088-01Wo
- 88 9	erec ID No.	leen:emi Ree or ReiSeg (D	प्रिटवंबा एक्ट	Human Homologous Human Homologous Known Gene Name	Human Homologous Known Gene Name: Human Homologous/Sequence (Gluster/Mic
3536	17227	NM_024131		D-dopachrome tautomerase	D-dopachrome tautomerase, EST, Moderately similar to DOPD_HUMAN D-DOPACHROME TAUTOMERASE [H.sapiens]
4055	18356	R47042	D	decorin	RIKEN cDNA 5530600M07 gene, decorin, expressed sequence C85409, extracellular matrix protein 2, female organ and adipocyte specific
				degenerative	
_	,			spermatocyte homolog (Drosophila),	
				•	
				spermatocyte homolog, lipid	ESTs, Moderately similar to degenerative spermatocyte homolog (Drosophila) [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 2210008A03 gene, degenerative
3748	23597	NM_053323	>	desaturase (Drosophila)	spermatocyte homolog (Drosophila), degenerative spermatocyte homolog, lipid desaturase (Drosophila)
			S, U, RR,		
			CCC, LLL, RRR, SSS	oeiodinase	ESTs, Moderately similar to IOD1_RAT_TYPE I IODOTHYRONINE DEIODINASE
3428	19679	NM_021653	nnn	ne, type I	iodothyronine, type I
				diazepam binding	
				binding inhibitor	
				(GABA receptor	
				modulator, acyl-	
3709	16535	NM 031853	Q, R, U, YY	protein)	
			B, L, III, JJJ, 000, QQQ,		
2871	811	D63704	General Core Tox Markers	dihydropyrimidinase	ESTs, Weakly similar to DPY1 MOUSE DIHYDROPYRIMIDINASE RELATED PROTEIN 1 [M.musculus], dihydropyrimidinase
				,	

TABUE 3	3.3				Attorney Docket 44921-5059-01W0
		leemisent Aee er Reßeg (D)	Model Gode	HumaniHomologous Known Gene Name	Human Homologous Known Gene Namer Human/Homologous/Sequence(Gluster/IIII)อ
			OOO, PPP, QQQ, General		
2871	812	D63704	Core Tox Markers	dihydropyrimidinase	ESTs, Weakiy similar to DPY1 MOUSE DIHYDROPYRIMIDINASE RELATED PROTEIN 1 [M.musculus], dihydropyrimidinase
					ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to
				dimethylarginine	dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine
673	6377	AA894273	nn	dimethylaminohydrola se 1	dimethylaminohydrola  dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus], dimethylarginine se 1
					ESTS, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYI AMINOHYDBOI ASE 1 IH saniens! ESTS, Weakly similar to
·				dimethylarginine	dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine
				dimethylaminohydrola	dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus], dimethylarginine
854	19425	AA943842	N	_	dimethylaminohydrolase 1, dimethylarginine dimethylaminohydrolase 2
					ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE
					DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to
					dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine
905	19421	AA945152	S, NNN	dimemylaminonydrola se 1	olmetnylaminonydrolase [kattus norvegicus] [k.norvegicus], dimetnylariginine dimethylaminohydrolase 1. dimethylarginine dimethylaminohydrolase 2
					ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE
					DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to
					dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine
			EE, PP, QQ,	dimethylaminohydrola	dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus], dimethylarginine
2349	19427	AI179510	۲۲		dimethylaminohydrolase 1, dimethylarginine dimethylaminohydrolase 2
					ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE
<del></del>		·			DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to
····-				dimethylarginine	dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine
	0,0	(	-	dimethylaminohydrola	dimethylaminohydrola  dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus], dimethylarginine
4024	13428	K4/028	H	Se 1	dimethylaminohydrolase 1, dimethylarginine dimethylaminohydrolase 2

TABLES	ଜ				Attorney Docket 44924-5038-011W0
Seq. Description	erec Id No.	GEMISEM Age Or RefSeq (D	ित्र हैं या किन्तु  Madal Gada	Human Homologous Knowni Genei Name	tumani Homologous knowni GenetiName:   Human Homologous/SequenceiGluster, littis
	-			dipeptidylpeptidase 4, dipeptidylpeptidase IV	dipeptidylpeptidase 4, ESTs, Weakly similar to DPP4 MOUSE DIPEPTIDYL PEPTIDASE IV [M.musculus], dipeptidylpeptidase IV (DPP IV) (GP110
				(CD26, adenosine deaminase	glycoprotein) (Bile canaliculus domain-specific membrane glycoprotein) [R.norvegicus], dioeptidylpeptidylpeptidase 8. fibroblast activation protein, fibroblast
3140	7784	NM_012789	BB, CC, II, OO	complexing protein 2)	activation protein, alpha
				DNA polymerase	
	7,70	77777	0		Mus musculus, Similar to DNA polymerase beta, clone MGC:6386 IMAGE:3581916,
3200	70147	ININ 017 141	רד, עע	(DINA directed), peta	mKNA, complete cas, polymerase (DINA directed), beta
			1 1 1 1	script 3,	UNA-damage inducible transcript 3, DNA-damage-inducible transcript 3, ESTs, Highly
,	7	4 6 0 0 4 10	Z, K, EEE,		SIMILATIO GROWIN AKKESI AND UNA-DAMAGE-INDUCIBLE PROTEIN GADD 153
2	0001	AA6864/0	MMM	Inducible transcript 3	[M.musculus], ESTs, Weakly similar to 1916411A TLS-CHOP protein [H.sapiens]
					DnaJ (Hsp40) homolog, subfamily A, member 2, DnaJ (Hsp40) homolog, subfamily B,
					member 11, DnaJ (Hsp40) homolog, subfmaily B, member 1, ESTs, Weakly similar to
				DnaJ (Hsp40)	DnaJ (Hsp40) homolog, subfamily A, member 2 [Rattus norvegicus] [R.norvegicus],
				homolog, subfamily A,	homolog, subfamily A, RIKEN cDNA 2810451A06 gene, RIKEN cDNA 5730496F10 gene, expressed sequence
3727	18492	NM_032079	王	member 2	AI506245
					DnaJ (Hsp40) homolog, subfamily A, member 2, DnaJ (Hsp40) homolog, subfamily B,
					member 11, DnaJ (Hsp40) homolog, subfmaily B, member 1, ESTs, Weakly similar to
				DnaJ (Hsp40)	DnaJ (Hsp40) homolog, subfamily A, member 2 [Rattus norvegicus] [R.norvegicus],
				homolog, subfamily A,	homolog, subfamily A, RIKEN cDNA 2810451A06 gene, RIKEN cDNA 5730496F10 gene, expressed sequence
3727	18494	NM_032079	РРР, ФОО	member 2	AI506245
				DnaJ (Hsp40)	
				homolog, subfamily B,	
3121	15616	NM_012699 Q	٥	member 9	

	Kenes Kenes				
	elec Idae	Content Recor Refsed ID	Model Gode	Human Homologous Known Gene Name Human Homologous	Sequence Cluster IIItle
2840	18686	D00729	B, I, J, U, FF, LL, XX, YY	A delta 3,2 trans- yme A A delta A delta 3,2 trans-	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
3335	18687	NM_017306		I- A delta (3,2 trans- Iyme A I- A delta (3,2 trans- Izyme A	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
1558	1431	Al044610	I, J, CC, II, General Alternate	dopa decarboxylase, dopa decarboxylase (aromatic L-amino acid decarboxylase)	EST, Highly similar to DDC_RAT Aromatic-L-amino-acid decarboxylase (AADC) (DOPA decarboxylase) (DDC) [R.norvegicus], EST, Moderately similar to DDC_RAT Aromatic-L-amino-acid decarboxylase (AADC) (DOPA decarboxylase) (DDC) [R.norvegicus], Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610109021:dopa decarboxylase, full insert sequence, dopa decarboxylase, dopa decarboxylase)

	ତ୍ର ୧୯				Afterney Boeket 44.921-5638-61W0
- 80 - 80 - 90 - 90 - 90 - 90 - 90 - 90 - 90 - 9	9 9 9 1	ලේකුවෙක්රි / Xee ලේ   Reise ලේ [ලි	Model Gede		มีขั้นกลัก เมื่อเมื่อใช้สู่อับระ  ได้เจิพภ Gene Namer   Human Homologous Sequence Gluster IIItle)
			TT, DDD, General Core	dopa decarboxvlase.	EST, Highly similar to DDC_RAT Aromatic-L-amino-acid decarboxylase (AADC) (DOPA decarboxylase) (DDC) [R.norvegicus], EST, Moderately similar to DDC_RAT Aromatic-Lamino-acid decarboxylase (AADC) (DOPA decarboxylase) (DDC) [R.norvegicus], Mus
			Tox Markers, General	dopa decarboxylase (aromatic L-amino	musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610109021:dopa decarboxylase, full insert sequence, dopa decarboxylase,
3046	1430	M84648	Alternate	acid decarboxylase)	dopa decarboxylase (aromatic L-amino acid decarboxylase)
				dopamine receptor 3,	
4218	492	X53944	RR	dopamine receptor D3	dopamine receptor D3 dopamine receptor 3, dopamine receptor D3
4229	1719	X59267	Z, AA, SS	drebrin 1	drebrin 1
3631	19096	NM_031352	<u> </u>	drebrin-like	
				dual specificity	
				phosphatase 1,	Mus musculus, clone MGC:11703 IMAGE:3964527, mRNA, complete cds, RIKEN
				protein tyrosine	cDNA 2310076D10 gene, RIKEN cDNA 4930527G07 gene, dual specificity
				phosphatase, non-	phosphatase 1, expressed sequence BB104621, protein tyrosine phosphatase, non-
3825	15995	NM_053769	I, J, Q, R	receptor type 16	receptor type 16
				dual specificity	
				phosphatase 1,	Mus musculus, clone MGC:11703 IMAGE:3964527, mRNA, complete cds, RIKEN
				protein tyrosine	cDNA 2310076D10 gene, RIKEN cDNA 4930527G07 gene, dual specificity
				phosphatase, non-	phosphatase 1, expressed sequence BB104621, protein tyrosine phosphatase, non-
3825	15996	NM_053769	C, I, J, R, LLL	receptor type 16	receptor type 16
				dual specificity	
				phosphatase 1,	Mus musculus, clone MGC:11703 IMAGE:3964527, mRNA, complete cds, RIKEN
				protein tyrosine	cDNA 2310076D10 gene, RIKEN cDNA 4930527G07 gene, dual specificity
				phosphatase, non-	phosphatase 1, expressed sequence BB104621, protein tyrosine phosphatase, non-
3825	15997	NM_053769	l, J, R	receptor type 16	receptor type 16

	ଞ				Attorney Bocket 44921-5665-01000   Attorney Bocket 44921-566508.1
89	elec Id No.	Comernik Ace or Rekseg (D		Human Homologous Known Gene Namer	Ruman Romologous Knowni Gener Nameri   Human Homologous Sequence (Gluster Mille)
				dynein, cytoplasmic, light chain 1, dynein,	ESTs, Moderately similar to protein inhibitor of nitric oxide synthase [M.musculus],
3747	17473	NM_053319	999	cytoplasmic, light polypeptide	dynein, axon, light chain 4, dynein, axonemal, light polypeptide 4, dynein, cytoplasmic, light chain 1, dynein, cytoplasmic, light polypeptide
				E26 avian leukemia	
				oncogene 1, 5	E26 avian leukemia oncogene 1, 5' domain, ESTs, Moderately similar to A53988
				domain, v-ets	transcription factor ets-1, splice form a - rat [R.norvegicus], Mus musculus ETS-domain
				erythroblastosis virus	transcription factor mRNA, complete cds, Rattus norvegicus ETS domain transcription
				E26 oncogene	factor Pet-1 mRNA, complete cds, v-ets erythroblastosis virus E26 oncogene homolog 1
3077	21836	NM_012555	NM_012555 O, P, PP, QQ	homolog 1 (avian)	(avian), v-ets erythroblastosis virus E26 oncogene like (avian)
			A, BB, CC,	early growth response	
3075	23868	NM_012551	NNN	1	early growth response 1, expressed sequence AI835008
			A, BB, CC,	early growth response	
3075	23869	NM_012551	NNN	-	early growth response 1, expressed sequence AI835008
				early growth response	
3075	23871	NM_012551	W	-	early growth response 1, expressed sequence AI835008
			(	early growth response	-
30/2	7,387	NM_012551	NM 012551 A, OO, NNN	1	early growth response 1, expressed sequence AI835008
				early growth response	
3355	16227	NM_019137	SS, XX, YY	4	RIKEN cDNA 4930563M09 gene, early growth response 4
				ectonucleotide	
				pyrophosphatase/pho	
				sphodiesterase 2,	
				ectonucleotide	
			E, Y, CC, HH,	pyrophosphatase/pho	
			General	sphodiesterase 2	ectonucleotide pyrophosphatase/phosphodiesterase 2, ectonucleotide
3878	9527	NM_057104   Alternate	Alternate	(autotaxin)	pyrophosphatase/phosphodiesterase 2 (autotaxin)

3028-011WG . 1985323.1						siial tgolipid G- 1-coupled ate hydro- lus 14, 17	
Altomay Docks (492/45	nan Homologous Seguence Chister Title	ectonucleotide pyrophosphatase/phosphodiesterase 2, ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	pancreatic	edpha =	e alpha	endothelial differentiation sphingolipid G-protein- coupled receptor 1, endothelial differentiation sphingolipid G-protein-coupled receptor 1, endothelial differentiation, differentiation, sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G- sphingolipid G-protein-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G- sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G- sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G-protein-coupled coupled receptor, 3 EST, Moderately similar to ENOA_RAT Alpha enolase (2-phospho-D-glycerate hydro-lyase) (NON-neural enolase) (NNE) (Enolase 1) [R.norvegicus], Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, enolase 1, alpha non-clone:3230402G19:enolase 1, alpha non-neuron, full insert sequence, enolase 1, alpha non-neuron, full insert sequence, enolase 1, alpha non-neuron, full insert sequence, enolase 1, alpha non-neuron, full insert sequence, enolase 1, alpha non-neuron, full insert sequence, enolase 1, alpha non-neuron, full insert sequence, enolase 1, alpha non-neuron, full insert sequence, enolase 1, alpha non-neuron, full insert sequence, enolase 1, alpha non-neuron, full insert sequence, enolase 1, alpha non-neuron, full insert sequence, enolase 1, alpha non-neuron, full insert sequence, enolase 1, alpha non-neuron, full insert sequence, enol	(alpha), enolase 1, alpha non-neuron, expressed sequence ALUZZ/84
	Human Ho	ectonuclec	elastase 1	endosulfine alpha	endosulfine alpha	endothelial differentiati protein-cou receptor, 3 EST, Mode lyase) (NOI days embry clone:3230,	(alpna), er
	Human Homologous Known Gene Name	ectonucleotide pyrophosphatase/pho sphodiesterase 2, ectonucleotide pyrophosphatase/pho sphodiesterase 2 (autotaxin)	elastase 1, pancreatic elastase 1, pancreatic	endosulfine alpha	endosulfine alpha	endothelial differentiation sphingolipid G-protein- coupled receptor 1, endothelial differentiation, sphingolipid G-protein- coupled receptor, 1 enolase 1, (alpha), enolase 1, alpha non-	neuron
	ी किया हिन्द्री	HH, General Alternate	F, M, Y	99	88, CC, PP, QQ	Z, General Core Tox Markers	G, ਜ, ∨∨
	Aee මැි යියේදීගේ (ම	NM_057104		AI169421	NM_021842	AA943737	NM_012554  G, H, VV
33	ecec: Idino	9528		24341	20114		1940/
MABLE 3	Seq. [D]	3878	2940	2019	3441	850	3076

TABLES	G.E.				Aftionney Boeket 44924-4668-61W0
 		ලිකි.   Age or   Re(Seg (D)	E TOTAL	Human Homologous Known Gene Name	lumen Homologous Sequence (luster Tille)
1497	1114	AI029917	E, DD, KKK, NNN	enolase 2, (gamma, neuronal), enolase 2, gamma neuronal	enolase 2, (gamma, neuronal), enolase 2, gamma neuronal
3495	20925	NM_022594	U, FF, LL, CCC, RRR, SSS	enoyl Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1,	EST, Moderately similar to Peroxisomal enoyl hydratase-like protein; enoyl hydratase-like protein, peroxisomal [Rattus norvegicus] [R.norvegicus], enoyl Coenzyme A.hydratase 1, peroxisomal, enoyl coenzyme A.hydratase 1, peroxisomal
3196	20926	NM 013013	Q Q	enoyl Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1, peroxisomal, prosaposin, prosaposin (variant Gaucher disease and I variant metachromatic feukodystrophy)	enoyl Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1, prosaposin (variant metachromatic gene, enoyl Coenzyme A hydratase 1, peroxisomal [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 2310020A21 variant metachromatic gene, enoyl Coenzyme A hydratase 1, peroxisomal, prosaposin (peroxisomal, prosaposin)
3897	21562	NM_078623	Ø	AU RNA b coenzyme hydrolase, enoyl Coenzyme A 1300017C hydratase, short enoyl Coechain, 1, mitochondrial FLJ10948	AU RNA binding protein/enoyl-Coenzyme A hydratase, AU RNA binding protein/enoyl-coenzyme A hydratase, Mus musculus, Similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase, clone MGC:31364 IMAGE:4238681, mRNA, complete cds, RIKEN cDNA 1300017C12 gene, RIKEN cDNA 1810022C23 gene, RIKEN cDNA 2310005D12 gene, enoyl Coenzyme A hydratase, short chain, 1, mitochondrial, hypothetical protein FLJ10948

TABLE	ভ্ৰ				The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
ි. මුල් මුල්	(CLGC)	<u>eensemx</u> Aecor Rasseplo	Model Godo	Human Homologous Known Gene Name	Humani Homologovs Sequence Gluster imite
				epidermal growth	
	,			ractor receptor,	
				factor receptor	
	-			(erythroblastic	EST, Moderately similar to EGFR_HUMAN EPIDERMAL GROWTH FACTOR
				leukemia viral (v-erb-	RECEPTOR PRECURSOR [H.sapiens], Homo sapiens truncated epidermal growth
				b) oncogene homolog,	o) oncogene homolog, factor receptor (EGFR) mRNA, partial cds; alternatively spliced, epidermal growth factor
694	17906	AA899762	NNN	avian)	receptor
				epidermal growth	
				factor receptor,	•
				epidermal growth	
				factor receptor	
				(erythroblastic	EST, Moderately similar to EGFR_HUMAN EPIDERMAL GROWTH FACTOR
····				leukemia viral (v-erb-	RECEPTOR PRECURSOR [H.sapiens], Homo sapiens truncated epidermal growth
				b) oncogene homolog,	b) oncogene homolog, factor receptor (EGFR) mRNA, partial cds; alternatively spliced, epidermal growth factor
2615	17907	AI233224	Ω	avian)	receptor
				epidermal growth	
				factor receptor,	
				epidermal growth	
				factor receptor	
				(erythroblastic	EST, Moderately similar to EGFR_HUMAN EPIDERMAL GROWTH FACTOR
		-	`	leukemia viral (v-erb-	RECEPTOR PRECURSOR [H.sapiens], Homo sapiens truncated epidermal growth
				b) oncogene homolog,	b) oncogene homolog, factor receptor (EGFR) mRNA, partial cds; alternatively spliced, epidermal growth factor
3022	16604	M37394	K, LLL, UUU	avian)	receptor
				epidermal growth	
				factor, epidermal	
	000	0,000		growth factor (beta-	Homo sapiens mRNA; cDNA DKFZp6670055 (from clone DKFZp6670055), epidermal
200	-T	NM 012842		urogastrone)	growth tactor, epidermal growth factor (beta-urogastrone), nidogen 2
2961	854	L20823	RR	epimorphin	

			<del></del>		
Attorney Doctract (1921-1938-6100)  Doctract No. 1935223.1	Human Homologous Sequence (cluster 1711)	epoxide hydrolase 1, microsomal, epoxide hydrolase 1, microsomal (xenobiotic)	EST, Weakly similar to S21055 translation elongation factor eEF-1 alpha chain - rat [R.norvegicus], ESTs, Highly similar to EFHU1 translation elongation factor eEF-1 alpha-1 chain [H.sapiens], ESTs, Weakly similar to S21055 translation elongation factor eEF-1 alpha chain - rat [R.norvegicus], G1 to S phase transition 1, G1 to phase transition 2, eukaryotic translation elongation factor 1 alpha 1	ESTs, Highly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], ESTs, Weakly similar to EF2_MOUSE Elongation factor 2 (EF-2) [M.musculus], ESTs, Weakly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], G elongation factor, Musmusculus, Similar to elongation factor G2, clone MGC:28160 IMAGE:3984129, mRNA, complete cds, U5 small nuclear ribonucleoprotein 116 kDa, U5 snRNP-specific protein, 116 kD, eukaryotic translation elongation factor 2, expressed sequence Al451340	ESTs, Highly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], ESTs, Weakly similar to EF2_MOUSE Elongation factor 2 (EF-2) [M.musculus], ESTs, Weakly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], G elongation factor, Musmusculus, Similar to elongation factor G2, clone MGC:28160 IMAGE:3984129, mRNA, complete cds, U5 small nuclear ribonucleoprotein 116 kDa, U5 snRNP-specific protein, 116 kD, eukaryotic translation elongation factor 2, expressed sequence Al451340
	Human Homologous Known Gene Name	epoxide hydrolase 1, microsomal, epoxide hydrolase 1, microsomal (xenobiotic)	eukaryotic translation elongation factor 1 alpha 2	eukaryotic translation elongation factor 2	eukaryotic translation elongation factor 2
	Modell Gode	F, N, S, CC, II, NN, OO, PP, QQ, TT, DDD, EEE, LLL, MMM, SSS, UUU, General Alternate	H	N, RR	ш
	Aee or Reisseg 10	NM_012844	NM_033539	NM_017245	NM_017245
E3	9979 100 (136)	17541	24420	17561	17563
MABL	(1)	3156	3738	3316	3316

TABLES	ଞ୍ଚ				
Seq. (D-	erec Idino.	Geneent Aeeor Refeq ID	Model Godo	Human Homologous Known Genei Name	ogovs Seqvence Guster Titue
					ESTs, Highly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], ESTs, Weakly similar to EF2_MOUSE Elongation factor 2 (EF-2) [M.musculus], ESTs, Weakly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], G elongation factor, Mus musculus Similar to elongation factor 62 close MGC 28160 [MAGE 3084129 mBNA
3316	17562	NM_017245	<b>&gt;</b>	2, mitogen-activated protein kinase kinase 2	complete cds, U5 small nuclear ribonucleoprotein 116 kDa, U5 snRNP-specific protein, 116 kD, eukaryotic translation elongation factor 2, expressed sequence Al451340, mitogen activated protein kinase kinase 2
				eukaryotic translation elongation factor 2,	
				mitogen activated protein kinase kinase	
3932	17560	NM 133283	Z	z, mitogen-activated protein kinase kinase	
				eukaryotic translation initiation factor 2 alpha	
				kinase 3, eukaryotic	EST, Weakly similar to eukaryotic translation initiation factor 2 alpha kinase 3 [Rattus
3655	14295	NM 031599		translation initiation ZZ, AAA, PPP, factor 2-alpha kinase QQQ	norvegicus] [R.norvegicus], eukaryotic translation initiation factor 2 alpha kinase 3, eukaryotic translation initiation factor 2 alpha kinase 4, eukaryotic translation initiation factor 2-alpha kinase 3
000	2	0.70	C	eukaryotic translation initiation factor 4A,	ESTs, Weakly similar to EUKARYOTIC INITIATION FACTOR 4A-II [M.musculus],
3414	18713	020078 870078	0 C	eukaryotic translation	eukaryolic translation initiation ractor 4A, Isolorm 2  DNA segment, Chr 1, ERATO Doi 692, expressed, ESTs, Highly similar to  EUKARYOTIC TRANSLATION INITIATION FACTOR 5 [R.norvegicus], KIAA1856
3414	18715	NM_020075		eukaryotic translation initiation factor 5	DNA segment, Chr 1, ERATO Doi 692, expressed, ESTs, Highly similar to EUKARYOTIC TRANSLATION INITIATION FACTOR 5 [R.norvegicus], KIAA1856 protein, eukaryotic translation initiation factor 5

. Attorney Docket 44924-5038-611W6	มีบักลาก Homologous Xnown Cene Name   Human Homologous Sequence @luster intle	farnesyl diphosphate farnesyl transferase 1, farnesyl-diphosphate farnesyltransferase 1	farnesyl diphosphate farnesyl transferase 1, farnesyl-diphosphate farnesyltransferase 1		geranyltranstransferas ESTs, Moderately similar to A34713 farnesyl-pyrophosphate synthetase, testis - rat [R.norvegicus], ESTs, Weakly similar to A34713 farnesyl-pyrophosphate synthetase, diphosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)
	Human Homologous Known Gene Name	farnesyl diphosphate farnesyl transferase 1, farnesyl-diphosphate farnesyltransferase 1	farnesyl diphosphate farnesyl transferase 1, farnesyl-diphosphate farnesyltransferase 1	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstrans ferase,	geranyltranstransferas e), farnesyl diphosphate synthetase
	Model Gode	SS, KKK, OOO, General Alternate	C, I, J, FF, OOO, General Alternate		
	consent Lecor Refseq (D=	NM_019238	NM_019238		3707 15069 NM_031840 Alternate
38	erec Dina	16449	16450		15069
TWEES	(D. Q.)	3378	3378		3707

TABEL	<u>ell</u> 33.				Altomey Docket (1927-5008-6100)
	elec Idon	ලබෙනිනෙන්යි.  නීමෙ ගේ.  යිස්තිලේ [1ව ු	जिल्ला (इन्ट्रा)	Human Homologous Known Gene Name	Numen Homologous ใก้อัพภ์ Gene Name   HumaniHomologous Sequence (duster ITMe
3707	15070	N N S S S S S S	H-	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstrans ferase, geranyltranstransferase), farnesyl diphosphate	farnesyl diphosphate synthase (farnesyl synthase (farnesyl synthetase, dimethylallyltranstrans ferase, geranyltranstransferas ESTs, Moderately similar to A34713 farnesyl-pyrophosphate synthetase, testis - rat [R.norvegicus], farnesyl diphosphate synthase (farnesyl pyrophosphate synthase (farnesyl pyrophosphate synthatase)
		I		hosphate arnesyl	
		··		synthetase, dimethylallyltranstrans ferase,	
				geranyltranstransferas e), farnesyl diphosphate	geranyltranstransferas ESTs, Moderately similar to A34713 farnesyl-pyrophosphate synthetase, testis - rat (R.norvegicus), ESTs, Weakly similar to A34713 farnesyl-pyrophosphate synthetase, testis - rat (R.norvegicus), farnesyl diphosphate synthase (farnesyl pyrophosphate
3157	25460 20819	NM 031840 NM 012847	I, J, T W, General Alternate	synthetase farnesyltransferase, CAAX box, alpha	synthetase, dimethylallyltranstransferase, geranyltranstransferase) farnesyltransferase, CAAX box, alpha
			A, B, III, JJJ, KKK, 000, PPP, 000,		
4162	851	U72497	General Core Tox Markers	hydrolase, fatty acid hydroxylase	RIKEN cDNA 2700038P16 gene, fatty acid amide hydrolase
3078	17676	NM_012556 N, HH	N, HH	fatty acid binding protein 1, liver	fatty acid binding protein 1, liver

TABL	31 <u>5</u> 3				Attorney Docket 4:1924-5038-01WO
See	લિલ્લ	<u>   ©emasani  </u>   Aee or		Rymenillomologous	
	ID No.	Raksali	(अन्त्रधा दन्त	Known Gene Name	HumaniHomologovs Sequence, Gluster, Jule
4087	40	U02096	II, MM, XX,	fatty acid binding protein 7, brain	Homo sapiens mRNA; cDNA DKFZp547J2313 (from clone DKFZp547J2313), fatty acid binding protein 7 brain
					ESTs. Weakly similar to fatty acid Coenzyme A ligase. long chain 2: acetyl-Coenzyme
					A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming);
					acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty-
					acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA,
					complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone
		-		fatty acid Coenzyme	MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long
			H, BBB, CCC,	A ligase, long chain 2,	chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-
			RRR, General	fatty-acid-Coenzyme	chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipidosis-related
628	20985	AA893242	Alternate	A ligase, long-chain 2	protein lipidosin
					ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme
			-		A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming);
	_				acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty-
					acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA,
					complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone
,			A, B, BBB,	fatty acid Coenzyme	MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long
			CCC, FFF,	A ligase, long chain 2,	chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-
			General	fatty-acid-Coenzyme	chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipidosis-related
628	20986	AA893242	Alternate	A ligase, long-chain 2	protein lipidosin
					ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme
					A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming);
-			A, FF, JJ, KK,		acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty-
			LL, FFF, HTH,		acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA,
			SSS, General		complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone
			Core Tox	fatty acid Coenzyme	MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long
			Markers,	A ligase, long chain 2,	chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-
			General	fatty-acid-Coenzyme	chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipidosis-related
1566	20983	A1044900	Alternate	A ligase, long-chain 2	protein lipidosin

	ල ლ				Attorney Dockst 44924-5038-01W0  Document No. 1995523.1
	GLGG BNo.	Consent. Ace or Rober 10	Model Gode	Ruman Homologous Knovin Gener Name	ໃນເກືອກ ເກືອກວໄວgous ໃດວະນາ Gene Name:   Human klomologous Sequence @luster Mile:
2881	20984	D90109	U, FF, FFF, HHH, General Alternate	fatty acid Coenzyme A ligase, long chain 2, fatty-acid-Coenzyme A ligase, long-chain 2	ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipidosis-related protein lipidosin
2858	3743	D30666	888	fatty acid Coenzyme A ligase, long chain 3, fatty-acid-Coenzyme A ligase, long-chain 3	fatty acid Coenzyme A ligase, long chain 3, fatty-acid-Coenzyme A ligase, long-chain 3
3803		209800 WN	Ф	fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-chain 5	ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone A ligase, long chain 5, MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long fatty-acid-Coenzyme A ligase, long-chain 5, hypothetical protein PRTD-NY3

Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Service   Complete Se		8 8 1				AMOGRACY BOCKET AND THE SECOND OF THE SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND
fatty acid Coenzyme A ligase, long chain 5, I, J, General fatty-acid-Coenzyme A ligase, long-chain 5 IL, BBB, CCC, fatty-acid-Coenzyme A ligase, long-chain 4, ILL, BBB, CCC, fatty-acid-Coenzyme A ligase, long-chain 4 Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of I	Sed Sed	@L@@ 10 No.	Keintenk Aeetr Reiseg ID	Medal Gede		HumaniHomologovis Segvence (Ruster-Intile)
fatty acid Coenzyme 15926 NM_053607 Alternate A ligase, long chain 5, 1, J, General fatty-acid-Coenzyme 13005 NM_053623 RRR A ligase, long-chain 4 LL, BBB, CCC, fatty-acid-Coenzyme A ligase, long-chain 4 RC fragment of IgG, low affinity IIIa, receptor for (CD16), O, P, NN, OO, Fc receptor, IgG, low affinity IIIa, receptor for (CD16), O, P, NN, OO, Fc fragment of IgG, low affinity IIIa, receptor for (CD16), O, P, V, NN, Fc receptor, IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III						ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA,
tatty acid-Coenzyme A ligase, long chain 4, LL, BBB, CCC, fatty-acid-Coenzyme A ligase, long-chain 4 Fc fragment of IgG, low affinity Illa, receptor for (CD16), O, P, NN, OO, Fc receptor, IgG, low affinity Illa Fc fragment of IgG, low affinity Illa Fc fragment of IgG, low affinity Illa Fc fragment of IgG, low affinity Illa Fc fragment of IgG, receptor, transporter, lgG, alpha chain 12363 NM 033351 N transporter	3803	15926	NM 053607		fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme	complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long-chain 5, fatty-acid-Coenzyme A ligase, long-chain 5, hypothetical protein PRTD, NY3
13005 NM 053623 RRR A ligase, long chain 4, LL, BBB, CCC, fatty-acid-Coenzyme A ligase, long-chain 4 Fc fragment of lgG, low affinity IIIa, receptor for (CD16), O, P, NN, OO, Fc receptor, lgG, low affinity III Fc fragment of lgG, low affinity IIIa, receptor for (CD16), O, P, V, NN, Fc receptor, lgG, low affinity III Fc fragment of lgG, low affinity III Fc fragment of lgG, low affinity III Fc fragment of lgG, receptor, transporter, lgG, alpha chain ltansporter				1		
13005 NM_053623 RRR					<u> </u>	
20868 NM 053843 VV affinity IIIa, receptor for (CD16), O, P, NN, OO, Fc receptor, IgG, low affinity III Fc fragment of IgG, low affinity IIIa, receptor for (CD16), O, P, V, NN, Fc receptor, IgG, low affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, receptor, IgG, low affinity III Fc fragment of IgG, receptor, transporter, lgG, alpha chain Itansporter	3806	13005	  NM_053623			
20868 NM 053843 VV affinity III receptor for (CD16), affinity III Fc fragment of IgG, low affinity III Fc fragment of IgG, low affinity III receptor for (CD16), O, P, V, NN, Fc receptor, IgG, low affinity III Fc fragment of IgG, receptor, transporter, lgG, alpha, Fc receptor, transporter, lgG, alpha, Fc receptor, lgG, low affinity III Fc fragment of IgG, receptor, transporter, lgG, alpha chain ltransporter					Fc fragment of IgG,	
20868 NM_053843 VV affinity III  For fragment of IgG, low affinity IIIa, receptor for (CD16), O, P, V, NN, For eceptor, IgG, low affinity III  For fragment of IgG, low affinity IIIa, For eceptor, IgG, low affinity III  For fragment of IgG, receptor, transporter, alpha, For eceptor, transporter, lgG, alpha chain Itansporter					receptor for (CD16).	
20869 NM_053843 OO, VV affinity III receptor, IgG, Iow affinity III receptor, IgG, Iow affinity III receptor, IgG, Iow affinity III receptor, IgG, Iow affinity III receptor, IgG, Iow affinity III receptor, Igg, Iow affinity III receptor, Igg, Iow affinity III receptor, Igg, Iow affinity III receptor, Inasporter, IgG, alpha chain Itansporter	3636	9900	NIM OF 2012		Fc receptor, IgG, low	
low affinity IIIa, receptor for (CD16), Co, P, V, NN, Fc receptor, IgG, low affinity III Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha, Fc receptor, IgG, alpha chain IgG, alpha chain Itansporter	3	20007	20000	,	Fc fragment of IgG,	
20869 NM_053843 OO, VV affinity III  For fragment of IgG, low affinity III  For fragment of IgG, low affinity III  For fragment of IgG, low affinity III  For fragment of IgG, low affinity III  For fragment of IgG, low affinity III  For fragment of IgG, low affinity III  For fragment of IgG, low affinity III  For fragment of IgG, low affinity III  For fragment of IgG, low affinity III  For fragment of IgG, low affinity III  For fragment of IgG, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low affinity III  For fragment in the Igg, low aff					low affinity Illa,	
20869 NM_053843 OO, VV affinity III For fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain Itansporter				O. P. V. NN.	Fc receptor, IqG, low	
Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain transporter	3838	20869	NM_053843		affinity III	
receptor, transporter, alpha, Fc receptor, lgG, alpha chain 12363 NM 033351 N transporter					Fc fragment of IgG,	
alpha, Fc receptor, lgG, alpha chain 12363 NM_033351 N transporter					receptor, transporter,	
12363 NM 033351 N transporter					alpha, Fc receptor,	
	3736				IgG, alpha chain transporter	Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain transporter

TABUE 8	ଜ				Aitomey Doeket (49221-5958-61W0 ************************************
ි ගිනීම් ම	ි මැම්ල 10 No.	ලෙක්වෙක්ද 	10 a No. 101	Human Homologous Known Gene Name	Model Code   Known Cene Name   Human Homologous Sequence (duster julie
				Fc fragment of IgG,	
				receptor, transporter,	
			·	alpha, Fc receptor,	ciodo edelo. On returnos el edelo returnos estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados estados est
3736	12365.	12365 . NM_033351	<b>LL</b>	transporter	re nagiment of 196, receptor, transporter, alpha, ne receptor, 196, alpha chain transporter
3282	21663	NM_017126	E, 888, CCC	ferredoxin 1	ferredoxin 1, similar to RIKEN cDNA B230118G17 gene
			CC, GG, HH, EEE, III, JJJ		
			MMM, General	٠	ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.noryegicus].
			Core Tox		ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus],
			Markers,	ferritin light chain 1,	RIKEN cDNA 2010009K05 gene, RIKEN cDNA 4933416E14 gene, cysteine conjugate-
			General	ferritin, light	beta lyase; cytoplasmic (glutamine transaminase K, kyneurenine aminotransferase),
2104	8215	A1171692	Alternate	polypeptide	ferritin light chain 1, ferritin light chain 2, ferritin, light polypeptide
					ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus],
		-	F, PP, QQ,	ferritin light chain 1,	ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus],
			Λ, LLL,	ferritin, light	RIKEN cDNA 4933416E14 gene, ferritin light chain 1, ferritin light chain 2, ferritin, light
2033	8213	AI169883	ດດດ	polypeptide	polypeptide
					ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus],
				ferritin light chain 1,	ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus],
	,	00000 1414	N, MM, UDU,	rerritin, lignt	KIKEN CUNA 4933416E14 gene, territin light chain 1, territin light chain 2, territin, light
04/3	1170	000270 MN	-+	polypeptide	polypeptide
			H H C	A character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the character of the char	ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus],
			, , ,	rerriin light chain 1,	ESTS, Moderately Similar to FRLZ MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus],
3473	8212	NM 022500 UUU	טטט, רגר,	territin, light polypeptide	RIKEN cDNA 4933416E14 gene, ferritin light chain 1, ferritin light chain 2, ferritin, light polynentide
_			IBB CC MM		ESTs Moderately similar to ferritin light chain 1 (Battus nonvenious) (P nonvenious)
			UU, TTT,	ferritin light chain 1,	ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus],
			General	ferritin, light	RIKEN cDNA 4933416E14 gene, ferritin light chain 1, ferritin light chain 2, ferritin, light
4063	8210	S61960	Alternate	polypeptide	polypeptide

TABLE 9	38 a				Aitomey/Docket 4492145039-01W0
See	କ୍ରା ଜିନ୍ତ ଜ୍ୟା ଜିନ୍ତ	(ජමබාවෙකුයි   වූල්ලේ බැ		Himsa Homologous	Human Homologons
<u>.</u>	lo kiể,	RefSeq (D	Model Gode	Known Gene Name	Human Homologous Sequence @luster mile
3753	14042	NM_053348 N, YY		fetuin B, fetuin beta	expressed sequence AW413091, fetuin B, fetuin beta, histidine-rich glycoprotein
				fibrinogen, A alpha	
				polypeptide, fibrinogen, alpha	
3019	20699	M35601	E, KKK	polypeptide	
				fibrinogen, A alpha	
				polypeptide,	
			E, L, S, X, Y,	fibrinogen, alpha	
3019	20700	M35601	NNN	polypeptide	
			BB, CC, DD,		
			EE, LL, SS,		
			DDD, III, JJJ,		
			LLL, NNN,	fibrinogen, gamma	
2027	6479	AI169690	ດດດ	polypeptide	
			E, N, LL, MM,		
			KKK, NNN,	fibrinogen, gamma	
3080	6477	NM_012559	E	polypeptide	
			E, J, S, X, Y,		
-			DD, EE, KKK,	fibrinogen, gamma	
280	6478	NM_012559	ZZZ	polypeptide	
				fibroblast growth	
		;		arouth factor 1	
4199	644	X14232	<i>≻</i> ×	(acidic)	fibroblast growth factor 1. fibroblast growth factor 1 (acidic)
				fibroblast growth	
3049	13488	M91599	^	factor receptor 4	
				fibroblast growth	
3049	13489	M91599	nnn	factor receptor 4	

TABLES	ଞ୍ଚ				Attorney Docket 44921-5039-01W0
8 9	elege Id No.	Centenik Acetor Refsee 10	Medell Gede	Human Homologous Known Gene Name	HumaniHomologous
			N. C. C. C.	Finkel-Biskis-Reilly	
				murine sarcoma virus	
				(FBR-MuSV)	
		-		ubiquitously	
				expressed (fox	
				derived), Finkel-Biskis-	
				Reilly murine sarcoma	
				virus (FBR-MuSV)	EST, Moderately similar to I48346 ribosomal protein fau - mouse [M.musculus], EST,
			_	ubiquitously	Weakly similar to UBIM_HUMAN UBIQUITIN-LIKE PROTEIN FUBI (SUB 1-74
				expressed (fox	[H.sapiens], EST, Weakly similar to UBIM_RAT UBIQUITIN-LIKE PROTEIN FUBI
				derived); ribosomal	[R.norvegicus], Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously
4243	20821	X62671	F, T	protein S30	expressed (fox derived)
				FK506 binding protein	
				1A (12kD), FK506	FK506 binding protein 10 (65 kDa), FK506 binding protein 1A (12kD), FK506 binding
				binding protein 1a (12	protein 1a (12 kDa), FK506 binding protein 5, FK506 binding protein 7 (23 kDa), FK506
2193	6782	AI176170	FFF	kDa)	binding protein 8 (38 kDa)
				FK506 binding protein 14 (12kD). FK506	
				binding protein 1a (12	
			•	kDa), FK506 binding	
				protein 2 (13 kDa),	FK506 binding protein 10 (65 kDa), FK506 binding protein 1A (12kD), FK506 binding
				FK506 binding protein	FK506 binding protein protein 1a (12 kDa), FK506 binding protein 5, FK506 binding protein 7 (23 kDa), FK506
3220	15295	NM_013102 P, HH, JJ	Р, НН, ЈЈ	2 (13kD)	binding protein 8 (38 kDa)

	8 8				Attorney Docket (4.92A-5959-0MW)
68 99 19	elec Dina	leomisemk Ace or Rekseq (D)	Medell Code	Human Homologous Known Gene Name	Hornologous Gene Name   Human Homologous Sequence ©lusterimile: 제가
				FK506 binding protein 1A (12kD), FK506	
				binding protein 1a (12 kDa), FK506 binding protein 2 (13 kDa),	=K506 binding protein 10 (65 kDa), FK506 binding protein 1A (12kD), FK506 binding
3220	15296	NM 013102	O H H	FK506 binding protein 2 (13kD)	FK506 binding protein protein 1a (12 kDa), FK506 binding protein 5, FK506 binding protein 7 (23 kDa), FK506 2 (13kD)
		A, GG, II, T	A, GG, II, TT,		EST, Weakly similar to FMO1 MOUSE DIMETHYLANILINE MONOOXYGENASE
			III, JJJ, LLL, SSS, UUU,		[M.musculus], ESTs, Weakly similar to S33758 flavin-containing monooxygenase 1 - rat [R.norvedicus], Mus musculus flavin-containing monooxygenase 4 mRNA, complete
			General Core	flavin containing	cds, expressed sequence AW107733, flavin containing monooxygenase 1, hypothetical
3141	23445	NM_012792		monooxygenase 1	protein PRO1257
3512	24345	NM_022701	g	flotillin 1	flotillin 1
3639	10167	NM_031830 PP, QQ		flotillin 2	flotillin 2
				forkhead box A3,	ESTs, Weakly similar to HN3G_RAT HEPATOCYTE NUCLEAR FACTOR 3-GAMMA
3274	1262	R, MM	R, MM, NN,	hepatocyte nuclear	(HNF-3G) [R.norvegicus], RIKEN cDNA 1200010K03 gene, expressed sequence
4174	906	U83112		forkhead box M1	Art 2002 I, Tot Micad Dox As, Tot Micad Dox DI, Tepanosyte Tucced Tacks S, gailing
					ESTs, Moderately similar to formiminotransferase cyclodeaminase; human
				rase	formiminotransferase cyclodeaminase [Homo sapiens] [H.sapiens],
3791	9267	NM_053567	00, PP, TT	cyclodeaminase	formiminotransferase cyclodeaminase
				fracture callus 1	EST, Moderately similar to IM9B_HUMAN MITOCHONDRIAL IMPORT INNER
				homolog (rat),	MEMBRANE TRANSLOCASE SUBUNIT TIM9 B (FRACTURE CALLUS PROTEIN 1)
209	3844	AA891857	U, FF, RRR, SSS, UUU	fractured callus expressed transcript 1	(FXC1) [H.sapiens], fracture callus 1 homolog (rat), fractured callus expressed transcript 1

	G E				Attorney Doelret 4492/1-5038-04W/0
	elec Ole Ole	ලේක්වෙක්ය . සරේපිලේ [ලි	   Modell ලිලේල	* 5. 5.	<u>บกาสกเหอกางใจจับรา</u> ภิจจังกา GenetName   หมีเกาสาเหมือกางใจจุดบรเรียดุบยกละ Gluster Tittle
3756	3842	NM_053371	ввв, ссс	fracture callus 1 homolog (rat), fractured callus expressed transcript 1	EST, Moderately similar to IM9B_HUMAN MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM9 B (FRACTURE CALLUS PROTEIN 1) (FXC1) [H.sapiens], fracture callus 1 homolog (rat), fractured callus expressed transcript
3422	21336	NM_021266	nnn	frizzled homolog 1 (Drosophila), frizzled homolog 1, (Drosophila)	frizzled homolog 1 (Drosophila), frizzled homolog 1, (Drosophila), frizzled homolog 7 (Drosophila)
1790	19373	A1102044	NNN FF	frizzled homolog 1 (Drosophila), frizzled homolog 1, (Drosophila)	
3248	15621	NM_017005	Υ,		fumarate hydratase, fumarate hydratase 1
3302	23961	NM_017181	PPP, QQQ	fumarylacetoacetate hydrolase, fumarylacetoacetate hydrolase (fumarylacetoacetase)	fumarylacetoacetate hydrolase, fumarylacetoacetate ESTs, Weakly similar to FAAA_RAT Fumarylacetoacetase (Fumarylacetoacetate hydrolase) (Beta-diketonase) (FAA) [R.norvegicus], fumarylacetoacetate hydrolase, (fumarylacetoacetase) [fumarylacetoacetase)
			F, General	FXYD domain containing ion transport regulator 1 (phospholemman), FXYD domain-containing ion	EST, Weakly similar to PLM_HUMAN PHOSPHOLEMMAN PRECURSOR [H.sapiens], FXYD domain containing ion transport regulator 1 (phospholemman), FXYD domain-
3663	18368	NM_031648 Alternate	Alternate	transport regulator 1	containing ion transport regulator 1, FXYD domain-containing ion transport regulator 6

TABLES	38				Altoriney Docket 4/192/1-5088-0/10/05 The Document No. 1995323.1
Seq.	erec ID No.	ලොකො Ae ගේ Rණිදීලේ ලි	Model Gode	Human Homologous Known Gene Name	Human Homologous Known Genen Name Human Homologous Séquence Guister Musi
				FXYD domain containing ion transport regulator 1 (phospholemman), FXYD domain-	EST. Weakly similar to PLM HUMAN PHOSPHOLEMMAN PRECURSOR (H saniens)
3663	18369	NM_031648	S, General Alternate		EXYD domain containing ion transport regulator 1 (phospholemman), FXYD domain-containing ion transport regulator 1, FXYD domain-containing ion transport regulator 6
2956	1228	L14684	BBB, CCC		
857	867	AA943963	<b>c</b> .		ESTs, Weakly similar to GRK6 MOUSE G PROTEIN-COUPLED RECEPTOR KINASE GRK6 [M.musculus], G protein-coupled receptor kinase 6, adrenergic receptor kinase, beta 1
3694	17194	NM_031814	ZZ, AAA	G protein-coupled receptor kinase-interactor 1	DKFZP434B203 protein, G protein-coupled receptor kinase-interactor 1, G protein- coupled receptor kinase-interactor 2
3018	1241	M35162	D, Z, AA	gamma-aminobutyric acid (GABA) A receptor, delta, gamma-aminobutyric acid (GABA-A) receptor, subunit delta	gamma-aminobutyric acid (GABA) A receptor, delta, gamma-aminobutyric acid (GABA-A)  MGC:28005 IMAGE:3602400, mRNA, complete cds, gamma-aminobutyric acid (GABA) receptor, subunit delta A receptor, delta
2400	2052	AI227854	RR	gamma-aminobutyric acid (GABA) B receptor, 1, gamma- aminobutyric acid (GABA-B) receptor, 1	

Altomay Dockat 4/92A-5008-0M	Homorogouss GeneuName   HumaniHomologous/Sequence(Gluster/IIIIIe	tor, gamma-aminobutyric acid (GABA) receptor, rho 1, gamma-aminobutyric acid (GABA-A)	gamma-glutamyl carboxylase	amma-glutamyl ydrolase, gamma- sonjugase, lylpolygammaglutam gamma-glutamyl hydrolase, gamma-glutamyl hydrolase (conjugase,	sp junction embrane channel oten alpha 5, gap junction membrane channel brotein alpha 5, gap junction protein, alpha 5, 40kD (connexin 40)	ta 32, th RIKEN cDNA D230044M03 gene, gap junction protein, beta 1, 32kD (connexin 32, ed) Charcot-Marie-Tooth neuropathy, X-linked)
	Humen Kaowa	gamma-aminobutyric acid (GABA) receptor, rho 1, gamma- aminobutyric acid (GABA-A) receptor, subunit rho 1	gamma-glutamyl carboxylase	gamma-glutamyl hydrolase, gamma-glutamyl hydrolase (conjugase, folylpolygammaglutayl hydrolase)	gap junction membrane channel protein alpha 5, gap junction protein, alpha g 5, 40kD (connexin 40) (	gap junction membrane channel protein beta 1, gap junction protein, beta 1, 32kD (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)
	Modell Gode	*	C, FF	, χ, χ	Z, AA	General Alternate
	ජෙකාවකායි  Aee මැ  RefSeq (D	NM_017291	NM_031756	U38379	NM_019280	X04070
න ම	elec Io No	16839	11611	368	1143	419
TABL		3332	3684	4125	3385	4188

rotein nosine DP) bitor 1 bitor 1 bed ed	म्लामह	<b>E</b> 33				
GATA binding protein  GATA binding protein  GATA binding protein  GATA binding protein  GDP dissociation  Inhibitor 1, guanosine diphosphate (GDP)  General  General  General  General  Glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose		@LGC ID No.		Model Gode		HumaniHomologous Sequence Cluster Title
GDP dissociation inhibitor 1, guanosine diphosphate (GDP)  18679 Al103496 AA dissociation inhibitor 1 General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General	3365	23481	NM_019185	<b>&gt;</b>	GATA binding protein 6	GATA binding protein 5, GATA binding protein 6
18679 A1103496 AA dissociation inhibitor 1    EEE, MMM, General General Glucagon receptor glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kDa, glucose regulated protein, 58 kD glucose regulated protein, 58 kD glucose-6-phosphatase, catalytic, glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease)					GDP dissociation inhibitor 1, guanosine diphosphate (GDP)	
EEE, MMM,  General  General  General  General  glucagon receptor  glucose regulated protein, 58 kDa,  glucose regulated protein, 58 kD  glucose regulated phosphatase, catalytic, glucose-6- phosphatase, catalytic, glucose-6- phosphatase, catalytic, glucose-6- phosphatase, catalytic, glucose-6- phosphatase, catalytic, glucose-6- phosphatase, catalytic (glycogen storage disease type I, von Gierke disease)	1842	18679	A1103496	AA	dissociation inhibitor 1	GDP dissociation inhibitor 1, guanosine diphosphate (GDP) dissociation inhibitor 2
1678 M96674 Alternate glucagon receptor glucose regulated protein, 58 kDa, glucose regulated protein, 58 kD glucose regulated protein, 58 kD glucose regulated protein, 58 kD glucose-6-phosphatase, catalytic, glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease)				EEE, MMM,		
glucose regulated protein, 58 kDa, glucose regulated glucose regulated glucose regulated protein, 58 kDa, glucose regulated protein, 58kD glucose-6-phosphatase, catalytic, glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease)	3055		M96674	Seneral	glucagon receptor	ES IS, Weakly Similar to GLUCAGON RECEPTOR PRECURSOR [M.musculus], glucagon receptor
20789 NM_017319 M, U, LL protein, 58kD glucose regulated protein, 58kD glucose-6-phosphatase, catalytic glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease)					glucose regulated	
20789 NM_017319 M, U, LL protein, 58kD glucose-6-phosphatase, catalytic, glucose-6-phosphatase, catalytic glucose-6-phosphatase, glycogen storage disease type I, von Gierke disease)					glucose regulated	
glucose-6- phosphatase, catalytic, glucose-6- phosphatase, catalytic (glycogen storage disease type I, von 1322 AA964628 W Gierke disease)	3339	20789	NM_017319		protein, 58kD	
catalytic, glucose-6-phosphatase, catalytic (glycogen storage disease type I, von 1322 AA964628 W Gierke disease)					glucose-6- phosphatase,	
phosphatase, catalytic (glycogen storage disease type I, von 1322 AA964628 W Gierke disease)					catalytic, glucose-6-	ESTs, Weakly similar to G6PT_RAT Glucose-6-phosphatase (G6Pase) (G-6-Pase)
(glycogen storage disease type I, von 1322 AA964628 W Gierke disease)					phosphatase, catalytic	[R.norvegicus], RIKEN cDNA 0710001K01 gene, glucose-6-phosphatase, catalytic,
disease type I, von 1322 AA964628 W Gierke disease)					(glycogen storage	glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease),
	1083		AA964628		disease type I, von Gierke disease)	glucose-6-phosphatase, catalytic, related sequence, hypothetical protein BC002494, islet-specific glucose-6-phosphatase catalytic subunit-related protein

	डाडि ३				
	GLGC Dive	ලෙකවෙකි? ෆිලෙගේ (දිරුලල්) [0	Model Godo	Ruman Honologous Known Gene Name	ister Mile
				glucose-6- phosphatase,	EQTe Moskly cimilar to GROT BAT Cluster, and assessing a passive section of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of th
				phosphatase, catalytic (glycogen storage	phosphatase, catalytic (R.norvegicus), RIKEN cDNA 0710001K01 gene, glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease),
3218	1321	NM_013098		disease type I, von Gierke disease)	glucose-6-phosphatase, catalytic, related sequence, hypothetical protein BC002494, islet-specific glucose-6-phosphatase catalytic subunit-related protein
				-g-esconig	
			EEE, LLL, www, prosphatase, EEE, LLL,	pnospnatase, transport (glucose-6-	Mus musculus. Similar to solute carrier family 37 (glycerol-3-phosphate transporter)
	•		χ.	phosphate) protein 1,	member 1, clone MGC:28167 IMAGE:3985469, mRNA, complete cds, glucose-6-
			J,	-9-esonlb	phosphatase, transport (glucose-6-phosphate) protein 1, glucose-6-phosphatase,
			General	phosphatase,	transport protein 1, solute carrier family 37 (glycerol-3-phosphate transporter), member
3653	5496	NM_031589	Alternate	transport protein 1	
				-g-esoon B	
				phosphatase,	
			50	ransport (giucose-o-	inus musculus, Similar to solute carrier family 37 (glycerol-3-phosphate transporter), member 1. close MCC 38467 MAACE 3085460 mDNA complete add. closes 6
			_	glucose-6-	phosphatase, transport (alucose-6-phosphate) protein 1. alucose-6-phosphatase
				phosphatase,	transport protein 1, solute carrier family 37 (glycerol-3-phosphate transporter), member
3653	5497	NM_031589	กกก	transport protein 1	
				glucose-6-phosphate	
				dehydrogenase,	
				glucose-6-phosphate	glucose-6-phosphate dehydrogenase, glucose-6-phosphate dehydrogenase 2, glucose-
- 0			!	dehydrogenase X-	6-phosphate dehydrogenase X-linked, hexose-6-phosphate dehydrogenase (glucose 1-
3249	1399	NM 01/006	G, FF	linked	denydrogenase)

Attorney Docket 4492/1-5068-01/Wo	Name Human Homologows Sequence Quister Muor		glutamate dehydrogenase, glutamate dehydrogenase 1			glutamate dehydrogenase, glutamate dehydrogenase 1											ESTs, Highly similar to AATM_RAT ASPARTATE AMINOTRANSFERASE,		•			transaminase 2, mitochondrial, glutamic-oxaloacetíc transaminase 2, mitochondrial					
Humani Homologo	nown Genell Itamate	dehydrogenase,	dehydrogenase 1	glutamate	dehydrogenase,	giotainate dehydrogenase 1	glutamate	oxaloacetate	transaminase 1,	soluble, glutamic-	oxaloacetic	transaminase 1,	soluble (aspartate	aminotransferase 1	glutamate	oxaloacetate	transaminase 2,	mitochondrial,	glutamic-oxaloacetic	transaminase 2,	mitochondrial	(aspartate	aminotransferase 2)	glutamate-ammonia	ligase (glutamine	synthase), glutamine	synthetase
	Mठ्यंत्री देव्यं		XX, YY			GG, OO, DDD					<u>`</u>	Ļ-		Alternate									Alternate			ج. ۲ ۲	
Consent	යිමේරිලේ (D		NM_012570			NM_012570								NM_012571									NM_013177			11, Ri	CIOLIO MAIN
33 F	ID No.		4573			4274								20744									17628			7	_
	<u>:</u>		3082			3082								3083		-							3230		<u></u>	976	9700

######################################	Aumen Homologous   Manan Homologous Sequence Guster Mile:				glutamate-cysteine ligase, modifler subunit, glutamate-cysteine ligase, modifler subunit	glutamate-cysteine ligase, modifier subunit, glutamate-cysteine ligase, modifier subunit	Homo sapiens, Similar to glutamate-cysteine ligase, catalytic subunit, clone MGC:26341 IMAGE:4814728, mRNA, complete cds, glutamate-cysteine ligase, catalytic subunit	glutaredoxin (thioltransferase), glutaredoxin 1 (thioltransferase), glutaredoxin 2 (thioltransferase)
	Human Homologous Known Gene Name	glutamate-ammonia ligase (glutamine synthase), glutamine synthetase	glutamate-ammonia ligase (glutamine synthase), glutamine synthetase	glutamate-ammonia ligase (glutamine synthase), glutamine synthetase	glutamate-cysteine ligase , modifier subunit, glutamate- cysteine ligase, modifier subunit	ine ate-	glutamate-cysteine ligase, catalytic Ho subunit IM	glutaredoxin (thioltransferase), glutaredoxin 1 glu (thioltransferase) (th
	Model Gode K	ļ Ž	II, LL, TT, UU, DDD, LLL, UUU	ζ, II, ΤΤ, D, GGG,	Q, R, S, X, Y, NN, OO, General Alternate	Q, R, T, KKK	Q, R, S	ес, нн
	ලෙබාවෙබා? රූලෙමා* දීරෙනිලේ (D	NM_017073	MM_017073	G, I DD DD_ NM_017073	NM_017305	NM_017305	J05181	NM_022278 GG, HH
₹3	att. Odec Odec	11151	11152	11153	14003	14004	1247	4561
	, Seq (D)	3268	3268	3268	3334	3334	2931	3459

TABLE 3	ें हुट हुट				Altorney Decket 44924-5038-01000 Decument No. 1935323.1
Seq.	elec Ibno	ලාමෙන්නෙන්   හිමෙන්   ලානුන්න්	epag jepawi		Kinovin Genej Namer Homologous Sequence) Cluster III e
				me A	expressed sequence Al266902, expressed sequence D17825, glutaryl-Coenzyme A
1897	23596	AI105435	>	dehydrogenase	dehydrogenase
					ESTs, Weakly similar to GSHC_RAT Glutathione peroxidase (GSHPX-1) (Cellular
				glutathione	glutathione peroxidase) [R.norvegicus], glutathione peroxidase 1, glutathione
3564	1853	NM_030826	NM_030826   MM, TT, TTT	peroxidase 1	peroxidase 2, glutathione peroxidase 2 (gastrointestinal)
				glutathione	
	<u>-</u>			peroxidase 4,	
			············	glutathione	ESTs, Weakly similar to GSHH_RAT Phospholipid hydroperoxide glutathione
				peroxidase 4	peroxidase, mitochondrial precursor (PHGPx) (GPX-4) [R.norvegicus], RIKEN cDNA
				(phospholipid	2310016C16 gene, RIKEN cDNA 3110050F08 gene, glutathione peroxidase 4,
3296	17686	NM_017165	I, J, LL	hydroperoxidase)	glutathione peroxidase 4 (phospholipid hydroperoxidase)
				glutathione S-	
				transferase A2,	
				glutathione S-	
				transferase, alpha 1	
				(Ya), glutathione S-	
				transferase, alpha 2	
3250	18988	NM_017013 V, NN, OO	V, NN, 00	(Yc2)	
			F, K, M, N,	glutathione S-	
			GG, HH, TT,	transferase A2,	
	-		DDD, EEE,	glutathione S-	ESTs, Weakly similar to GTA1_RAT GLUTATHIONE S-TRANSFERASE YA
			LLL, MMM,	transferase, alpha 2	(LIGANDIN) (CHAIN 1) (GST CLASS-ALPHA) (CLONES PGST94 & PGTR261)
3250	18989	NM_017013	ດດດ	(Yc2)	[R.norvegicus], glutathione S-transferase A2, glutathione S-transferase, alpha 2 (Yc2)
				glutathione S- transferase A2	
				glutathione S-	ESTs, Weakly similar to GTA1 RAT GLUTATHIONE S-TRANSFERASE YA
	,			transferase, alpha 2	(LIGANDIN) (CHAIN 1) (GST CLASS-ALPHA) (CLONES PGST94 & PGTR261)
3634	18990	NM_031509   G, K, T1	G, K, 11, SSS	[Yc2)	[R.norvegicus], glutathione S-transferase A2, glutathione S-transferase, alpha 2 (Yc2)

(VAISUE 3)	33				Attorney Docket 44924-5083-011W0
	<u>ම</u> ල්ල	General   Age or			Human Homologosis   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Sectio
<u> </u>	(ID) (No.	යන්නෙකු 10 -	e e		Human Homologous Sequence Gluster Titule
				glutathione S-	
		V	UU, III, JJJ,	transferase theta 2,	
			General	glutathione S-	
3143	096	NM_012796	Alternate	transferase, theta 2	glutathione S-transferase theta 2, glutathione S-transferase, theta 2
			G, H, JJ, KK,		EST, Highly similar to GSHB MOUSE GLUTATHIONE SYNTHETASE (M.musculus).
2974	6405	L38615	GGG	glutathione synthetase	utathione synthetase glutathione synthetase
		•			EST, Highly similar to GSHB MOUSE GLUTATHIONE SYNTHETASE IM. musculus].
2974	. 9049	L38615	999	glutathione synthetase glutathione synthetase	glutathione synthetase
			HHH, General		
			Core Tox		
			Markers,		ESTs, Weakly similar to GLPK MOUSE GLYCEROL KINASE IM, musculus). RIKEN
			General		cDNA 2310009E04 gene, glucokinase activity, related sequence 1, glucokinase activity.
3554	20380	NM 024381		glycerol kinase	related sequence 2, glycerol kinase, glycerol kinase pseudogene 2
			, ×, ×,	glycine N-	
624	1552	AA893219		methyltransferase	glycine N-methyltransferase
			Y, EEE, GGG,	glycine N-	
3273	1550	NM 017084 MMM	MMM	methyltransferase	glycine N-methyltransferase
			F, O, P, X,		
			GGG, LLL,	glycine N-	
3273	1551	NM_017084	UUU	methyltransferase	glycine N-methyltransferase
				glycine transporter 1,	
				solute carrier family 6	
				(neurotransmitter	
-			;	transporter, glycine),	
3833	16311	INM 053818	В, н	member 9	
323	9707	A A O A A A A A A A A A A A A A A A A A		glycoprotein	
353	4040	A4621014	0, ^^	(transmembrane) nmb	ansmembrane) nmb glycoprotein (transmembrane) nmb

TABLES	38.4				7. **/Attorney Doctret 4492A-5938-91WO
	erec IDNo.	Censeni Accor: Refect D	  Modell ලැරෙ	Human Homologous Known Gene Name	HumeniHomologovs Sequence Gluster Milo
1908	4049	AI112012	w, o	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb glycoprotein (transmembrane) nmb
3934	19456	NM_133298	0, P, W	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb glycoprotein (transmembrane) nmb
153	16756	AA818089	В, Н	głycyl-tRNA synthetase	glycyl-tRNA synthetase
3353	15977	NM_019132	S		ESTs, Moderately similar to S34421 GTP-binding regulatory protein Gs alpha chain [H.sapiens], GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus, GNAS complex locus, RIKEN cDNA 5530400H20 gene, Sang. XLas protein
2659	21156	A1234248	N, PP, QQ, XX, YY	golgi SNAP receptor complex member 1	Homo sapiens, Similar to golgi SNAP receptor complex member 1, clone MGC:13657 IMAGE:4250494, mRNA, complete cds, golgi SNAP receptor complex member 1
3794	21153	NM_053584	<b>-</b>	5	Homo sapiens, Similar to golgi SNAP receptor complex member 1, clone MGC:13657 iMAGE:4250494, mRNA, complete cds. golgi SNAP receptor complex member 1
	21152	X14848	F, S, FF, HH, SS, WW	golgi SNAP receptor complex member 1	Homo sapiens, Similar to golgi SNAP receptor complex member 1, clone MGC:13657 IMAGE:4250494, mRNA, complete cds, golgi SNAP receptor complex member 1
3280 3280	20745 20746	NM 017113 NM 017113	C, O, P O, P	granulin granulin	granulin granulin
				ecific int, group- component	
894	17471	AA944965	ור	(vitamin D binding protein)	

	1000			Attorney Docket 44924-5033-01W0
Selver Nee or Rolsse	3. Q	Model Gode	25.25	umenn Homologogus   France   France   Human Homologogus Seguence   Cluster Intile
			group specific	
			specific component	
			(vitamin D binding	
M12450	50	M, S, NNN	protein)	
			growth arrest and	
			DNA-damage-	
			inducible 45 alpha,	
_				
			DNA-damage-	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-
Σ̈́	NM_024127	ပ		inducible 45 beta, growth arrest and DNA-damage-inducible, alpha
			growth arrest and	
			DNA-damage-	
			inducible 45 alpha,	
			growth arrest and	
			DNA-damage-	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-
Σ	NM_024127	С, нн, РР, аа	inducible, alpha	inducible 45 beta, growth arrest and DNA-damage-inducible, alpha
			growth arrest and	
			DNA-damage-	
			inducible 45 alpha,	
			growth arrest and	
		; II, PP,	DNA-damage-	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-
Σ	NM_024127	NNN	inducible, alpha	inducible 45 beta, growth arrest and DNA-damage-inducible, alpha
			growth arrest and	
			DNA-damage-	growth arrest and DNA-damage-inducible 45 beta, growth arrest and DNA-damage-
A P	AI070068	I, J, L, M, Z	inducible, beta	inducible, alpha, growth arrest and DNA-damage-inducible, beta
			growth arrest specific	
	057100	NM 057100 BB 11	6, growth arrest-	ESTS, Highly similar to growth arrest specific 6 [Rattus norvegicus] [K.norvegicus], and arrest specific 6.
[]		12, 22, 22	2 2 2 2 2 2	

	88 89				
	elèc Mon	ල්බෝඩෝ   Aලේ ලෝ  Rමැපිල් [D	ि व्यक्त शिल्बंद्री एक्व	Human Homologous Known Genername H	umaniHomologousi Sequence(Cluster/IIIIe
				growth factor, augmenter of liver	
				homolog, S. cerevisiae), growth	
				factor, erv1 (S. cerevisiae)-like	
2859	1396	D30735	RR	ver	growth factor, augmenter of liver regeneration (ERV1 homolog, S. cerevisiae), growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
1362	17524	AI010568	General Core Tox Markers	ne	growth hormone receptor
			B, H, S, LLL,		
			General Core		
•			Tox Markers,	the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	
3274	10886	NM_017094	Alternate	grown normane receptor	growth hormone receptor
			A, B, T, FF, NN, OO,		
3274	10887	NM 017094	ക		growth hormone receptor
				ase	
				cyclohydrolase 1 (dopa-responsive	
3549	_	15350 NM_024356	_	dystonia)	GTP cyclohydrolase 1, GTP cyclohydrolase 1 (dopa-responsive dystonia)

	3.8				
WWW.	ar i	ලෙන්නොදී			
නිලේ ම	9 9 9 9 9	Ace or Prison in		Human Homologous Krawa Garo Nemo	Himanal Capita South and Chief Paritification
Ţ	200		HHH	ouanidinoacetate N-	
			PPP, QQQ,	methyltransferase,	
					expressed sequence AA571402, guanidinoacetate N-methyltransferase,
3142	16947	NM_012793	Alternate	methyltransferase	guanidinoacetate methyltransferase
				guanidinoacetate N-	
				methyltransferase,	
				guanidinoacetate	expressed sequence AA571402, guanidinoacetate N-methyltransferase,
3142	16948	NM_012793	РРР, ааа	<u> </u>	guanidinoacetate methyltransferase
			c, uu,	guanine	
			General	monphosphate	
1196	3082	AA999172	Alternate	synthetase	guanine monphosphate synthetase
				guanine nucleotide	
				binding protein (G	
				protein) alpha 12,	ESTs, Moderately similar to guanine nucleotide binding protein (G protein) alpha 12
				guanine nucleotide	[Rattus norvegicus] [R.norvegicus], guanine nucleotide binding protein (G protein), alpha
				binding protein, alpha	13, guanine nucleotide binding protein, alpha 12, guanine nucleotide binding protein,
3585	069	NM_031034	RR	12	alpha 13
				guanine nucleotide	
				binding protein (G	
				protein), alpha	
				inhibiting activity	
				polypeptide 3,	
				guanine nucleotide	
			=	binding protein, alpha	binding protein, alpha   guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3,
3775		19949 NM 013106 IL, HHH	L, HHH	Innibiting 3	guanine nucleotide binding protein, alpha innibiting 3

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- 6 © ©	- 997 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987 - 987	Consenix Acoor Rossop	Medel Gede	Human Homologous Known Gene Name	Homologous Gene Name Human Homologous Seguence (cluster Mills)
				guanine nucleotide	EST, Weakly similar to B33928 GTP-binding protein beta chain homolog [H.sapiens], EST, Weakly similar to GBLP_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN
				binding protein (G	BETA SUBUNIT-LIKE PROTEIN 12.3 (H.sapiens), Homo sapiens cDNA: FLJ21913 fis,
			A, B, JJ, KK,	protein), beta polypeptide 2-like 1,	cione HEPU3888, Mus musculus, Similar to hypotnetical protein FLJ 10385, clone MGC:28622 IMAGE:4220923, mRNA, complete cds, expressed seguence AL033335,
				guanine nucleotide	guanine nucleotide binding protein (G protein), beta polypeptide 1-like, guanine
			HHH, General	binding protein, beta	nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide
3924	14959	NM_130734	Alternate		binding protein, beta 2, related sequence 1
					EST, Weakly similar to B33928 GTP-binding protein beta chain homolog [H.sapiens],
					EST, Weakly similar to GBLP_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN
				guanine nucleotide	BETA SUBUNIT-LIKE PROTEIN 12.3 [H.sapiens], Homo sapiens cDNA: FLJ21913 fis,
				binding protein (G	clone HEP03888, Mus musculus, Similar to hypothetical protein FLJ10385, clone
				protein), beta	MGC:28622 IMAGE:4220923, mRNA, complete cds, SWI/SNF related, matrix
				polypeptide 2-like 1,	associated, actin dependent regulator of chromatin, subfamily b, member 1, expressed
				guanine nucleotide	sequence AL033335, guanine nucleotide binding protein (G protein), beta polypeptide 1-
				nding protein, beta	like, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine
2088	14960	AI171319	9	ce 1	nucleotide binding protein, beta 2, related sequence 1
				H1 histone family,	
3084	16024	NM_012578	WW, ZZ, AAA	member 0	H1 histone family, member 0, H1 histone family, member O (oocyte-specific)
				H1 histone family,	
3084	16025	NM_012578	WW, ZZ, AAA	member 0	H1 histone family, member 0, H1 histone family, member O (oocyte-specific)
				H1 histone family,	
3084	16026	NM_012578	ZZ, AAA	member 0	H1 histone family, member 0, H1 histone family, member O (oocyte-specific)
				H2A histone family,	
2763	1488	AI237016	DDD	member Y	H2A histone family, member Y, RIKEN cDNA 4933432H23 gene
			S, SS, WW,		
2937	1264	K01933	NNN	haptoglobin	

	3.8				Antorney Docket 4k924-6038-01W0
Seg	986	Content		Human Homologous	Human Homologous
<u>.</u>	ത്തി	പ്രത്യേട്ടിയ്	Model Gode	KNIOWAI GENE NAME	Administration of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation of the second representation o
				heat shock 10 kDa	
				protein 1 (chaperonin 10) heat shock 10kD	ESTs. Weakly similar to S47532 chaperonin groES [H.sapiens]. expressed sequence
				protein 1 (chaperonin	AW108200, heat shock 10 kDa protein 1 (chaperonin 10), heat shock 10kD protein 1
3184	5033	NM_012966	L, PPP, aga	10)	(chaperonin 10)
				heat shock 10 kDa	
				protein 1 (chaperonin	
				10), heat shock 10kD	ESTs, Weakly similar to S47532 chaperonin groES [H.sapiens], expressed sequence
				protein 1 (chaperonin	AW108200, heat shock 10 kDa protein 1 (chaperonin 10), heat shock 10kD protein 1
3184	5034	NM_012966	RR	10)	(chaperonin 10)
				heat shock 70kD	EST, Weakly similar to GR78_RAT 78 KD GLUCOSE-REGULATED PROTEIN
				protein 5 (glucose-	PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN)
		٠		regulated protein,	(BIP) (STEROIDOGENESIS-ACTIVATOR POLYPEPTIDE) [R.norvegicus], expressed
2990	1466	M14050	LL	78kD)	sequence AL022860, heat shock 70kD protein 5 (glucose-regulated protein, 78kD)
				-	EST, Moderately similar to HS7C_HUMAN HEAT SHOCK COGNATE 71 KDA PROTEI
					[H.sapiens], EST, Weakly similar to A27077 dnaK-type molecular chaperone
					[H.sapiens], EST, Weakly similar to A45935 dnaK-type molecular chaperone hsc70 -
					mouse [M.musculus], ESTs, Moderately similar to HS7C MOUSE HEAT SHOCK
				heat shock 70kD	COGNATE 71 KDA PROTEIN [M.musculus], ESTs, Weakly similar to HS7C MOUSE
3548	17764	NM_024351	Z, AA, FF	protein 8	HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], heat shock 70kD protein 8
					EST, Moderately similar to HS7C_HUMAN HEAT SHOCK COGNATE 71 KDA PROTEI
					[H.sapiens], EST, Weakly similar to A27077 dnaK-type molecular chaperone
					[H.sapiens], EST, Weakly similar to A45935 dnaK-type molecular chaperone hsc70 -
					mouse [M.musculus], ESTs, Moderately similar to HS7C MOUSE HEAT SHOCK
				heat shock 70kD	COGNATE 71 KDA PROTEIN [M.musculus], ESTs, Weakly similar to HS7C MOUSE
3548	17765	NM_024351	99	protein 8	HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], heat shock 70kD protein 8

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ි. ම්ල	GLGG TD No.	Iceneenk Aecor RéfSeq (D)	  Model Gods	Human Homologous Known Gene Name	
			A, B, RRR,	heat-responsive	
			SSS, UUU, General	protein 12, translational inhibitor	Mus musculus adult male liver cDNA, KIKEN full-length enriched library, clone:1300015121-heat-responsive
3675	21693	NM_031714		10	protein 12, translational inhibitor protein p14.5
			<u>م</u>		
2353	16081	AI179610			heme oxygenase (decycling) 1
				heme oxygenase	
3085	16080	NM_012580	EEE, MMM	(decycling) 1	heme oxygenase (decycling) 1
					EST, Highly similar to HFE_HUMAN HEREDITARY HAEMOCHROMATOSIS PROTEIN
2836	19703	AJ001517	E, 88, CC, II	hemochromatosis	PRECURSOR [H.sapiens], hemochromatosis
					EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS
					[R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND
					ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT
				hemoglobin alpha,	HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA
		-		adult chain 2,	2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1,
2323	18907	A1178971	T	hemoglobin, alpha 1	hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1
					EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS
					[R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND
					ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT
				hemoglobin alpha,	HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS (R.norvegicus), RIKEN cDNA
				adult chain 2,	2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, 🍦
2370	1687	AI179971	T	hemoglobin, alpha 1	hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1
					EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS
					[R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND
					ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT
				hemoglobin alpha,	HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA
264.0	7000	02000014	ŀ	adult chain 2,	2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1,
7107	1,000	A1230970		memogrami, alpita i	Hernogroum, aipria 1, Hernogroum, aipria 2, Hernogroum, meta 1

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88	GLGC In No.			Human Homologous	
2000	San Gn	ଳା ଜନ୍ମ କଥା ଥିଏ	alaga jegami	National Centernature	THE TRUTOR OF SOME SERVICES CONTRACTOR OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE SERVICES OF THE
					EST, Moderately similar to HBA_KAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS IB powaricus] EST Weakly similar to HBA_BAT HEMOGLOBIN ALBHA-1 AND
					ALPHA-2 CHAINS [R. norvegicus], ESTS. Moderately similar to HBA_RAT
				hemoglobin alpha,	HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA
				adult chain 2,	2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1,
2731	1689	AI236360	T, XX, YY	hemoglobin, alpha 1	hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1
					EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS
					[R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND
					ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT
				hemoglobin alpha,	HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA
				adult chain 2,	2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1,
3217	1684	NM_013096	T	hemoglobin, alpha 1	hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1
				hemoglobin beta	EST, Moderately simitar to HBB1_RAT Hemoglobin beta chain, major-form
				chain complex,	[R.norvegicus], expressed sequence Al036344, hemoglobin, beta, hemoglobin, beta
445	18897	AA875207	C, T, Z, AA	hemoglobin, beta	adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta
				hemoglobin beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form
				chain complex,	[R.norvegicus], expressed sequence Al036344, hemoglobin, beta, hemoglobin, beta
3734	17829	NM_033234	T, HH, NNN	hemoglobin, beta	adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta
				hemoglobin beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form
					[R.norvegicus], expressed sequence Al036344, hemoglobin, beta, hemoglobin, beta
3734	17832	NM_033234	Ţ	hemoglobin, beta	adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta
				hemoglobin beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form
			K, T, HH, XX,	chain complex,	[R.norvegicus], expressed sequence Al036344, hemoglobin, beta, hemoglobin, beta
3734	25468	NM_033234	₩	hemoglobin, beta	adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta
			E, S, PP, QQ,		
3746	13164	NM_053318	ww	hemopexin	
				n antimicrobial	
3770	22586	NM_053469 L, M	L, M	peptide	hepcidin antimicrobial peptide

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				To be a first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of t	ESTs, Weakly similar to HEPS_RAT SERINE PROTEASE HEPSIN [R.norvegicus], ESTs, Weakly similar to TMS2_MOUSE TRANSMEMBRANE PROTEASE, SERINE 2 (EPITHELIASIN) (PLASMIC TRANSMEMBRANE PROTEIN X) [M.musculus], Mus
4256	1548	X70900	V, General Alternate	hepsin, hepsin (transmembrane protease, serine 1)	musculus airway trypsin-like protease mRNA, complete cds, Mus musculus, Similar to transmembrane protease, serine 4, clone MGC:29209 IMAGE:5030266, mRNA, complete cds, hepsin, hepsin (transmembrane protease, serine 1)
1875	4235	A1104524	HHH, General Alternate	heterogeneous nuclear ribonucleoprotein A/B	DAZ associated protein 1, Musashi homolog 1(Drosophila), Musashi homolog 2 (Drosophila), RIKEN cDNA 4933434H11 gene, expressed sequence AA959857, heterogeneous nuclear ribonucleoprotein A/B, musashi homolog 1 (Drosophila)
3626	4234	NM 031330	A, B, I, L, Y, MM, HHH, KKK, OOO, TTT, General Alternate	heterogeneous nuclear ribon Icleoprofein A/B	DAZ associated protein 1, Musashi homolog 1(Drosophila), Musashi homolog 2 (Drosophila), RIKEN cDNA 4933434H11 gene, expressed sequence AA959857,
		4		<del></del>	ESTs, Highly similar to 152962 FBRNP [H.sapiens], ESTs, Highly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Moderately similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar to ROA1 RAT Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein)
3317		O, P, JJ, 17502 NM_017248 VV, HHH	О, Р, ЈЈ, КК, VV, ННН	heterogeneous nuclear ribonucleoprotein A1	(Single-strand binding protein) (hnRNP core protein A1) (HDP) [R.norvegicus], Homo sapiens cDNA: FLJ22720 fis, clone HSI14320, Mus musculus, Similar to TAR DNA binding protein, clone MGC:19284 IMAGE:4016437, mRNA, complete cds, RIKEN cDNA 4930547K05 gene, heterogeneous nuclear ribonucleoprotein A1

UABU	ें 8 ह				Atterney Doctret (1927) 4038-4038-4018-4018-4018-4018-4018-4018-4018-401
(B)  Model Code	Known Gene Name	Kaowa Gene Name   Humaniyonologous Sequence Ouster Tidlo			
					ESTs, Highly similar to 152962 FBRNP [H.sapiens], ESTs, Highly similar to S12520 core protein A1 [H.sapiens], ESTs, Highly similar to heterogeneous ribonuclear particle
					protein A1 [H.sapiens], ESTs, Moderately similar to heterogeneous ribonuclear particle
					protein A1 [H.sapiens], ES1s, Weakiy similar to KOA1_KA1 Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP
					core protein A1) (HDP) [R.norvegicus], Homo sapiens cDNA: FLJ22720 fis, clone
-					HSI14320, Mus musculus, Similar to TAR DNA binding protein, clone MGC:19284
				heterogeneous	IMAGE:4016437, mRNA, complete cds, RIKEN cDNA 2610510D13 gene, RIKEN cDNA
					4930547K05 gene, heterogeneous nuclear ribonucleoprotein A1, heterogeneous
3317	15012	NM_017248	≥	ribonucleoprotein A1	nuclear ribonucleoprotein A3
					ESTs, Highly similar to heterogeneous nuclear ribonucleoprotein K, isoform b; dC-
					stretch binding protein; transformation upregulated nuclear protein [Homo sapiens]
				snoaual	[H.sapiens], ESTs, Weakly similar to heterogeneous nuclear ribonucleoprotein K
				nuclear	[Rattus norvegicus] [R.norvegicus], heterogeneous nuclear ribonucleoprotein K, poly(rC)
က	2417	AA684857	≯	ribonucleoprotein K	binding protein 3, poly(rC) binding protein 4
					ESTs, Highly similar to heterogeneous nuclear ribonucleoprotein K, isoform b; dC-
					stretch binding protein; transformation upregulated nuclear protein [Homo sapiens]
_				heterogeneous	[H.sapiens], ESTs, Weakly similar to heterogeneous nuclear ribonucleoprotein K
				nuclear	[Rattus norvegicus] [R.norvegicus], heterogeneous nuclear ribonucleoprotein K, poly(rC)
2766	2416	AI237051	ור	ribonucleoprotein K	binding protein 3, poly(rC) binding protein 4
				heterogeneous	
				nuclear	
789	16944	AA925541	SSS	in L	heterogeneous nuclear ribonucleoprotein L
				heterogeneous	
1	1,00,		: : :		
8	16345	AA925541	С, ввв, ннн	ribonucleoprotein L	heterogeneous nuclear ribonucleoprotein L

TABLE 8	88				Attorney Decket 44921-5038-61W0
	@ @ @ @ @	Consent Récor Réseq D	Modell Gode	Human Homologous Known Gene Name	Homologous Homologous Gene Namer HumaniHomologous Sequence Guster IIII e
				heterogeneous nuclear	
				ribonucleoprotein U,	
					E1B-55kDa-associated protein 5, EST, Weakly similar to heterogenous nuclear
				ribonucleoprotein U	ribonucleoprotein U; scaffold attachment factor A; nuclear matrix protein sp120 [Mus
					musculus] [M.musculus], expressed sequence Al465155, heterogeneous nuclear
3886	19833	NM_057139	GG	1	ribonucleoprotein U
,	101	707070	2		ESTs, Weakly similar to A35244 hexokinase [M.musculus], Mus musculus, Similar to
5	13/1	NW 012/34	٥, ٧, ٥٥	nexokiliase	HEXDRIII 1356 I, CIOITE INICO. 200 I INICOE. 4304302, HITARA, COTTORES COS, HEXDRIII 1336 I
2434	41620	NIM 01072E 7 AA NININ	7 00 1010	C escriptored	EST, Weakly Similar to DAKZ MOUSE DEXONIVASE TIPE II [M.:IIIuscuius], ESTS, Massky similar to HXX2 MOUSE HEXOKINASE TYPE II [M.m.scriples] hexokinase 2
010	1	10 17 1 23 1 33 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2, CC, INININ		
					ESTs, Weakly similar to HGF-regulated tyrosine kinase substrate [Mus musculus]
				tyrosine kinase	[M.musculus], HGF-regulated tyrosine kinase substrate, RIKEN cDNA 1700013B03
				tocyte	gene, WD40- and FYVE-domain containing protein 2, hepatocyte growth factor-
				growth factor-	regulated tyrosine kinase substrate, myotubularin related protein 3, phosphoinositide-
				sine	binding protein SR1, target of myb1 homolog (chicken), zinc finger protein, subfamily 2A
1258	10108	AI007857	a,	kinase substrate	(FYVE domain containing), 1
					ESTs, Highly similar to HIPP_HUMAN Neuron specific calcium-binding protein
					hippocalcin (P23K) (Calcium-binding protein BDR-2) [R.norvegicus], ESTs, Weakly
					similar to HIPP RAT NEURON SPECIFIC CALCIUM-BINDING PROTEIN
2845	1375	D12573	Z, AA	hippocalcin	HIPPOCALCIN [M.musculus], hippocalcin
			,00	stidine ammonia	
			General	lyase, histidine	
3027	20	M58308	Alternate	ammonia-lyase	histidine ammonia lyase, histidine ammonia-lyase
				transcript 1, HLA-B-	ESTs, Highly similar to S33681 translation initiation factor eIF-4A.I [H.sapiens], ESTs,
				associated transcript	Weakly similar to A42811 nuclear RNA helicase (DEAD family) homolog - rat
3036	17344	M75168	ပ	1A	[R.norvegicus], RIKEN cDNA 2610307C23 gene, hypothetical protein MGC6664

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				HLA-B associated	HLA-B associated transcript 3, HLA-B-associated transcript 3, Mus musculus, clone
				transcript 3, HLA-B-	IMAGE:4010394, mRNA, partial cds, Mus musculus, clone IMAGE:5321785, mRNA,
				associated transcript	cystin 1, enabled homolog (Drosophila), expressed sequence AA408914, hypothetical
1347	11460	AI010293	쏘	3	protein MGC10820, zinc finger protein, multitype 1
					EST, Moderately similar to ANM1_HUMAN PROTEIN ARGININE N-
					METHYLTRANSFERASE 1 [H.sapiens], EST, Weakly similar to ANM1_HUMAN
					PROTEIN ARGININE N-METHYLTRANSFERASE 1 [H.sapiens], ESTs, Moderately
				HMT1 hnRNP	similar to ANM1_MOUSE PROTEIN ARGININE N-METHYLTRANSFERASE 1
				methyltransferase-like	[M.musculus], ESTs, Weakly similar to ANM1_MOUSE PROTEIN ARGININE N-
				2 (S. cerevisiae),	METHYLTRANSFERASE 1 [M.musculus], HMT1 hnRNP methyltransferase-like 2 (S.
				heterogeneous	cerevisiae), RIKEN cDNA 2410018A17 gene, coactivator-associated arginine
				nuclear	methyltransferase 1, coactivator-associated arginine methyltransferase-1,
				ribonucleoproteins	heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae),
				methyltransferase-like	heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae),
3550	20772	NM_024363	А	2 (S. cerevisiae)	related sequence
					ESTs, Weakly similar to R107_RAT H-rev 107 protein [R.norvegicus], H-rev107-like
					protein 5, HRAS-like suppressor, HRAS-like suppressor 2, HRAS-like suppressor 3, Ha-
					Ras suppressor A-C1, Harvey rat sarcoma virus oncogene relatedsuppressor, Mus
				ppressor	musculus, Similar to HRAS-like suppressor 3, clone MGC:37701 IMAGE:5065247,
	•			3, HRAS-like	mRNA, complete cds, RIKEN cDNA 4921526K24 gene, expressed sequence C78643,
4261	1955	X76453	M	suppressor 3	retinoic acid receptor responder (tazarotene induced) 3
_					EST, Weakly similar to UBC1_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-25
		-			KD [H.sapiens], ESTs, Weakly similar to ubiquitin-conjugating enzyme E2D 2 [Rattus
					norvegicus] [R.norvegicus], RIKEN cDNA 0910001J09 gene, RIKEN cDNA 1700013N18
					gene, RIKEN cDNA 6720465F12 gene, huntingtin interacting protein 2, ubiquitin-
				huntingtin interacting	conjugating enzyme E2D 2, ubiquitin-conjugating enzyme E2L 3, ubiquitin-conjugating
2362	23120	AI179857	S	protein 2	enzyme E2N

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संकृत्यन्त्र । Doefret 4492त-5068-601770 न्ह्रांन्य ' Doeument No. 1986822.1									SOLA SOLA		gene,	olase							zyme	cus},	C:303		se 1,	ducta	
1-500 10, 119									¥DK	clone	51.15	hydr					<b>⊕</b>		3, iso	rvegi	e MG		gena	se/re	
44.922 Jeint B	1								SNE	ase, (	1002	hione					-beta	3DR3	enase	[R.70	Clou	3908	ydro	gena	
(व्याप्त अस्याप्त									SHI)	ydrol	A 06	glutat					id (1)	e rets	drog	301)	e 11,	1 <u>GC:6</u>	a) det	hydro	
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		4							SYLG	utathi	SKE)	'drox					droxy	e/red	-beta	11-b	ydrog	us, cl	oid (1	r-ch	
$\otimes$									Χ¥	cyl gl	cds, F	17, hy					 	genas	oid 11	e 1) (	ta del	nscn	yster	al sho	
		5							ORG/	roxya	plete	otein .					, type	ydro	oster	genas	17-be	lus m	ydrox	retini	
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		Ž							imilar	us m	AGE:3	5000					penzy	e 10,	simila	sta-hy	, Simi	42, m	55, m	11-b	
		2							ghly s	is], M	7 IM/	NA 1					S-KS	enas	eakly	(11-be	culus	1323	6558	teroid	
		0							ESTs, Highly similar to GLO2_HUMAN HYDROXYACYLGLUTATHIONE HYDROLASE	[H.sapiens], Mus musculus, Similar to hydroxyacyl glutathione hydrolase, clone	MGC:6697 IMAGE:3583919, mRNA, complete cds, RIKEN cDNA 0610025L15 gene,	RIKEN cDNA 1500017E18 gene, brain protein 17, hydroxyacyl glutathione hydrolase					hydroxyacyl-Coenzyme A dehydrogenase, type II, hydroxysteroid (17-beta)	dehydrogenase 10, retinal short-chain dehydrogenase/reductase retSDR3	ESTs, Weakly similar to DHI1_RAT Corticosteroid 11-beta-dehydrogenase, isozyme	(11-DH) (11-beta-hydroxysteroid dehydrogenase 1) (11-beta-HSD1) [R.norvegicus]	Mus musculus, Similar to hydroxysteroid 17-beta dehydrogenase 11, clone MGC:30360	IMAGE:5132342, mRNA, complete cds, Mus musculus, clone MGC:6908	IMAGE:2655855, mRNA, complete cds, hydroxysteroid (11-beta) dehydrogenase 1,	roxys	DR2
	Human Homologous				~		L		ES	H.	Σ		_				hyd	<del>g</del>	ES	Ė	Š	Σ		, hydroxysteroid 11- hydroxysteroid 11-beta dehydrogenase 1, retinal short-chain dehydrogenase/reductase	peta dehydrogenase 1 retSDR2
	fuman Homologous	5	ase	se) 3,	nydroxyacid oxidase 3							glutathione hydrolase			dehydrogenase, type	I, hydroxysteroid (17-	oeta) dehydrogenase					<del>-</del>	peta) dehydrogenase	d 11-	nase
	jo E		XOD	oxidae	d oxid	hain)					<u>~</u>	hydr	÷	4	nase,	steroi	droge					roid (	droge	steroi	droge
			ydroxyacid oxidase	glycolate oxidase) 3	xyaci	medium-chain)					nydroxyacyl	hione	ydroxyacyl-	Soenzyme A	droge	droxy	dehy					ydroxysteroid (11-	dehy	droxy	dehyc
			hydro	(glyc	hydro	(med					hydro	glutaí	hydro	Coen	dehy	<u>.</u> Б	beta)	9				hydro	beta)	7, h	beta
	\$ 6	200	A, B, M, 000, I	eral			H,			neral					c S	ιń	-							ت.	
		) D	Ž.	J. Ger	Core Tox	(ers	, M, F	SS, UU, III,	XX,	000, General	Core Tox	(ers		A, B, P, U,	S	۶, SS	eral	nate						T, U, RRR	
	3 1		Ą M	3	<u>8</u>	Markers	A, B	SS,	33	8	Š	Markers		Ą B	888	RR	General	Alter						<u>⊢</u>	SSS
	الم الم	J.				97						05						NM_031682 Alternate							NM_017080 SSS
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		Ž.				2558						1430						3667							3272

Aiterney Dockst 44921-5939-01W0 Document No. 1855223.1	hypoxanthine guanine phosphoribosyl transferase, hypoxanthine phosphoribosyltransfe ESTs, Weakly similar to The Crystal Structure Of Icam-2 (SUB 25-216 [H.sapiens], phosphoribosyltransferase (EC 2.4.2.8) - rase 1 (Lesch-Nyhan rat [R.norvegicus], hypoxanthine phosphoribosyltransferase, hypoxanthine syndrome)	Mus musculus inhibitory PAS domain protein (ipas) mRNA, complete cds, hypoxia inducible factor 1, alpha subunit, hypoxia-inducible factor 1, alpha subunit, hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor), neuronal PAS domain protein 1, single-minded 1, single-minded bomolog 1 (Drosophila)	l factor (complement), complement component factor i	importin beta, karyopherin (importin) beta 1, karyopherin (importin) beta 3	
Human Homologous KnowniGene Name	hypoxanthine guanine phosphoribosyl transferase, hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	hypoxia inducible factor 1, alpha subunit, hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	I factor (complement), complement component factor i	importin beta, karyopherin (importin) beta 1	inhibitor of DNA binding 1, inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
Medel Gode	Ш	WW	BBB, CCC	0, P, X, Y, W	۸
Consontal	M63983	Y09507	NM_024157	L38644	NM_012797_V
33 (1) (1) (1) (1) (1) (1) (1)	13547	. 1146	22079	1427	10247
TABLES Seq (C)	3033	4284	3543	2975	3144

Attorney Docket 44921-5033-01W0 Document No. 1935323.1 Homologous   Human Homologous Sequence (cluster Mite)		ESTs, Weakly similar to JC2112 helix-loop-helix protein, Id2 - rat [R.norvegicus], inhibitor of DNA binding 2, inhibitor of DNA binding 2, dominant negative helix-loop-helix protein, inhibitor of DNA binding 4, inhibitor of DNA binding 4, dominant negative helix-nop-helix protein	inositol (myo)-1(or 4)-monophosphatase 1, inositol (myo)-1(or 4)-monophosphatase 2, inositol(myo)-1(or 4)-monophosphatase 1	iositol polyphosphate EWS/FL11 activated transcript 2, SH2 domain protein 1A, inositol polyphosphate hosphatase-like 1	ESTs, Moderately similar to A Chain A, Inositol Monophosphatase [H.sapiens], RIKEN cDNA 2900059K10 gene, inositol(myo)-1(or 4)-monophosphatase 1, inositol(myo)-1(or 4)-monophosphatase 2	apoptosis-associated tyrosine kinase, insulin receptor	EST, Highly similar to IG1R_MOUSE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR [M.musculus], EST, Moderately similar to IG1R_MOUSE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR [M.musculus], ESTs, Highly similar to IG1R_MOUSE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR [M.musculus] insulin recentor-related recentor insulin-like growth factor 1 recentor.	[in:dacodica], "Isaami Jacepiol-Leigied Tecepiol, "Isaami-line glowin factor i tecepiol,
Kalown Gene Name	inhibitor of DNA binding 1, inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	inhibitor of DNA binding 2, inhibitor of ESTs, Weakly sin DNA binding 2, inhibitor of DNA b dominant negative protein, inhibitor of	inositol (myo)-1(or 4)- monophosphatase 1, inositol(myo)-1(or 4)- monophosphatase 1	inositol polyphosphate phosphatase-like 1	inositol(myo)-1(or 4)- monophosphatase 2	insulin receptor	insulin-like growth factor 1 receptor,	I DAO B DAILLING
Model Gods	DD, EE, JJJ, General Core Tox Markers	<b>⊢</b> 	C, I, J, TT, 000	22	U, GG, HH, BBB, CCC, RRR	RR		
r Seeder - Réfiseq (D	NM_012797	Al137583	NM_032057	NM_022944	AA859981	NM_017071		
33.000 GLGC IDNO.	10248	16510	18640	19669	23336	24719		
TABU Seq D	3144	1958	3723	3523	409	3266		

	8.5 5.5				Attorney Docket 44921-5038-01W0
Seg	9979	(एटका-हामार   श्रेव्ह वर्ग्-		Human Homologous	
	llo No-	යිසේපිලේ [ම	Wodel  Gode ;	Kinown Gene Name.	Known: Genei Name.   Human Homologous Sequence: @Wsterfillde:
				insulin-like growth	
				factor 1, insulin-like	
			D, G, H, GG,	growth factor 1	
2839	21051	D00698	000	(somatomedin C)	
   			H, S, GGG,	insulin-like growth	
			PPP, QQQ,	factor 1, insulin-like	
			General	growth factor 1	
2993	21052	M15481	Alternate	(somatomedin C)	
				insulin-like growth	
				factor 1, insulin-like	
			G, H, PPP,	growth factor 1	
2993	21053	M15481	aaa	(somatomedin C)	
				insulin-like growth	
				factor 1, insulin-like	
			G, H, M, S,	growth factor 1	
4190	21054	X06107	999	(somatomedin C)	
				insulin-like growth	
				factor binding protein	
3088	15097	NM_012588	7	3	insulin-like growth factor binding protein 3
				insulin-like growth	
				factor binding protein	
3088	15098	NM_012588 GG, II	GG, II	3	insulin-like growth factor binding protein 3

			_									$\neg$
Attorney Docket 49921-5038-01W0  Line Homologous   Attorney Document No. 1995828.0  Kinowin Reprologous   Attorney Sequence Observation	ESTs, Weakly similar to A41915 insulin-like growth factor-binding complex acid-labile chain precursor [H.sapiens], ESTs, Weakly similar to ALS MOUSE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN	PRECURSOR [M.musculus], RIKEN cDNA 1200009022 gene, glycoprotein A repetitions predominant, glycoprotein 1b (platelet), alpha polypeptide, insulin-like growth factor binding protein, acid labile subunit, toll-like receptor 3, toll-like receptor 4, toll-like	receptor 5	ESTs, Weakly similar to A41915 insulin-like growth factor-binding complex acid-labile chain precursor [H.sapiens], ESTs, Weakly similar to ALS MOUSE INSULIN-LIKE COMMENTAL EACTOR BINDING PROTEIN COMMENTS ACID I ARII E CHAIN	PRECURSOR [M.musculus], RIKEN cDNA 1200009022 gene, glycoprotein A	repetitions predominant, glycoprotein Ib (platelet), alpha polypeptide, insulin-like growth factor binding protein, acid labile subunit, toll-like receptor 3, toll-like receptor 4, toll-like	receptor 5	chain precursor [H.sapiens], ESTs, Weakly similar to ALS MOUSE INSULIN-LIKE	GROW IN FACTOR BINDING PROTEIN COMPLEA ACID LABILE CHAIN PRECURSOR [M.musculus], RIKEN cDNA 1200009022 gene, glycoprotein A	repetitions predominant, glycoprotein lb (platelet), alpha polypeptide, insulin-like growth	actor binding protein, factor binding protein, acid labile subunit, toll-like receptor 3, toll-like receptor 4, toll-like	receptor 5
Hinternational Services of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Contr		insulin-like growth factor binding protein,	acid labile subunit			insulin-like growth factor binding protein,	acid labile subunit			insulin-like growth	factor binding protein,	acid labile subunit
Modell Gode	G, BB, CC, GGG, III, JJJ, KKK, LLL, NNN, OOO,	PPP, QQQ, SSS, General Core Tox	Markers		BB, PPP,	QQQ, General Core Tox	Markers	G, S, CC,	GGG, III, JJJ, KKK, 000,	PPP, QQQ,	General Core	Tox Markers
Kenseni Reger			NM_053329  Markers				NM_053329  Markers					NM_053329 Tox Markers
33 Gues			21977				21978		_			25480
IIABIL See			3749				3749					3749

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9	ie No.	Re(Seq 10	Model Gode	Known Gene Name	Modell Goden   Known Gene Namer   Human Homologous Sequence Gluster Mile.
				integrin beta 1	
				(fibronectin receptor	
				(fibronectin receptor,	
					integrin beta 1 (fibronectin receptor beta), integrin beta 2, integrin beta 7, integrin, beta 1
				antigen CD29	(fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12), integrin, heta 2 (antigen CD18 (nd5) tymphocyte function, accordated antigen 1: macrophage
2266	14989	A1177366	HHH		antigen 1 (mac-1) beta subunit), integrin, beta 7
				cionent adala	
				inter alpha-trypsin	
				filmibitor, neavy chain	COT Wheeler similar to 10,6062 interplaced challed and 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March 1400 March
				(clobulin) inhibitor H4	IR populations   ESTs   Weakly similar to INTER-AI DHA-TRYPSIN INHIBITOR HEAVY
			D. E. S. CC.	(plasma Kallikrein-	CHAIN H2 PRECURSOR IM musculus]. inter alpha-trosin inhibitor, heavy chain 4, inter-
4285	1818	Y11283		sensitive glycoprotein)	sensitive glycoprotein) alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)
				intercellular adhesion	
				ă	ESTs, Weakly similar to ICA1_HUMAN INTERCELLULAR ADHESION MOLECULE-1
				τ-	PRECURSOR [H.sapiens], intercellular adhesion molecule, intercellular adhesion
					molecule 1 (CD54), human rhinovirus receptor, intercellular adhesion molecule 3,
3185	2554	NM_012967	W	rhinovirus receptor	intercellular adhesion molecule 5, telencephalin
				intercellular adhesion	
				<u>_</u>	ESTs, Weakly similar to ICA1_HUMAN INTERCELLULAR ADHESION MOLECULE-1
				ule 1	PRECURSOR [H.sapiens], intercellular adhesion molecule, intercellular adhesion
			W, BB, CC,		molecule 1 (CD54), human rhinovirus receptor, intercellular adhesion molecule 3,
3185	2555	NM_012967	NM_012967 NN, OO, PP	Irhinovirus receptor	intercellular adhesion molecule 5, telencephalin

tomey Docket 4492/1-5939-6910VO S	200	regulation 2,	musculus, similar i evisiae), clone	quence A1646973,	on regulatory factor	n regulation 2,	regulation 2,	regulation 2,		eron regulatory		ELOPMENTAL	IN PC4) (IRPR)	ron-related			•						<ul><li>macrophage),</li></ul>			
eksenney Docke († 1974) 1908 – Paris Joseph († 1974)	ในเกิลท์ เห็อเกอโอยูอับรู  ไก้อันนา์ Geneiname:   Human≣Homologoับธ\Sequence (cluster/litite	ESTs, Moderately similar to sirtuin 2 (silent mating type information regulation 2,	nomotog) z (s. cerevisiae) [Kattus norvegicus] [K.norvegicus], inus musculus, similar to sirtuin silent mating type information regulation 2 homolog 7 (S. cerevisiae), clone	MGC:37560 IMAGE:4987746, mRNA, complete cds, expressed sequence Al646973,	interferon regulatory factor 1, interferon regulatory factor 2, interferon regulatory factor 4,	interferon regulatory factor 5, sirtuin 1 ((silent mating type information regulation 2,	homolog) 1 (S. cerevisiae), sirtuin 2 (silent mating type information regulation 2,	homolog) 2 (S. cerevisiae), sirtuin 3 (silent mating type information regulation 2,	homolog) 3 (S. cerevisiae)	expressed sequence Al646973, interferon regulatory factor 1, interferon regulatory	factor 2, interferon regulatory factor 4, interferon regulatory factor 5	ESTs, Weakly similar to IFR1_RAT INTERFERON-RELATED DEVELOPMENTAL	REGULATOR 1 (NERVE GROWTH FACTOR-INDUCIBLE PROTEIN PC4) (IRPR)	R.norvegicus], interferon-related developmental regulator 1, interferon-related	developmental regulator 2						interleukin 18, interleukin 18 (interferon-gamma-inducing factor)		nterleukin 4 receptor,  colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage),	nterleukin 4 receptor, interleukin 4 receptor, alpha		
	HumaniHomologous KnownGeneiname	ŭ i	<u> </u>	Σ	<u>.i.</u>	<u>.</u>	<u>ĕ</u> .	interferon regulatory ho		interferon regulatory ex		ŭ	interferon-related R	developmental [[F	regulator 1	interleukin 1 beta,	interleukin 1, beta	interleukin 18,	interleukin 18	(interferon-gamma-	inducing factor) in	interleukin 4 receptor,	interleukin 4 receptor,  α	alpha	interleukin 6 receptor,	interleukin 6 receptor,
	गठवंवा द्ववंव								T, W		<b>A</b>			Q, W, MM,	<b>QQ, TTT</b>		W				^			٨		DD, EE, SS,
がある。	ලෙකවෙකාය Aee or RefSeg (D)								NM_012591		NM_012591				NM_019242		NM_031512				77777U			NM_133380		DD, EE, S
33	erec Dino								20126		21162				17908		247.10				1520	•		656		0
TABLE :	- 6 8 9								3089		3089				3379		3636				4171			3937		0

TABUES PARTIES	8				/Atterney Docket(4492/1-5038-0/1W0)
Sed D	elec. Idine.	ලකසක්දැ Aee ලැ Refiseg (Dි	Model Gode	HumaniHomologous KnowniGene Name	Human: Homologous Sequence (Gluster Mille)
				iron responsive element binding	
				protein 2, iron-	
4106	202	U20181	z	responsive element binding protein 2	
			Q, R, GG,		ESTs, Highly similar to IDHC_RAT ISOCITRATE DEHYDROGENASE [NADP]
			PPP, ada,	isocitrate	CYTOPLASMIC (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC
3635	17427	NM 031510	General	dehydrogenase 1 (NADP+), soluble	ICDH) (IDP) [R.norvegicus], expressed sequence AI788952, isocitrate dehydrogenase 1 (NADP+), soluble, isocitrate dehydrogenase 2 (NADP+), mitochondrial
	Т –			isocitrate	
				dehydrogenase 3	
3809	15090	15090 NM_053638	В, ннн	(NAD+) alpha	isocitrate dehydrogenase 3 (NAD+) alpha
				isocitrate	
				dehydrogenase 3	
3809	23305	NM_053638		(NAD+) alpha	isocitrate dehydrogenase 3 (NAD+) alpha
	٠		F, V, Z, AA,	isovaleryl Coenzyme	
			×, √<,	A dehydrogenase,	A dehydrogenase,   ESTs, Moderately similar to IVD_HUMAN ISOVALERYL-COA DEHYDROGENASE,
				isovaleryl coenzyme A	MITOCHONDRIAL PRECURSOR [H.sapiens], isovaleryl Coenzyme A dehydrogenase,
3090	4449	NM_012592	_	dehydrogenase	isovaleryl coenzyme A dehydrogenase
			A, B, V, BB,	isovaleryl Coenzyme	
			CC, II, 000,	A dehydrogenase,	ESTs, Moderately similar to IVD_HUMAN ISOVALERYL-COA DEHYDROGENASE,
			General	isovaleryl coenzyme A	isovaleryl coenzyme A MITOCHONDRIAL PRECURSOR [H.sapiens], isovaleryl Coenzyme A dehydrogenase,
3090	4450	NM_012592	Alternate	dehydrogenase	isovaleryl coenzyme A dehydrogenase
			-	isovaleryl Coenzyme	
				A dehydrogenase,	ESTs, Moderately similar to IVD_HUMAN ISOVALERYL-COA DEHYDROGENASE,
				isovaleryl coenzyme A	isovaleryl coenzyme A MITOCHONDRIAL PRECURSOR (H.sapiens), isovaleryl Coenzyme A dehydrogenase,
3090	4451	NM_012592	Alternate	dehydrogenase	isovaleryl coenzyme A dehydrogenase

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· 교요	Jeie Sei Sei	centenk Necot P Refreq ID	Model Gode	Human/Homologous Known Gene Name	Uman/Homologous
				isovaleryl Coenzyme A dehydrogenase	ESTs. Moderately similar to IVD. HUMAN ISOVALERYL-COA DEHYDROGENASE.
			W, General	isovaleryl coenzyme A	isovaleryl coenzyme A MITOCHONDRIAL PRECURSOR [H.sapiens], isovaleryl Coenzyme A dehydrogenase,
3090 44	4452	NM_012592	Alternate	dehydrogenase	isovaleryl coenzyme A dehydrogenase
				Janus kinase 1, Janus	
				kinase 1 (a protein	
2834 25	25233 /	AJ000556	⊢	tyrosine kinase)	
				jumping translocation	ESTs, Highly similar to jumping translocation breakpoint [Rattus norvegicus] umping translocation [R.norvegicus], ESTs, Moderately similar to jumping translocation breakpoint [Rattus
3372 26	2632	NM_019213	S	breakpoint	norvegicus] [R.norvegicus], jumping translocation breakpoint
				Jun oncogene, v-jun	
				sarcoma virus 17	
				oncogene homolog	
3438 22	22352	NM_021835	'c'	(avian)	Jun oncogene, v-jun sarcoma virus 17 oncogene homolog (avian)
				,	ESTs, Weakly similar to dJ1170K4.2 [H.sapiens], Mus musculus mRNA for serine protease-like 1, complete cds, Mus musculus, Similar to mosaic serine protease, clone
					IMAGE:3490022, mRNA, partial cds, RIKEN cDNA 1600027G01 gene, RIKEN cDNA
-				kallikrein B, plasma	1700049K14 gene, RIKEN cDNA 2010015P21 gene, RIKEN cDNA 4931440B09 gene,
				(Fletcher factor) 1,	coagulation factor XI (plasma thromboplastin antecedent), distal intestinal serine
27 24	1722	NM 012725	3127 24722 NM 012725 F, G, U, WW	kallikrein B, plasma 1	protease, kallikrein B, plasma (Fletcher factor) 1, kallikrein B, plasma 1

TABLES Section (Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Contro	33 000 000	Conservative   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Reference   Ref	Wodellcode	Kinowai Genei Name	Attorney Doctret (4522) - 5055-01000 Document No. 1955523.1 Human Homologous Sequence Chuster IIII (6)
3691		NM_031797	ww, 000	kangai 1 (suppression of tumorigenicity 6, prostate), kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))	kangai 1 (suppression of tumorigenicity 6, prostate), kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)), tetraspan 1
3710	16726	NM_031855	A, B, BB, CC, HH, OO, EEE, GGG, III, JJJ, MMM, General Core Tox Markers	ketohexokinase, ketohexokinase (fructokinase)	ketohexokinase, ketohexokinase (fructokinase)
2291	659	A1178208	M	KIAA0618 gene product, nuclear pore membrane protein 121	EST, Moderately similar to N121_HUMAN NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KDA) (P145) [H.sapiens], EST, Weakly similar to N121_HUMAN NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KDA) (P145) [H.sapiens], ESTs, Weakly similar to nuclear pore membrane glycoprotein 121 kD [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to DDX9 MOUSE ATP-DEPENDENT RNA HELICASE A [M.musculus], KIAA0410 gene product, KIAA0618 gene product, Mus musculus, clone IMAGE:5148310, mRNA, Mus musculus, clone IMAGE:5321620, mRNA, partial cds, POM (POM121 rat homolog) and ZP3 fusion, Snf2-related CBP activator protein, melanoma antigen, family D, 3

	ABUE 3				Atterney Docket 44924-5068-01WVO
	erec orec orec	leemeenkk. Aee or RefSeel D	Model Gode		fuman flomologous (nown Gene Name Human Homologous:Sequence Gluster IIII)
				<u> 11 – 1</u>	
				protein receptor,	
				kinase insert domain	
				receptor (a type III	
				receptor tyrosine	
3209	16472	NM_013062	222	kinase)	
			D, E, M, BB,		
3120	1850	NM_012696 CC, III, JJJ	CC, III, JJJ	kininogen	Kininogen
3120	1854	NM_012696	NM_012696 D, E, M, BB	kininogen	kininogen
				Kirsten rat sarcoma	
				oncogene 2,	ESTs, Weakly similar to RASL MOUSE TRANSFORMING PROTEIN P21/K-RAS 2B
				expressed, v-Ki-ras2	[M.musculus], Mus musculus, Similar to v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene
					homolog, clone MGC:6244 IMAGE:3158212, mRNA, complete cds, RAS-like protein
				viral oncogene	expressed in many tissues, Ric-like, expressed in many tissues (Drosophila), v-Ki-ras2
1586	2699	A1045340	MM, TTT	homolog	Kirsten rat sarcoma 2 viral oncogene homolog
3782	14380	NM_053536	W	Kruppel-like factor 15	
				Kruppel-like factor 9,	
				basic transcription	ESTs, Moderately similar to Kruppel-like factor 9 [Rattus norvegicus] [R.norvegicus],
				element binding	Kruppel-like factor 9, basic transcription element binding protein 1, expressed sequence
3895	8640	NM_057211	KKK	protein 1	AL022736
				Kruppel-like factor 9,	
				basic transcription	ESTs, Moderately similar to Kruppel-like factor 9 [Rattus norvegicus] [R.norvegicus],
				element binding	Kruppel-like factor 9, basic transcription element binding protein 1, expressed sequence
3895	8641	NM_057211	NM_057211 C, DD, EE, SS	protein 1	AL022736

17ABLE 3 Seq. (CLGG 100.00 13889 (613 3255 17807 3285 24885	Keneank Aeejer Refesque NM_057186 NM_017025	B, G, M, GG, HH, NN, OO, FFF, GGG, III, JJJ, General Core Tox Markers A, U C, U, FF, HH, YY YY F, G, H, General Alternate	kynureninase (L-kynurenine hydrolase) L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain lactate dehydrogenase 1, A chain, lactate dehydrogenase A laminin receptor 1 (67kD, ribosomal protein SA)	Mus musculus, Similar to kynureninase (L-kynurenine hydrolase)   Mus musculus, Similar to kynureninase (L-kynurenine hydrolase)   Mus musculus, Similar to kynureninase (L-kynurenine hydrolase)   Mus musculus, Similar to kynureninase (L-kynurenine hydrolase)   Mus musculus, Similar to kynureninase (L-kynurenine hydrolase)   Mus musculus, Similar to kynureninase (L-kynurenine hydrolase)   Mus musculus, Similar to kynureninase (L-kynurenine hydrolase)   Mus musculus, Similar to L-3-hydroxyacyl-Coenzyme A dehydrogenase (L-kynurenine hydrolase)   Musculus   ESTs, Highly similar to JC4879 3-hydroxyacyl-Coenzyme A dehydrogenase 1, A chain, lactate dehydrogenase 1, A lactate dehydrogenase 1, A lactate dehydrogenase 2   A chain, lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase B lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase A lactate dehydrogenase B lactate dehydrogenase B lactate dehydrogenase B lactate dehydrogenase B lactate dehydrogenase A lactate dehydrogenase B lactate dehydrogenase B lactate dehydrogenase B lactate B lactate dehydrogenase B lactate B lactate B lactate B lactate B lactate B lactate B lactate B lactate B
24886	3285 24886 NM_017138 F, G, H, VV	F, G, H, W	laminin receptor 1 (67kD, ribosomal protein SA)	KSP4 MOUSE 40S KIBOSOMAL PROTEIN SA [M.musculus], ESTS, Highly similar to A31233 ribosomal protein RS.40K, cytosolic [H.sapiens], ESTS, Moderately similar to laminin-binding protein [H.sapiens], expressed sequence AL022858, laminin receptor 1 (67kD, ribosomal protein SA)

	38				Attorney   Docket 4492A-5038-64WG
	GLGG ID No.	centeni: Ase or Refsig (D	Model Gode	HumaniHomologous KnowniGereinamen	Tumantikomologous Knownicenelvämen kluman Homologous Seguence (cluster ilitiae
					EST, Weakly similar to LCAT MOUSE PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR [M.musculus], EST, Weakly similar to LCAT_HUMAN PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR [H.sapiens], ESTs, Moderately similar to LCAT_HUMAN
			33		PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR [H.sapiens], expressed sequence C87498, lecithin cholesterol acyltransferase, lecithin-cholesterol
4219	670	X54096	XX, YY, CCC, PPP, QQQ	lectrnin-cholesterol acyltransferase	acylitransterase, lysopnospholipase 3, lysopnospholipase 3 (lysosomal phospholipase A2)
				lecithin retinol acyltransferase	
				(phosphatidylcholine	
				acyltransferase), lecithin-retinol	
				acyltransferase	
			General	(phosphatidylcholine- retinol-O-	lecithin retinol acyltransferase (phosphatidylcholineretinol O-acyltransferase), lecithin-
3460	10562	NM_022280	Alternate	acyltransferase)	retinol acyltransferase (phosphatidylcholine-retinol-O-acyltransferase)
			O BB PP W	lectin, galactose binding, soluble 3	
			EEE, MMM,		
			General	binding, soluble, 3	EST, Weakly similar to A35820 galectin 3 [H.sapiens], galectin-related inter-fiber protein,
3700	22321	NM_031832	Alternate	(galectin 3)	ectin, galactoside-binding, soluble, 3 (galectin 3)
902	22283	AA945172		leucine aminopeptidase 3	aminopeptidase-like 1, leucine aminopeptidase 3
				LIM domain kinase 2,	
2861	1351	D31874	RRR	LIM motir-containing protein kinase 2	EST, Moderately similar to LIKZ_KAT LIM domain kinase 2 (LIMK-2) [K.norvegicus], LIM domain kinase 2, LIM motif-containing protein kinase 2

TABLE 3	33				Attention of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
% (% (%)	@ <u>r</u> @@ 10 No.	ලිකින්නේ  යිලේගේ  යිරෙහිලේ [මි	Model Gode	Human Homologous Known Gene Name	
÷-	· =			linker of T-cell receptor pathways,	ESTs, Weakly similar to linker of T-cell receptor pathways [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to ShcC [M.musculus], linker of T-cell receptor
845	1682	AA943555	SS	lymphocyte adaptor protein	pathways, lymphocyte adaptor protein, src homology 2 domain-containing transforming protein C1, src homology 2 domain-containing transforming protein D
		·		lipase A, lysosomal acid, cholesterol	
				esterase (Wolman	ESTs, Weakly similar to cholesterol esterase (pancreatic), see D3Wox12, D3Wox13,
3129	10260	NM_012732	T, GG, HH, LL	disease), lysosomal acid lipase 1	D3Wox26 and D3Mgh25 [Rattus norvegicus] [R.norvegicus], lipase A, lysosomal acid, cholesterol esterase (Wolman disease), lysosomal acid lipase 1
				lipase A, lysosomal	
_				esterase (Wolman	ESTs, Weakly similar to cholesterol esterase (pancreatic), see D3Wox12, D3Wox13.
				disease), lysosomal	D3Wox26 and D3Mgh25 [Rattus norvegicus] [R.norvegicus], lipase A, lysosomal acid,
3129	25563	NM_012732		acid lipase 1	cholesterol esterase (Wolman disease), lysosomal acid lipase 1
			B, F, G, NN,		
			00, 666,		
			LLL, General		
			Core Tox		
2995	2505	M16235	Markers	lipase, hepatic	ESTs, Weakly similar to S15893 triacylglycerol lipase [M.musculus], lipase, hepatic
					ESTs, Weakly similar to 156246 lipopolysaccharide binding protein - rat [R.norvegicus],
					ESTs, Weakly similar to LBP MOUSE LIPOPOLYSACCHARIDE-BINDING PROTEIN
			A, D, E, V, W,	•	PRECURSOR [M.musculus], bactericidal/permeability-increasing protein, cholestery!
			BB, NN, EEE,	lipopolysaccharide	ester transfer protein, plasma, lipopolysaccharide binding protein, phospholipid transfer
3309	20529	NM_017208	NM_017208 [III, JJJ, MMM	binding protein	protein
			O, P, EEE,		ESTs, Highly similar to JH0790 lipoprotein lipase (EC 3.1.1.34) precursor - rat
3091	18385	NM_012598   MMM	MMM	lipoprotein lipase	[R.norvegicus], lipase, endothelial, lipoprotein lipase

oeket 44921-4056-011Wo Doeument No. 1995223.1		lase,	lase,			
Attorney Docket 44921-5038-01W0	maniklomologous Seguence @luster mitte	liver glycogen phosphorylase, muscle glycogen phosphorylase, phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	liver glycogen phosphorylase, muscle glycogen phosphorylase, phosphorylase, glycogen storage disease type VI)			utheran blood group (Auberger b antigen included)
	ในเกล้าแHomologious  ใต้own GeneiName Hur	liver glycogen phosphorylase, phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type liver (VI)	liver glycogen phosphorylase, phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type liver (VI)		L-kynurenine/alpha- aminoadipate aminotransferase, kynurenine aminotransferase II	Lutheran blood group (Auberger b antigen ncluded)
	7 D-  Model Gode	B, I, J, V, GGG, OOO, General Core General Core Tox Markers	I, FF, General	L.	F, XX, YY	٥
	ලෙක්වෙකියි නීලේ ගේ Refපිලේ (D	NM_022268	NM_022268	Z50144	250144	AA851637
E3.	GLGC DNS	10509	25814	1541	1542	21713
	Seq Di	3457	3457	4291	4291	317

	33				Attorney Docket 4492/1-5039-01/WO
ි ලින්	ම්ලල ම්ලල ම්	<u>  Genternik</u>   Aec.or   Refisia   ID = 1	Modell Gode	HumaniHomologous Known Gene Name	HumaniHomologous Sequence (cluster/little)
3160	18770	NM 012857	u u	lysosomal membrane glycoprotein 1, lysosomal-associated membrane protein 1	CD68 antigen, ESTs, Weakly similar to LMP1_RAT LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 1 PRECURSOR (LAMP-1) (120 KD LYSOSOMAL MEMBRANE GLYCOPROTEIN) (LGP-120) (CD107A) [R.norvegicus], chromosome 20 open reading frame 103, lysosomal membrane glycoprotein 1, lysosomal-associated membrane protein 3.
3265	6653	NM_017068	LL, XX, YY,		CD68 antigen, ESTs, Weakly similar to JC4317 lysosome-associated membrane protein 2 precursor, splice form B [H.sapiens], lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2
3265	6654	NM_017068	ור	lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2	CD68 antigen, ESTs, Weakly similar to JC4317 lysosome-associated membrane protein 2 precursor, splice form B [H.sapiens], lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2
588	12118	AA892775	00, W, XX, YY	lysozyme, lysozyme (renal amyloidosis)	EST, Weakly similar to LYC1_RAT Lysozyme C, type 1 precursor (1,4-beta-N-acetylmuramidase C) [R.norvegicus], RIKEN cDNA 9530003J23 gene, lysozyme, lysozyme (renal amyloidosis), similar to lysozyme C-1 (1,4-beta-N-acylmuramidase C, EC 3.2.1.17)
3367	15242	NM_019191	O, P, EE		MAD homolog 2 (Drosophila), MAD, mothers against decapentaplegic homolog 2 (Drosophila)
4155	871	U66479	BB, CC	MAD homolog 3 (Drosophila), MAD, mothers against decapentaplegic homolog 3 (Drosophila)	Homo sapiens cDNA: FLJ23037 fis, clone LNG02036, highly similar to HSU68019 Homo sapiens mad protein homolog (hMAD-3) mRNA, MAD homolog 3 (Drosophila), MAD, mothers against decapentaplegic homolog 3 (Drosophila)

	3.8 3.8				Attorney Docket 44921-5038-0/1W0
Seq. 10.	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	ලේඛවේඛැ /\ලේ ගේ ීි  යිම්හිමු [D]	जिन्द्र होते । जिन्द्रवादिन्द्र	Kuman Homologous Known Gene Name	ใบเทลากไม่อักภอใจgอบรา ใก้อังมาเรียกะ INumani Homologous (Sequence Gluster Tiltle)
0.00	6		( ( ( (	malic enzyme 1, NADP(+)-dependent, cytosolic, malic	
6071	2007	Alguadzu	agg, ccc	enzyme, supernatant malic enzyme 1, NADP(+)-dependent,	
3093	18746	NM_012600	888	cytosolic, malic enzyme, supernatant	
			T, X, Y, BBB,	malic enzyme 1, NADP(+)-dependent,	
3093	18747	NM_012600	SSS, UUU	enzyme, supernatant	
			X, Y, BBB,	malic enzyme 1, NADP(+)-dependent,	
3093	18749	NM_012600	LLL, RRR, SSS, UUU	cytosolic, malic enzyme, supernatant	
		70-0-1		malignancy- associated protein,	CD33 antigen (gp67), ESTs, Weakly similar to MAG_RAT Myelin-associated glycoprotein precursor (L-MAG/S-MAG) (Brain neuron cytoplasmic protein 3)
3304	24437	NM_017190		myelin-associated glycoprotein	[R.norvegicus], Mus musculus sialic acid-binding lectin Siglec-F mRNA, complete cds, myelin-associated glycoprotein, sialic acid binding Ig-like lectin 5
				mannose binding lectin, serum (C),	
		=,.=	H, S, HH, FFF, R	mannose-binding lectin (protein C) 2,	
3513	24434	Core To:	Core Tox Markers		mannose binding lectin, serum (C), mannose-binding lectin (protein C) 2, soluble (opsonic defect)

TABUES	8 E				Attorney Docket 44921-5038-01W0
8960	<u>@</u>	Ceneral		Humen Homologous	Human Homologous
<u> </u>	(D) (D)	RefSeq [D	ിയുട	Known Gene Name	Human Homologous Sequence Guster Mile
				matrix	
				metalloproteinase 7,	
				matrix	
_				metalloproteinase 7	
2962	395	L24374	SS	(matrilysin, uterine)	
					RIKEN cDNA 1700056A17 gene, RIKEN cDNA 1700080O16 gene, RIKEN cDNA
				na antigen,	2410003J06 gene, RIKEN cDNA 3830417A13 gene, melanoma antigen, family D, 1,
3762	19322	NM_053409	99	family D, 1	melanoma antigen, family L, 2
			U, BBB, CCC,	membrane interacting	
3731	17933	NM_032615	RRR, SSS	protein of RGS16	
			U, V, BBB,	membrane interacting	
3731	17934	NM_032615	၁၁၁	protein of RGS16	
				membrane interacting	
3731	17935	NM_032615	RRR, SSS	protein of RGS16	
					EST, Moderately similar to Cd-7 Metallothionein-2 [H.sapiens], EST, Moderately similar
_			C, E, L, T, W,	metallothionein 1,	to SMHU1E metallothionein 1E [H.sapiens], ESTs, Moderately similar to MT1_RAT
				metallothionein 1A	METALLOTHIONEIN-I (MT-I) [R.norvegicus], metallothionein 1, metallothionein 4,
3982	15189	NM_138826	NNN	(functional)	metallothionein IV
					EST, Moderately similar to Cd-7 Metallothionein-2 [H.sapiens], EST, Moderately similar
			C, E, L, T, DD,		to SMHU1E metallothionein 1E [H.sapiens], ESTs, Moderately similar to MT1_RAT
			SS, WW, KKK,		METALLOTHIONEIN-I (MT-I) [R.norvegicus], metallothionein 1, metallothionein 4,
3982	15190	NM_138826		NNN (functional)	metallothionein IV
					ESTs, Highly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus],
					ESTs, Weakly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus],
				metastasis associated	letastasis associated KIAA1266 protein, KIAA1610 protein, metastasis associated 1, metastasis associated 1-
3493	20762	NM_022588	YY	1	like 1, metastasis associated 3, metastasis-associated 1-like 1
				methionine	methionine adamosultransfarase   Mus musculus plana MGC:6545 IMAGE:085444 mRNA complete pds avorassed
203	975	AA819118	ς, ΥΥ	ateriosymansiciase i,	sequence AI046368, methionine adenosyltransferase I, alpha

	<u>ඉලබ</u> ඩබොද _{ැදි}		1, 17, 18, 18, 18, 18, 18, 18, 18, 18, 18, 18	
Accor Referend	的影響	ි. ගින්න් ලින්න	Human Homologousi Known Cene Name	HumanaHomologous Sequence Gusterville
		F, L, T, RR,	methionine	
		SS, WW, SSS,	adenosyltransferase I,	SS, WW, SSS, adenosyltransferase I, Mus musculus, clone MGC:6545 IMAGE:2655444, mRNA, complete cds, expressed
X15734		ດດດ	alpha	sequence AI046368, methionine adenosyltransferase I, alpha
			nine	
			aminopeptidase 2,	
			methionyl	ESTs, Moderately similar to AMP2 MOUSE METHIONINE AMINOPEPTIDASE 2
NM_022539	2539	۵	aminopeptidase 2	[M.musculus], methionine aminopeptidase 2, methionyl aminopeptidase 2
		B, K, GGG,	methionine	
		HHH, PPP,	aminopeptidase 2,	
		QQQ, General methionyl	methionyl	ESTs, Moderately similar to AMP2 MOUSE METHIONINE AMINOPEPTIDASE 2
NM_022539	2539	Alternate	aminopeptidase 2	[M.musculus], methionine aminopeptidase 2, methionyl aminopeptidase 2
			microsomal	
		M, S, DD, EE,	glutathione S-	
NA 1	NM_134349		transferase 1	
				EGF-like repeats and discordin I-like domains 3, ESTs, Weakly similar to JC4915 ags
				protein precursor - rat [R.norvegicus], milk fat globule-EGF factor 8 protein, retinoschisis
OW	NM_012811	χ, <del>′</del> χ	factor 8 protein	1 homolog (human)
			mitochondrial	
M 1	NM_133539	G, н	ribosomal protein L17	
			mitochondrial	
Σ	NM_133539	G, H	ribosomal protein L17	
			mitochondrial	
O M	NM_022529	D, JJ, KK	ribosomal protein L23	
			mitogen activated	
			protein kinase kinase	
			2, mitogen-activated	
			protein kinase kinase	
(C) N	2223	INM 133283 II . I DD FF	2	

TENSIT!	ABUE 8				Attorney Docket 4492/1-5098-0/1070
Seq. Tu	elec Idno	ලෙබු.හොයි.ි රුලේ ගේ Rප්රිලිලේ (D	FriedelfCede Kno	Human Homologous KnownicenelName	man Homologous own Genen Name Human Homologous Sequence Gluster, Title
3932	21848	I, J, I	· · · · · ·	mitogen activated protein kinase kinase 2, mitogen-activated protein kinase kinase	
				mitogen activated protein kinase kinase 2, mitogen-activated protein kinase kinase	
3932	21849	NM_133283	U, RRR	2	
				mitogen activated. protein kinase kinase kinase 12, mitogen- activated protein kinase kinase	ESTs, Highly similar to A55318 serine/threonine protein kinase [M.musculus], Mus musculus, Similar to mitogen-activated protein kinase kinase klnase 9, clone MGC:27778 IMAGE:3156324, mRNA, complete cds, RIKEN cDNA 9130019115 gene, expressed sequence C81508, mitogen activated protein kinase kinase kinase kinase 11, mitogen activated protein kinase kinase kinase kinase kinase kinase kinase 10, mitogen-activated protein kinase kinase kinase kinase kinase 13, protein kinase kinase kinase kinase kinase 13,
3207	12371	NM_013055	င	12	mitogen-activated protein kinase kinase kinase 7
3659	14956	NM_031622	ပ	mitogen-activated protein kinase 6	ESTs, Weakly similar to B40033 protein kinase (EC 2.7.1.37) ERK3 - rat [R.norvegicus], mitogen-activated protein kinase 6
3659	14957	NM_031622	c, T	mitogen-activated protein kinase 6	ESTs, Weakly similar to B40033 protein kinase (EC 2.7.1.37) ERK3 - rat [R.norvegicus], mitogen-activated protein kinase 6
4095	88	009870	W, General Alternate	Mitral valve prolapse, familial, major vault protein	
3972	12215	NM_138502 K,	K, 888	monoglyceride lipase	Homo sapiens cDNA: FLJ22330 fis, clone HRC05729, highly similar to AF131821 Homo monoglyceride lipase sapiens clone 24877 mRNA sequence, monoglyceride lipase

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r. SiSe	11, Br nhibit							r to M encep		oligode
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die in	NA se							STs, F Ayelin		myelin-assoc basic protein
	itor DI	တ ဖ	-	es S	se.					sic m
ologo Nami	ng-zin inhib (TAT)	tol esphata sphata ssitol ee		tol :e sphata spitol	rc sphata	-	protei	protei	iated yte ba in-	ytic ba
	eractir Proteir ated S	inosii sphat phos ple inc sphat		inosii sphat phos ple inc	e phos	-	nding 1a	basic	assoc ndroc myel tted	ndroc
(nown)(Gene,Name)	Msx-interacting-zinc finger, Protein inhibit of activated STAT X	multiple inositol solyphosphate istidine phosphatase 1, multiple inositol solyphosphate		nultiple inositol bolyphosphate histidine phosphatase 1, multiple inositol	onypriospriate nistidine phosphatase,		MYB binding protein (P160) 1a	nyelin basic protein	myelin-associated bligodendrocyte basic protein, myelin-associated	oligode
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Mode	T, 00	Q, MM, T General	Alternate	<i>y</i> ,	General	Alternate	C, PPP, ( General Alternate	ж Ж		AA, SS
10 10	3337		14		_	2		78		NM_012720
ee or t	NM_053337		AF012/14			AI111401	NM_031668	AI169378		M 01
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2   2   2   2   2   2   2   2   2   2	14934		15292	·····		15291	17448	7253		22294
	3751		1220			1898	3666	2017	<u> </u>	3126

TABLE 3	38.	N. Y.			Attorney Dearet 4A92A-5038-0AWO
	ලැලේ 10 No.	Genzenik Ağe ör RefSeq (D	Model Gode	Human Homologous Modell Gode: Known Gene Name	Human Homologous Sequence Guster Mille
				myelocytomatosis	
				oncogene, v-myc	
				myelocytomatosis viral oncodene	
3094	2629	NM_012603	>	homolog (avian)	myelocytomatosis oncogene, v-myc myelocytomatosis viral oncogene homolog (avian)
					EST, Highly similar to MY1A_RAT Myosin IA (Myosin I alpha) (MMI-alpha) (MMIa) (Myosin heavy chain myr 1) [R.norvegicus], EST, Weakly similar to MYOSIN I ALPHA
			C, SS, WW,		[M.musculus], Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010010B23:myosin, heavy polypeptide-like (110kD), full insert
3864	17653	NM_053986   SSS, UUU	SSS, UUU	myosin IB	sequence, myosin IB
	•			N-acylaminoacyl-	
2929	1421	104733	N, BBB, CCC, RRB	N, BBB, CCC, peptide hydrolase,	Mus musculus, clone IMAGE:4974221, mRNA, partial cds, N-acylaminoacyl-peptide
				NAD/DIH	ESTE Moothly similar to A34469 MAD/DND dobydzagango (minana) (EC 4 6 00 0) ast
			HH CC X	רו( די )טראיו ספריסריסראילסר	ESTS, Weakly Silling 10 A34 102 NAD(P)H denydrogenase (quinone) (EC 1.5.99.2) - rat IR non-enicus) NAD(P)H debydrogenase aninone 1 NAD(D)H debydrogenase
3247	1698	NM_017000		quinone 1	quinone 2, NAD(P)H menadione oxidoreductase 2, dioxin inducible
				NADH	
				dehydrogenase	
				(ubiquinone) Fe-S	
				(NADH-coenzyme O	MANH debydraces (canalisation of control of the MANH) (MANH)
2090	4428	AI171362	၁၁၁	3 2 11 6	reductase)
				NADH	
				dehydrogenase	
				(ubiquinone) Fe-S	
2471	3099	A1229680	RRR	(NADH-coenzyme Q reductase)	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)

DABLE 3	ଞ				Attorney Docket 44924-5038-01000 Document No. 1935828.1
	GLGC B No.	ලෙබන්නොයි දැ 	Ks. F. William		Human Homologous Known Gene Namer Human Homologous Sequence ©luster ∏ttle
				NADH	
				dehydrogenase	
				(ubiquinone) Fe-S	
				protein 6 (13kD)	
				(NADH-coenzyme Q	
	•			reductase), NADH	ESTs, Highly similar to NUMM MOUSE NADH-UBIQUINONE OXIDOREDUCTASE 13
				enase Fe-S	KD-A SUBUNIT [M.musculus], NADH dehydrogenase (ubiquinone) Fe-S protein 6
3375	20938	NM_019223	V, EE	protein 6	(13kD) (NADH-coenzyme Q reductase)
				NADH	
				dehydrogenase	
				(ubiquinone) Fe-S	
				protein 8 (23kD)	
				(NADH-coenzyme Q	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q
20	16901	AA799479	FF	reductase)	reductase)
				natriuretic peptide	
				precursor B,	EST, Moderately similar to ANFB MOUSE BRAIN NATRIURETIC PEPTIDE
				natriuretic peptide	PRECURSOR [M.musculus], natriuretic peptide precursor B, natriuretic peptide
3644	18389	NM 031545	PP, UU, III	precursor type B	precursor type B
				nerve growth factor	
				receptor, nerve	
				growth factor receptor	growth factor receptor Mus musculus, clone IMAGE:5097359, mRNA, partial cds, nerve growth factor receptor
			_	(TNFR superfamily,	nerve growth factor receptor (TNFR superfamily, member 16), p75-like apoptosis-
3095	1299	NM_012610	^	member 16)	inducing death domain protein PLAIDD

TABLE	33 	<u>িভ্রিক্ত হিলার ্</u>			Attorney Docket 44921-5088-611W0
ම ම	GLEG ID No.	Acc or .  Re(Seq 10	Model Gode   KA	HumaniHomologousi Known GeneiName	Human Homologous Sequence Cluster Mile
				N-ethylmaleimide	
				sensitive fusion	
				protein attachment	
				protein alpha, N-	
				ethylmaleimide-	N-ethylmaleimide sensitive fusion protein attachment protein alpha, N-ethylmaleimide
				sensitive factor	sensitive fusion protein attachment protein beta, N-ethylmaleimide sensitive fusion
				attachment protein,	protein attachment protein gamma, N-ethylmaleimide-sensitive factor attachment
3902	16108	NM_080585	Z, AA	alpha	protein, alpha, N-ethylmaleimide-sensitive factor attachment protein, gamma
				N-ethylmaleimide	
				sensitive fusion	
				protein attachment	
				protein alpha, N-	
				ethylmaleimide-	N-ethylmaleimide sensitive fusion protein attachment protein alpha, N-ethylmaleimide
				sensitive factor	sensitive fusion protein attachment protein beta, N-ethylmaleimide sensitive fusion
				attachment protein,	protein attachment protein gamma, N-ethylmaleimide-sensitive factor attachment
3902	16109	NM_080585	RR, SS	alpha	protein, alpha, N-ethylmaleimide-sensitive factor attachment protein, gamma
				neuromedin,	
3452	20450	NM_022239	Z, AA, SS	neuromedin U	neuromedin, neuromedin U
				nuclear distribution	ESTs, Moderately similar to A55897 prolactin-induced T cell protein c15 - rat
				gene C homolog (A.	[R.norvegicus], KIAA1068 protein, Mus musculus, Similar to KIAA1068 protein, clone
				nidulans), nuclear	IMAGE:4236345, mRNA, partial cds, expressed sequence AL022907, nuclear
				distribution gene C	distribution gene C homolog (A. nidulans), nuclear distribution gene C homolog
4269	570	X82445	BBB, CCC	homolog (Aspergillus)	(Aspergillus)
					nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor
3188	763	NM_012988	χ¥	nuclear factor I/A	I/X (CCAAT-binding transcription factor)
					nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor
4273	764	X84210	F, HH, JJ, KK	nuclear factor I/A	I/X (CCAAT-binding transcription factor)
			General		Nuclear Factor IA, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor
1209	17962	AB012230	Alternate	nuclear factor I/B	I/X, nuclear factor I/X (CCAAT-binding transcription factor)

	8 ETTEN				Attorney Bocket 4492A-5038-04W0
8 8 9	erec Ida Ida	Ceneank Kee or Resea 10	Modell Gode	Humani Homologous Knowni Genei Name	flumaniffomologous Goown Genei Name   Humaniffomologous Sequence Ourster Witto
			FFF, General		
			Core Tox		
			Markers,		
			General		Nuclear Factor IA, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor
1210	17963	AB012231	Alternate	nuclear factor I/B	I/X, nuclear factor I/X (CCAAT-binding transcription factor)
L			Y, LLL,		
			General Core		
			Tox Markers,		
			General		Nuclear Factor IA, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor
2209	24763	A1176488	Alternate	nuclear factor I/B	I/X, nuclear factor I/X (CCAAT-binding transcription factor)
				nuclear factor I/X,	
				nuclear factor I/X	
					Nuclear Factor IA, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor
1211	24414	AB012234	D, SS	<u></u>	I/X, nuclear factor I/X (CCAAT-binding transcription factor)
				nuclear factor of	
				kappa light chain gene	
		<del></del> -		enhancer in B-cells	
				inhibitor, alpha,	
				nuclear factor of	
				kappa light	
				polypeptide gene	
				enhancer in B-cells	
4244	25089	X63594	٦' ٦	inhibitor, alpha	

	ଚ୍ଚ				Attorney Docket 44924-5938-04000
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				nuclear factor of kappa light chain gene	
				enhancer in B-cells	
				inhibitor, alpha,	
_				nuclear factor of	
				kappa light	
				polypeptide gene	
				enhancer in B-cells	
4244	25090	X63594	7	inhibitor, alpha	
				nuclear protein 1, p8	
				protein (candidate of	EST, Weakly similar to P8_HUMAN P8 PROTEIN [H.sapiens], nuclear protein 1, p8
1221	1597	AF014503	W, MM, TTT	metastasis 1)	protein (candidate of metastasis 1)
			W, DD, EE,		EST, Moderately similar to NRH3_RAT Oxysterols receptor LXR-alpha (Liver X receptor
			KKK, NNN,	nuclear receptor	alpha) (Nuclear orphan receptor LXR-alpha) (RLD-1) [R.norvegicus], EST, Weakly
			General	subfamily 1, group H,	similar to 138975 nuclear orphan receptor LXR-alpha (H.sapiens), expressed sequence
4099	1639	U11685	Alternate	member 3	AU018371, nuclear receptor subfamily 1, group H, member 3
			A, B, General		
			Core Tox		
			Markers,	nuclear receptor	EST, Weakly similar to 138975 nuclear orphan receptor LXR-alpha [H.sapiens], ESTs,
			General	subfamily 1, group H,	subfamily 1, group H,  Moderately similar to JC4014 steroid hormone-nuclear receptor NER [H.sapiens],
3433	19712	NM_021745	Alternate	member 4	expressed sequence Al957360, nuclear receptor subfamily 1, group H, member 4
				nuclear RNA export	
_				factor 1, nuclear RNA	
				export factor 1	
			1	homolog (S.	
1247	18731	AF093139	R	cerevisiae)	

### 17394 NM 012992 D. JJ, HHH Interest properties    Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t									
4339 AA875121 UU fit 16163 NM_031563 MM, TTT P 16165 NM_031563 D D P 17393 NM_012992 D, JJ, HHH D 17394 NM_012992 Alternate D P		epunz		ESTs, Highly similar to 139382 Y box-binding protein 1 - human [H.sapiens], ESTs, Moderately similar to PS0015 DNA-binding protein B [H.sapiens], RIKEN cDNA 1700102N10 gene, Y box protein 2, nuclease sensitive element binding protein 1	ESTs, Highly similar to 139382 Y box-binding protein 1 - human [H.sapiens], ESTs, Moderately similar to PS0015 DNA-binding protein B [H.sapiens], RIKEN cDNA 1700102N10 gene, Y box protein 2, nuclease sensitive element binding protein 1	ESTs, Highly similar to 139382 Y box-binding protein 1 - human [H.sapiens], ESTs, Moderately similar to PS0015 DNA-binding protein B [H.sapiens], RIKEN cDNA 1700102N10 gene, Y box protein 2, nuclease sensitive element binding protein 1	ESTs, Highly similar to A32915 nucleophosmin [H.sapiens], nucleophosmin 1	ESTs, Highly similar to A32915 nucleophosmin [H.sapiens], nucleophosmin 1	nucleoporin 88kD, preimplantation protein 2
16165 NM 031563 16165 NM 031563 16165 NM 031563 16165 NM 031563 17393 NM 012992		Known Cene Name	nuclear transcription factor Y, gamma, nuclear transcription factor-Y gamma	nuclease sensitive element binding protein 1	nuclease sensitive element binding protein 1	nuclease sensitive element binding protein 1	nucleophosmin (nucleolar phosphoprotein B23, numatrin), nucleophosmin 1	nucleophosmin (nucleolar phosphoprotein B23, numatrin), nucleophosmin 1	nucleoporin 88kD, preimplantation protein 2
16163 16165 16165 16165 17393		Modeli ලික්ව	nn	MM, TTT	RR, W	Q	О, JJ, ННН	FFF, General Alternate	ZZ, AAA
16163 16165 16165 17393		ලේඛවෙකයි.  කිලේ ලේ  යිලේහිලේ (D	AA875121		NM_031563	NM_031563	NM_012992	NM_012992	U93692
	8	elêê Dino	4339	16163	16164	16165	17393	17394	1401
318 364 435		ි. මුල්	438	3648	3648	3648	3189	3189	4178

TABLES	33				Attorney Doetst 44921-5038-01W0
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୍ଟ ଅକ୍ର	Series Dina	Aee or Refseq (D)	Model Gode	32.53	uman Homologous  nown/GenenName=  Human/Homologous/Sequence/Glusten/Iffle
			General Core		
			Tox Markers,		ESTs, Highly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], ESTs,
			General	nucleosome assembly	Icleosome assembly Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], SET translocation, SET
1515	7665	A1030668	Alternate	protein 1-like 1	translocation (myeloid leukemia-associated), nucleosome assembly protein 1-like 1
				opioid receptor, sigma	
3579	1792	NM_030996	K, KKK	1	opioid receptor, sigma 1, sigma receptor (SR31747 binding protein 1)
				ornithine	
			WW, FFF,	carbamoyltransferase,	
			General	ornithine	
3214	13282	NM_013078	Alternate	transcarbamylase	ornithine carbamoyltransferase, ornithine transcarbamylase
				ornithine	
				carbamoyltransferase,	
				ornithine	
3214	13283	NM_013078	A, B, NN, 00	transcarbamylase	ornithine carbamoy/transferase, ornithine transcarbamylase
				ornithine	ESTs, Highly similar to DCOR MOUSE ORNITHINE DECARBOXYLASE [M.musculus],
				decarboxylase 1,	ESTs, Weakly similar to DCOR MOUSE ORNITHINE DECARBOXYLASE [M.musculus],
					ESTs, Weakly similar to DCOR_HUMAN ORNITHINE DECARBOXYLASE [H.sapiens],
				decarboxylase,	ornithine decarboxylase 1, ornithine decarboxylase, structural, ornithine decarboxylase-
3096	23522	NM_012615	A	structural	like protein
				ornithine	ESTs, Highly similar to DCOR MOUSE ORNITHINE DECARBOXYLASE [M.musculus],
				decarboxylase 1,	ESTs, Weakly similar to DCOR MOUSE ORNITHINE DECARBOXYLASE [M.musculus],
				ornithine	ESTs, Weakly similar to DCOR_HUMAN ORNITHINE DECARBOXYLASE [H.sapiens],
				decarboxylase,	ornithine decarboxylase 1, ornithine decarboxylase, structural, ornithine decarboxylase-
3096	23523	NM_012615	В, Н, І, Ј	structural	like protein
				ornithine	
			DD, EE, MM,	decarboxylase	ESTs, Weakly similar to ODCI_MOUSE Ornithine decarboxylase antizyme inhibitor
3492		21062 NM_022585	UU, TTT	antizyme inhibitor	[M.musculus], ornithine decarboxylase antizyme inhibitor

TABLES	88	F			Atterney Docket 4492/1-5038-01/WO
- (		Geneenia			
	GLGG (D) No	Mee or RefSeq (D	Model Gode	-5"	tuman Homologous (nownicene Names Human Homologous Sequence Gluster) ii de
			111	ornithine	Total Windows and an analysis of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
3492	21063	NM_022585	7. Miw., 90,	antizyme inhibitor	ESTS, weakly stilling to ODOL_MOOSE Officiality decarboxylase analytice initibility [M.musculus], ornithine decarboxylase antizyme inhibitor
				ornithine	
				decarboxylase	
				antizyme, ornithine	
_				decarboxylase	
3998	15134	NM_139081	E, K	antizyme 1	
				ornithine	
				decarboxylase	
				antizyme, ornithine	
				decarboxylase	
3998	25250	NM_139081	<u></u>	antizyme 1	
			D, E, BB, CC,		
4181	412	V01216	111, JJJ	orosomucoid 1	orosomucoid 1, orosomucoid 2, orosomucoid 3
3697	15840	NM_031817	WW	osteomodulin	osteoglycin, osteomodulin
			l, L, ww,		
			000, General	P450 (cytochrome)	
2883	1921	E01524	Alternate	oxidoreductase	
				P450 (cytochrome)	
3651	1919	NM_031576  I, L, WW	I, L, WW	oxidoreductase	
			C, I, L, MM,		
			ww, 000,		
			TTT, General	P450 (cytochrome)	
3651	1920	NM_031576	Alternate	oxidoreductase	

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See 1	etec Da	Ceneent Ace or Rasse ID	Model Gode	ในที่สามหอักอใจอูดบร Known.GeneyName	Human Homologous Known Genei Name Human Homologous Sequence Cluster, Title
				paired basic amino	
				4, proprotein	EST, Highly similar to 153282 gene PACE4 protein - rat [R.norvegicus], RIKEN cDNA
				convertase	A930029K19 gene, paired basic amino acid cleaving system 4, proprotein convertase
3192	24263	NM_012999	BB, CC	subtilisin/kexin type 6	subtilisin/kexin type 6
				paired basic amino	
				acid cleaving system	
				4, proprotein	EST, Highly similar to 153282 gene PACE4 protein - rat [R.norvegicus], RIKEN cDNA
				convertase	A930029K19 gene, paired basic amino acid cleaving system 4, proprotein convertase
3192	24264	NM_012999	MM, TTT	subtilisin/kexin type 6	subtilisin/kexin type 6
270	1000	100000 FAIN	2	palmitoyl-protein	
2405	10020	NM_01936/	٥,٠	tnioesterase 2	palmitoyi-protein thioesterase 2
				partner of RAC1	
1600	24374	AI045973	ш	(arfaptin 2)	partner of RAC1 (arfaptin 2)
				peptidylglycine alpha-	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING
				amidating	MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating
37	1647	AA799575	G, H, ≡	monooxygenase	monooxygenase
				peptidylglycine alpha-	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING
ŀ				amidating	MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating
133	1650	AA817825	=	monooxygenase	monooxygenase
			-	peptidylglycine alpha-	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING
				amidating	MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating
465	1644	AA891068	G, =	monooxygenase	monooxygenase
				peptidylglycine alpha-	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING
				amidating	MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating
1853	1649	Al103782	Ξ	monooxygenase	monooxygenase
				peptidytglycine alpha-	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING
		1	ı	amidating	MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating
2411	1651	AI228068	±.	monooxygenase	monooxygenase

	38				11
Sed (10)	ලෝලේ ලෝලේ	(eeneen Ree or Resea (D'	් දැන්නම් මාන්තම් මෙමෙම		Aluman Homologous  Kiñown Genei Namer   Human Homologouss Sequencei ©luster ™©
				peptidylglycine alpha-	Deptidylglycine alpha- ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING amidating mondating and alpha-amidating mondating and alpha-amidating amidating mondating and alpha-amidating mondating and alpha-amidating amidating and alpha-amidating amidating and alpha-amidating amidating and alpha-amidating amidating amidating and alpha-amidating amidating and alpha-amidating amidating amidating and alpha-amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidating amidat
2642	1653	AI233806	F, G, II, UUU	Jenase	monooxygenase
				peptidylglycine alpha-	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING
				amidating	MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating
2660	1654	AI234258	X, Y, II	monooxygenase	monooxygenase
			BB, CC, PP,	peptidylglycine alpha-	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING
			QQ, EEE,	amidating	MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating
2884	1641	E03428	MMM, UUU	monooxygenase	monooxygenase
				peptidylglycine alpha-	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING
				amidating	MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating
3193	1640	NM_013000   II, LLL, UUU	II, LLL, UUU	monooxygenase	monooxygenase
			_		EST, Moderately similar to A Chain A, Cyclophilin A [H.sapiens], ESTs, Highly similar to
					CYPH MOUSE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [M.musculus], ESTs,
					Moderately similar to A Chain A, Human Cyclophilin A Complexed With 2-Thr
					Cyclosporin [H.sapiens], ESTs, Weakly similar to A Chain A, Cyclophilin A [H.sapiens],
				peptidylprolyl	ESTs, Weakly similar to A Chain A, Human Cyclophilin A Complexed With 2-Thr
				isomerase A,	Cyclosporin [H.sapiens], ESTs, Weakly similar to CYPH_RAT Peptidyl-prolyl cis-trans
				peptidylprolyl	isomerase A (PPlase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) (P31)
				isomerase A	[R.norvegicus], RIKEN cDNA 2510026K04 gene, expressed sequence Al256741,
3278	4391	NM_017101	=	(cyclophilin A)	expressed sequence AW457192, peptidylprolyl isomerase A

	NEW 8				Afterney Docket (49271-5939-61)Wo
(8) (8)	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	<u>Consent : .</u> Ace or . RetSeq ID .	X) (-epos) (dpow)	Human Homologous Known Genei Name	0
					EST, Moderately similar to A Chain A, Cyclophilin A [H.sapiens], ESTs, Highly similar to CYPH MOUSE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [M.musculus], ESTs,
<del></del> -					Moderately similar to A Chain A, Human Cyclophilin A Complexed With 2-Thr Cyclosporin IH,sapiensl, ESTs, Weakly similar to A Chain A, Cyclophilin A IH,sapiensl
				peptidylprolyl	ESTs, Weakly similar to A Chain A, Human Cyclophilin A Complexed With 2-Thr
				isomerase A,	Cyclosporin [H.sapiens], ESTs, Weakly similar to CYPH_RAT Peptidyl-prolyl cis-trans
				peptidylprolyl	isomerase A (PPlase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) (P31)
				isomerase A	[R.norvegicus], RIKEN cDNA 2510026K04 gene, expressed sequence Al256741,
3278	4392	NM_017101	, γ Χ, ΥΧ	(cyclophilin A)	expressed sequence AW457192, peptidylprolyl isomerase A
<u></u>					Homo sapiens cDNA FLJ12333 fis, clone MAMMA1002198, highly similar to
3298	14498	NM_017169	EE	peroxiredoxin 2	THIOREDOXIN PEROXIDASE 1, expressed sequence AL022839, peroxiredoxin 2
			U, LL, BBB,	peroxisomal acyl-CoA	
			CCC, LLL,	thioesterase,	EST, Moderately similar to PTE1_MOUSE Peroxisomal acyl-coenzyme A thioester
_				peroxisomal acyl-CoA	peroxisomal acyl-CoA hydrolase 1 (Peroxisomal long-chain acyl-coA thioesterase 1) [M.musculus],
3927	9268	NM_130756	ກກາ	thioesterase 1	peroxisomal acyl-CoA thioesterase, peroxisomal acyl-CoA thioesterase 1
	2000	77217004	L L	peroxisomal	
7171	/0077	AB01/544	W, UU, EE		peroxisomal biogenesis factor 14
				peroxisomal	
			( (	membrane protein 2	
				(ZZKU), peroxisornal	EDIS, WEAKIY SIMILIAN TO WILVE I MICHOLDE IMPORT PROFEIN [M.MUSCUIUS], MIDVIN
			General	membrane protein 2,	transgene, murine homolog, glomerulosclerosis, Mpv17 transgene, kidney disease
4253	405	X70223	Alternate	22 kDa	mutant, peroxisomal membrane protein 2, 22 kDa
			WW, LLL,		
3098	6055	NM 012619	RRR, SSS,	phenylalanine hydroxylase	ESTs, Highly similar to WHHUF phenylalanine 4-monooxygenase [H.sapiens], phenylalanine hydroxylase
1	2222	21.2	222	ospiton ptu	

	<u> </u>				. Attorney Docket 44921-5058-011WO
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					ESTs, Weakly similar to PM34_MOUSE PEROXISOMAL MEMBRANE PROTEIN PMP34 (34 KDA PEROXISOMAL MEMBRANE PROTEIN) (SOLUTE CARRIER
					FAMILY 25, MEMBER 17) [M.musculus], ESTS, Weakly similar to TXTP_HUMAN TRICABBOXY, ATE TRANSPORT DECISION DECISIONS (1) CARISTO MARKY
					similar to TXTP_RAT Tricarboxylate transport protein, mitochondrial precursor (Citrate
					transport protein) (CTP) (Tricarboxylate carrier protein) [R.norvegicus], Mus musculus, Similar to bynothetical protein FI 120554 close MCC:18873 IMACE:4235245, mBNA
					complete cds, RIKEN cDNA 1300019P08 gene, expressed sequence Al194714,
			_	phosphate	expressed sequence AW108044, ornithine transporter 2, solute carrier family 25
				cytidylyltransferase 1,	(mitochondrial carrier), member 18, solute carrier family 25 (mitochondrial
3336	23130	NM_017307	V, FF	١	oxodicarboxylate carrier), member 21, uncoupling protein 2, mitochondrial
				mine binding protein,	Homo sapiens, clone MGC:22776 IMAGE:4700840, mRNA, complete cds, RIKEN
				prostatic binding	cDNA 1700023A18 gene, RIKEN cDNA 1700081D17 gene, phosphatidylethanolamine 🍦
3315	15598	NM_017236	^	protein	binding protein, prostatic binding protein
				phosphatidylethanola	
				mine binding protein,	Homo sapiens, clone MGC:22776 IMAGE:4700840, mRNA, complete cds, RIKEN
				prostatic binding	cDNA 1700023A18 gene, RIKEN cDNA 1700081D17 gene, phosphatidylethanolamine
3315	15599	NM_017236	l, J, GG	protein	binding protein, prostatic binding protein
				phosphatidylinositol	EST, Weakly similar to PP11_RAT PHOSPHATIDYLINOSITOL TRANSFER PROTEIN
				transfer protein,	ALPHA ISOFORM (PTDINS TRANSFER PROTEIN ALPHA) (PTDINSTP) (PI-TP-
				phosphotidylinositol	ALPHA) [R.norvegicus], phosphatidylinositol transfer protein, phosphotidylinositol
3313	24598	NM_017231	L	transfer protein	transfer protein, retinal degeneration B2 homolog (Drosophila)
					ESTs, Highly similar to CN3B MOUSE CGMP-INHIBITED 3',5'-CYCLIC
					PHOSPHODIESTERASE B [M.musculus], ESTs, Highly similar to CN3B RAT CGMP.
1				phosphodiesterase	similar to CN3B_HUMAN CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE B
4288	442	Z22867	Z, AA	3B, cGMP-inhibited	[H.sapiens], expressed sequence AI847709, phosphodiesterase 3B, cGMP-inhibited

TABLE					ANDING CASA ASSA SISTEMAN OF A CANDING DOCKES ASSA SISTEMAN OF SISSES OF A CONTROL OF SISSES OF A CONTROL OF SISSES OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A CONTROL OF A C
ි. නිලෝ (ම	elec on on on	Geneeni Vee or Rekse (D.:	Opogaj (Godo)	Ruman Homologous Known Gene Namer	Humani Homologousi Sequence Guster, mue
				phosphodiesterase 4A, cAMP specific, phosphodiesterase	
3219	24	NM_013101	Z, AA, RRR, SSS	4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	
				phosphodiesterase 4B, cAMP specific, phosphodiesterase	
		<b>.</b>			
22	14250	AA799729	W	E4 dunce homolog, Drosophila)	phosphodiesterase 4B, cAMP specific, phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila), phosphodiesterase 9A
4113	1340	U25651	SS	phosphofructokinase, muscle	ESTs, Highly similar to phosphofructokinase, muscle; phosphofructokinase-1 A isozyme [Mus musculus] [M.musculus], expressed sequence Al131669, phosphofructokinase, muscle
	•			phosphoglucomutase E 1,	ESTs, Highly similar to PMRT phosphoglucomutase (EC 5.4.2.2) 1 - rat [R.norvegicus], ESTs, Highly similar to S62628 phosphoglucomutase-related protein - mouse
3256	24861	NM_017033	<b>-</b>	2	[w.mosculus], ESTS, would arely strilling to Socioto priospringlucorrutase-related protein - mouse [M.musculus], RIKEN cDNA 2610020G18 gene, phosphoglucomutase 1
				phosphoglucomutase 1,	ESTs, Highly similar to PMRT phosphoglucomutase (EC 5.4.2.2) 1 - rat [R.norvegicus], ESTs, Highly similar to S62628 phosphoglucomutase-related protein - mouse
3256	24862	NM_017033	HH, UU	phosphoglucomutase 2	[M.musculus], ESTs, Moderately similar to S62628 phosphoglucomutase-related protein - mouse [M.musculus], RIKEN cDNA 2610020G18 gene, phosphoglucomutase 1
3012	1312	M31788	ו' ז' ררר	phosphoglycerate kinase 1	ESTs, Highly similar to A33792 phosphoglycerate kinase (EC 2.7.2.3) - rat [R.norvegicus], phosphoglycerate kinase 1, phosphoglycerate kinase 2

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Sed [D	OF CONTRACT	Consent Ass or 4 Refisio (D)	Medell Cede	Human Homologous Knowni Gene Name	Human Homologous Known Cenei Name Human Homologous Sequence Gluster Mille
			X, Y, FFF, GGG, General		
			Core Tox Markers	phosphoglycerate	
2018	4091	A1169417		phosphoglycerate	ESTs, Highly similar to PMGB_HUMAN PHOSPHOGLYCERATE MUTASE, BRAIN
				phosphoglycerate	י מיניין (ייסקומים), אינטקומים (ייסקימים וומנססט ייסקומים וומנססט (עומון)
			_	mutase 1,	
2437	4092	A1228723	K, DDD	phosphoglycerate mutase 1 (brain)	ESTs, Highly similar to PMGB_HUMAN PHOSPHOGLYCERATE MUTASE, BRAIN FORM IH.sapiensl. phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate mutase 1, phosphoglycerate m
				phosphoglycerate	
				mutase 1,	
2552	4003	01222001	111 555 8	phosphoglycerate	ESTs, Highly similar to PMGB_HUMAN PHOSPHOGLYCERATE MUTASE, BRAIN
1		100707	Ι.	(1) (a) (a) (b) (a) (b) (a) (b) (b) (b) (b) (c) (c) (c) (c) (c) (c) (c) (c) (c) (c	rockii (11. sapieris), prospriogrycerate mutase 1, prospriogrycerate mutase 1 (prain)
				phosphoglycerate	
			JJ, KK, GGG.	phosphodivcerate	ESTs. Highly similar to PMGB HUMAN PHOSPHOGLYCERATE MUTASE BRAIN
3743	4090	NM_053290	HHH	mutase 1 (brain)	FORM [H.sapiens], phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)
				phosphoglycerate	
				mutase 1,	
				phosphoglycerate	ESTs, Highly similar to PMGB_HUMAN PHOSPHOGLYCERATE MUTASE, BRAIN
3743	25499	NM_053290	G, H, X, ≺	mutase 1 (brain)	FORM [H.sapiens], phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)
				phospholipase A2,	
				activating protein,	
			Q, R, PPP,	phospholipase A2-	
3844	11405	NM_053866		activating protein	phospholipase A2, activating protein, phospholipase A2-activating protein
				phospholipase A2,	
4207	1000	VE4 F.20	NN, EEE,	group IIA (platelets,	phospholipase A2, group IIA (platelets, synovial fluid), phospholipase A2, group IID,
4507	280	870104	IVIIVIIVI	synoviai riula)	pnospnoiipase Az, group IIF

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			phospholipase A2,	
			group IIC,	
			phospholipase A2,	Mus musculus, Similar to hypothetical gene LOC127733, clone MGC:32424
•			group IIC (possible	IMAGE:5041000, mRNA, complete cds, phospholipase A2, group IIC, phospholipase
20435	35 NM_019202	2   UU	(bsendogene)	A2, group IIF, phospholipase A2, group V
			phosphorylase,	liver glycogen phosphorylase, muscle glycogen phosphorylase, phosphorylase,
4832	2 AA800190	ZZ, AAA	glycogen; brain	glycogen; brain
			phosphorylase,	liver glycogen phosphorylase, muscle glycogen phosphorylase, phosphorylase.
4833	3 Al009178	Е	glycogen; brain	glycogen; brain
			phosphotidylinositol	ESTs, Highly similar to PPI2_HUMAN PHOSPHATIDYLINOSITOL TRANSFER
13368	1	NM_053742 T, PP, QQ	transfer protein, beta	PROTEIN BETA ISOFORM [H.sapiens], phosphotidylinositol transfer protein, beta
		C, UU, HHH,		
		General	phosphotidylinositol	ESTs, Highly similar to PPI2_HUMAN PHOSPHATIDYLINOSITOL TRANSFER
13369	39 NM_053742	2 Alternate	transfer protein, beta	PROTEIN BETA ISOFORM [H.sapiens], phosphotidylinositol transfer protein, beta
		V, II, RRR,		
		General Core	plasma glutamate	
6554	I NM_031640	Tox Markers		plasma glutamate carboxypeptidase
			platelet derived	
			growth factor	
			receptor, alpha	
			polypeptide, platelet-	
			derived growth factor	
			receptor, alpha	platelet derived growth factor receptor, alpha polypeptide, platelet-derived growth factor
19287	37 AI232379	LLL, UUU	polypeptide	receptor, alpha polypeptide, platelet-derived growth factor receptor, beta polypeptide

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				pleiotropic regulator 1 (PRL thomolog,	
	•			pleiotropic regulator 1,	pleiotropic regulator 1, WD repeat domain 12, f-box and WD-40 domain protein 4, katanin p80 (WD40-PRL1 homolog
3435	20090	NM_021757	E, TT, ZZ, JJJ	(Arabidopsis)	regulator 1, PRL1 homolog (Arabidopsis), transducin (beta)-like 2
				polo-like kinase	polo-like kinase
				(Drosophila), polo-like	Rattus norvegicus polo-like kinase isoform mRNA, partial cds, endoplasmic reticulum
				kinase homolog,	(ER) to nucleus signalling 1, polo-like kinase (Drosophila), polo-like kinase homolog,
4096	1392	U10188	۸	(Drosophila)	(Drosophila)
					EST, Weakly similar to T42723 probable DNA-directed RNA polymerase (EC 2.7.7.6) I
		<b></b>			second largest chain - mouse [M.musculus], ESTs, Weakly similar to RNA polymerase I
					(127 kDa subunit) [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to T42723
					probable DNA-directed RNA polymerase (EC 2.7.7.6) I second largest chain - mouse
				polymerase (RNA) II	[M.musculus], RIKEN cDNA 2700078H01 gene, RNA polymerase 1-2 (128 kDa
					subunit), RNA polymerase I (127 kDa subunit), polymerase (RNA) II (DNA directed)
2616	5778	AI233246	В, Н	polypeptide B (140kD) polypeptide B (140kD)	oolypeptide B (140kD)
			-	polymerase (RNA) II	
				(DNA directed)	
3854	15857	NM_053948	ZZ, AAA	polypeptide G	polymerase (RNA) II (DNA directed) polypeptide G
				postsynaptic protein	
				CKIP1, postsynaptic	
3413	15911	NM_019907	ZZ, AAA	protein Cript	
				potassium inwardly-	
				rectifying channel,	
	,	300		subfamily J, member	
32//	1551/	OO 'NN 660/10 MN	NN, OO	8	potassium inwardly-rectifying channel, subfamily J, member 8

	33				Altomey Docket 44924-5038-01000
ි. ගියේ ඩ	GLGG BNG	consent Recor Reksq ID	epoolepow	Human Homo logous Known Gene Name	Human Homologous  Godes   Known Gene Name   Human Homologous Sequence © USign 可能を
				potassium voltage- gated channel,	RIKEN CONA CO30044P22 gang expressed semience A11019351 potassium voltage.
3279	15776	NM_017108	SS	elated), member 3	gated channel, subfamily H (eag-related), member 3
				preimplantation	
2677	2789	AI234949	MM, TTT	protein 3	preimplantation protein 3
4281	1620	X97374	D, Z, AA	prepronociceptin	
				presenilin 1, presenilin	
3363	20256	NM_019163 JJ, KK	JJ, KK	(	presenilin 1, presenilin 1 (Alzheimer disease 3)
					ESTs, Weakly similar to Ser/Arg-related nuclear matrix protein; plenty-of-prolines-101;
					serine/arginine repetitive matrix protein 1 [wius musculus] [w.musculus], wus musculus, Similar to hypothetical protein MGC13125, clone MGC:38070 IMAGE:5252666, mRNA,
				is,	complete cds, PRKC, apoptosis, WT1, regulator, expressed sequence Al480556,
3737	23895	NM_033485 A, B, HHH	A, B, HHH	WT1, regulator	glucocorticoid-induced gene 1, serine/arginine repetitive matrix 1
					EST, Weakly similar to PCO1_HUMAN PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR IH saniens I ESTs Weakly similar to PCO1_RAT Procollagen
				procollagen C-	C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COOH-terminal
					proteinase enhancer) (Type 1 procollagen C-proteinase enhancer protein)
_				enhancer, procollagen	enhancer, procollagen [R.norvegicus], expressed sequence Al043106, membrane frizzled-related protein,
			NN, EEE,	C-proteinase	procollagen C-endopeptidase enhancer, procollagen C-endopeptidase enhancer 2,
3377	15503	15503 NM_019237 MMM	MMM	tein	procollagen C-proteinase enhancer protein

TABLES	33 13				Alienney Docket (4.92/1-5038-6/1006)  Document No. 1935523.1
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					EST, Weakly similar to PCO1_HUMAN PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PCO1_RAT Procollagen
				procollagen C- endopeptidase	C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COOH-terminal proteinase enhancer) (Type 1 procollagen C-proteinase enhancer protein)
				enhancer, procollagen	enhancer, procollagen [R.norvegicus], expressed sequence AI043106, membrane frizzled-related protein,
į				C-proteinase	procollagen C-endopeptidase enhancer, procollagen C-endopeptidase enhancer 2,
3377	15504	NM_019237	NN	enhancer protein	procollagen C-proteinase enhancer protein
				procollagen-proline, 2-	
				oxoglutarate 4-	
				dioxygenase (proline	
				4-hydroxylase), beta	
				polypeptide (protein	
				disulfide isomerase;	
-				thyroid hormone	
	_			binding protein p55),	
				prolyl 4-hydroxylase,	
3191	19391	NM_012998	U, FF, RRR	beta polypeptide	
				procollagen-proline, 2-	
				oxoglutarate 4-	
				dioxygenase (proline	
				4-hydroxylase), beta	
				polypeptide (protein	
				disulfide isomerase;	
				thyroid hormone	
				binding protein p55),	
				prolyl 4-hydroxylase,	
3191	19392	NM_012998	D, BB	beta polypeptide	

TABLES	3 3 8				. Attorney Doctot 44924-5066-011WO
) (Sed	@ @ @	Centenk		Hüman Hömologous	
<u>.</u> @	(19) (19) (19)	යිස්පිල් (ම්	Medel Gede	Known Gene Name	രൂർല ം  Knowni Gene Name   Human Homologous Sequence GusterMile 🕆 🗥
				procollagen-proline, 2-	
				oxoglutarate 4-	
				dioxygenase (proline	
				4-hydroxylase), beta	
				polypeptide (protein	
				disulfide isomerase;	
				thyroid hormone	
				binding protein p55),	
				prolyl 4-hydroxylase,	
3191	19393	NM_012998	H H	beta polypeptide	
3406	20298	NM_019374	0, P, 8B, CC	prodynorphin	
				progesterone receptor	
				membrane component	membrane component Homo sapiens, clone MGC:32124 IMAGE:4877960, mRNA, complete cds, RIKEN
3437	17936	NM_021766	٨	1	cDNA 4631434O19 gene, progesterone receptor membrane component 1
				programmed cell	ESTs, Weakly similar to A41257 apoptosis protein RP-8 - rat (fragment) [R.norvegicus],
3040	21670	M80601	Я	death 2	RIKEN cDNA 6030457N17 gene, programmed cell death 2
					EST, Moderately similar to T14756 hypothetical protein DKFZp564F0923.1 [H.sapiens],
		المسيون ا			EST, Weakly similar to proline rich protein 2 [Mus musculus] [M.musculus], EST,
					Weakly similar to PRP4_HUMAN SALIVARY PROLINE-RICH PROTEIN PO
					PRECURSOR [H.sapiens], ESTs, Weakly similar to proline rich protein 2 [Mus
					musculus] [M.musculus], ESTs, Weakly similar to T14355 protein-tyrosine-phosphatase
					[R.norvegicus], expressed sequence AA408880, expressed sequence AI462446, proline
				programmed cell	rich protein 2, proline-rich protein BstNI subfamily 3, proline-rich protein BstNI subfamily
				death 6 interacting	4, protein tyrosine phosphatase TD14, protein tyrosine phosphatase, non-receptor type
2296	5459	A1178246	RR	protein	23

灵态	3.8				Attorney Bocket (A1924-5939-91WO
	eltee Dina	ල්බෝනිබාදි ර්ල්ගේ වි ගිරෙහිමේ [D	XII (1900) (1900) (1900) (1900) (1900) (1900)	Knownikeneristaneri	Iumani Homologous Inowni Geneinamen   Humani Homologous Sequence (Guster Title)
			U, LL, RR, SS,		B-cell receptor-associated protein 37, EST, Moderately similar to PHB_MOUSE PROHIBITIN (B-CELL RECEPTOR ASSOCIATED PROTEIN 32) (BAP 32)
			BBB, CCC,		[R.norvegicus], ESTs, Moderately similar to PHB MOUSE PROHIBITIN [M.musculus],
3708	15601	NM_031851	SSS	prohibitin	Homo sapiens, clone MGC:20874 IMAGE:4547239, mRNA, complete cds, hypothetical protein MGC13071, prohibitin, repressor of estrogen receptor activity
					ESTs, Highly similar to PREB_RAT Prolactin regulatory element-binding protein [R.norvegicus], Homo sapiens cDNA FLJ1114 fis. clone PLACE1005951. Homo
					sapiens cDNA FLJ13343 fis, clone OVARC1001987, highly similar to Homo sapiens
2638	22866	AI233754	I	prolactin regulatory	prolactin regulatory element-binding protein (PREB) mRNA, prolactin regulatory element binding
1					D
3463	11454	NM_022381	N	nuclear antigen	proliferating cell nuclear antigen
3463	11455	NM_022381	VV, General Alternate	proliferating cell nuclear antigen	proliferating cell nuclear antigen
				prosaposin	
				prosaposin (variant	
				Gaucher disease and	
3196	23543	NM_013013	v, vu	variant metachromatic leukodystrophy)	
				prosaposin,	
				prosaposin (variant	
				Gaucher disease and	
3196	23544	NM_013013   MM,	E	variant metachromatic leukodystrophy)	
			*		

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(O) G					<u> </u>		
###   Altonney Docket 4/921-5059-01W0	luman Homologous Mownicenenel HumaniHomologous Sequence @uster/IIIII		prostaglandin D2 synthase 2, hematopoietic, prostaglandin D2 synthase, hematopoietic	RIKEN cDNA 4833439017 gene, immunoglobulin superfamily, member 2, immunoglobulin superfamily, member 3, immunoglobulin superfamily, member 8, prostaglandin F2 receptor negative regulator	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1, proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	proteasome (prosome, macropain) 28 subunit, alpha, proteasome proteasome (prosome macropain)	28 subunit, alpha, proteasome (prosome, macropain) activator subunit 1 (PA28 alpha),
	Human Homologous KnowniGeneiName	prostaglandin D2 synthase 2, hematopoietic, prostaglandin D2	synthase, hematopoietic	prostaglandin F2 receptor negative regulator	proteasome (prosome, macropain) 26S subunit, non- ATPase, 1	proteasome (prosome, macropain) 28 subunit, alpha, proteasome	activator subunit 1
	Model Gode	-	000	PP, QQ, BBB, CCC	ر ج		
	leconsent Recorda Reseq ID:		D82071	NM_019243	NM_031978		
ନ୍ଧ ଓଡ଼	@ @ @ @		1125	21109	15469		
TABLES	නි. ම ම		2872	3380	3717		2220

Attorney Decket 44921-5033-01W0	proteasome (prosome, macropain) 28 subunit, alpha, proteaseome (prosome, macropain) 29 subunit, alpha, proteaseome (prosome, macropain) 20 subunit, alpha, proteasome (prosome, macropain) 30 subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, proteasome (prosome, macropain) activator subunit, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alpha, alp	proteasome (prosome, macropain) 28 subunit, alpha, proteaseome (prosome, macropain) 28 subunit, 3, proteasome (prosome, macropain) activator subunit 1 28 subunit, alpha, proteasome (prosome, macropain) activator subunit 1 (PA28 alpha), proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	proteasome (prosome, macropain) 28 subunit, beta, proteasome (prosome, macropain) expressed sequence AA589371, expressed sequence AI788882, proteasome activator subunit 2 (prosome, macropain) 28 subunit, beta, proteasome (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome, macropain) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (prosome) activator (pros
Known Cenewame	proteasome (prosome, macropain) 28 subunit, alpha, proteasome (prosome, macropain) p activator subunit 1	proteasome (prosome, macropain) 28 subunit, alpha, proteasome (prosome, macropain) gactivator subunit 1 (PA28 alpha)	proteasome (prosome, macropain) 28 subunit, beta, proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
Model Gede	z	HH	II, EEE, MMM
consent consent laccorri	NM_017264	NM_017264	NM_017257
33	15225	15227	18750
TABLE 3	3320	3320	3318

<b>S</b> 45 5				Attorney Docket 44924-5059-01000
Generalak Aecor Reksegild		Model Gode	** E X	umanittomologous   novmicenciNamer   Humanittomologous Sequence Cluster IIIIe
NM_017278	m	A, D, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 1, proteasome (prosome, macropain) subunit, alpha type, 1	proteasome (prosome, macropain) subunit, alpha type 1, proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, alpha type 1, proteasome (prosome, macropain) subunit, alpha type, 1 macropain) subunit, alpha type, 1
NM_017279	<u>စ</u> ျ	D, General Alternate	proteasome (prosome, macropain) subunit, alpha type 2, proteasome (prosome, macropain) subunit, alpha type, 2	proteasome (prosome, macropain) subunit, alpha type 2, proteasome (prosome, macropain) RIKEN cDNA 5430437J10 gene, proteasome (prosome, macropain) subunit, alpha type subunit, alpha type, 2
NM_017279 X, Y	62	<i>≻</i>	proteasome (prosome, macropain) subunit, alpha type 2, proteasome (prosome, macropain) subunit, alpha type, 2	proteasome (prosome, macropain) subunit, alpha type 2, proteasome (prosome, macropain) subunit, alpha type 2, proteasome (prosome, macropain) subunit, alpha type subunit, alpha type, 2 2, proteasome (prosome, macropain) subunit, alpha type, 2

proteasome (prosome, macropain) EST, Weakly similar to SNHUC8 multicatalytic endopeptidase complex [H.sapiens], proteasome (prosome, macropain) subunit, alpha type, 2 2, proteasome (prosome, macropain) subunit, alpha type, 2 2, proteasome (prosome, macropain) subunit, alpha type, 2 2, proteasome (prosome, macropain) subunit, alpha type, 2 2, proteasome (prosome, macropain) subunit, alpha type, 3 2, proteasome (prosome, macropain) subunit, alpha type, 3 2, proteasome (prosome, macropain) subunit, alpha type, 3 2, proteasome (prosome, macropain) subunit, alpha type, 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	(prosome, macropain) [M.musculus], proteasome (prosome, macropain) subunit, alpha type 3, proteasome subunit, alpha type 3, forosome, macropain) subunit, alpha type, 3, forosome, macropain) subunit, alpha type, 3
Misormeny Doctress 44:9201-5031-5031-5031-5031-5031-5031-5031-50	in) subunit, alpha type 3, proteaso
weigney Docket 44920  The macropain subunity peptidase complex [H.s. ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME COMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.ME CAMPONENT C8 [J.M	in) subunit, alpha type 3, pro
ome, macropain) su type, 2  peptidase complex ME COMPONENT  Deptidase complex ME COMPONENT  ME COMPONENT  ME COMPONENT  ME COMPONENT  ME COMPONENT  ME COMPONENT  ME COMPONENT  ME COMPONENT  ME COMPONENT	in) subunit, alpha type 3
me, macropa peptidase con ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON ME COMPON	in) subunit, alpha t
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Attorney Docket (1/92/1-5928-0/1Wo	proteasome (prosome, macropain) subunit, alpha type 4, EST, Moderately similar to PRC9_HUMAN PROTEASOME COMPONENT C9 (prosome, macropain) [H.sapiens], proteasome (prosome, macropain) subunit, alpha type 4, proteasome subunit, alpha type, 4 (prosome, macropain) subunit, alpha type, 4 (prosome, macropain) subunit, alpha type, 4	proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, subunit, alpha type, 5 macropain) subunit, alpha type, 5	proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, subunit, alpha type, 5, macropain) subunit, alpha type, 5
Known Gene Name	proteasome (prosome, macropain) subunit, alpha type 4, proteasome (prosome, macropain) subunit, alpha type, 4	proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) subunit, alpha type, 5	proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) subunit, alpha type, 5
Medal Gode	A, BBB, CCC, GGG, PPP, QQQ	H, K, LLL, SSS, UUU	
Centenik   Centenik   Ace or     Rakseg ID	NM_017281	A1169479	NM_017282 ZZ, AAA
E 3 GLGC IDINO.	1447	3256	3253
TABL Seq.	3326	2021	3327

Attorney Docket (1927-5036-611W0)  Attorney Document No. 1995823.1  Attorney Document No. 1995823.1  Attorney Document No. 1995823.1	roteasome prosome, macropain) ubunit, alpha type 5, proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) subunit, alpha type, 5 macropain) subunit, alpha type, 5	proteasome (prosome, macropain) subunit, alpha type 6, proteasome ESTs, Highly similar to S30274 multicatalytic endopeptidase complex [H.sapiens], proteasome (prosome, macropain) ESTs, Weakly similar to JX0230 multicatalytic endopeptidase complex (EC 3.4.99.46) aubunit, alpha type, 6 jota chain - rat [R.norvegicus], proteasome (prosome, macropain) subunit, alpha type, 6 jota chain - rat [R.norvegicus], proteasome (prosome, macropain) subunit, alpha type 6	proteasome (prosome, macropain) subunit, alpha type 6, ESTs, Highly similar to S30274 multicatalytic endopeptidase complex [H.sapiens], (prosome, macropain) ESTs, Weakly similar to JX0230 multicatalytic endopeptidase complex (EC 3.4.99.46) subunit, alpha type, 6 jota chain - rat [R.norvegicus], proteasome (prosome, macropain) subunit, alpha type, 6
Codes Known/Genelvame	proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) subunit, alpha type, 5	proteasome (prosome, macropain) subunit, alpha type 6, proteasome (prosome, macropain) subunit, alpha type, 6	proteasome (prosome, macropain) subunit, alpha type 6, proteasome (prosome, macropain) subunit, alpha type, 6
Model Code	Т, GGG, РРР, QQQ	S, GGG, PPP.	NNN
Centernia Ree or Roiseq (D)	TT, GGG, NM_017282 PPP, QQQ	S, GC NM_017283 QQQ	15538. NM_017283
39 III	3254	15535	
	3327	3328	3328

TANBL Seq 10	33 GLGG ID No.	eensenk Vee or The Reiseg (D	Model Code	Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrews Andrew	Attorney Docket 4492/1-5038-01/Wolfenstand No. 1933828.1  Turnamikomologous  Known/Gene Name   Humanikomologous/Sequence/Giuster/IIII
2860	9029	D30804	A, B, RR, WW, SSS		EST, Highly similar to PSA7_HUMAN PROTEASOME SUBUNIT ALPHA TYPE 7  (PROTEASOME SUBUNIT RC6-1) (PROTEASOME SUBUNIT XAPC7) [H.sapiens], (prosome, macropain) EST, Highly similar to S60038 multicatalytic endopeptidase complex (EC 3.4.99.46) subunit, alpha type 7, alpha chain RC6-1 - rat [R.norvegicus], Homo sapiens, similar to Proteasome subunit alpha type 7 (Proteasome subunit RC6-1), clone MGC:26605 IMAGE:4829939, mRNA, (prosome, macropain) complete cds, RIKEN cDNA 2410072D24 gene, proteasome (prosome, macropain) subunit, alpha type, 7 subunit, alpha type, 7
2860	25281	D30804	G, H, K, X, Y, LLL, SSS, UUU	proteasome (prosome, macropain) subunit, alpha type 7, proteasome (prosome, macropain) subunit, alpha type, 7	
3329	. 8956	NM_017284 PPP, QQQ	PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 2, proteasome (prosome, macropain) subunit, beta type, 2	prosome, macropain) ubunit, beta type 2, inoteasome prosome, macropain) proteasome (prosome, macropain) subunit, beta type 2, proteasome (prosome, macropain) subunit, beta type, 2

	proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type 2, macropain) subunit, beta type 2, macropain) subunit, beta type 2, macropain) subunit, beta type 2, macropain) subunit, beta type 2, proteasome (prosome, macropain) subunit, beta type, 2	proteasome (prosome, macropain) EST, Moderately similar to S40468 proteasome subunit RC10-li - rat [R.norvegicus], subunit, beta type 3, ESTs, Weakly similar to proteasome (prosome, macropain) subunit, beta type, 3 (M.musculus), ESTs, Weakly similar to S40468 proteasome subunit RC10-li - (prosome, macropain) rat [R.norvegicus], proteasome (prosome, macropain) subunit, beta type, 3, proteasome subunit, beta type, 3.	proteasome (prosome, macropain) EST, Moderately similar to S40468 proteasome subunit RC10-li - rat [R.norvegicus], subunit, beta type 3, ESTs, Weakly similar to proteasome (prosome, macropain) subunit, beta type 3, proteasome (prosome, macropain) rat [R.norvegicus], proteasome (prosome, macropain) subunit, beta type 3, proteasome subunit, beta type 3, proteasome (prosome, macropain) subunit, beta type 3, proteasome (prosome, macropain) subunit, beta type 3, proteasome (prosome, macropain) subunit, beta type 3, proteasome (prosome, macropain) subunit, beta type, 3
man)	proteasome (prosome, macropain) subunit, beta type 2, proteasome (prosome, macropain) proteasome, macropain) proubunit, beta type, 2 m	proteasome (prosome, macropain) subunit, beta type 3, proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit, beta type 3, proteasome (prosome, macropain)
	Medetall COO , and a	ррр,	G, H, S, X, Y, GGG, PPP, QQQ
GEBBERRA Kee on	NM 017284	G, H,	NM_017285
33 @@@@	8957		12524
TABLES Sed @	3329	3330	3330

Aitoman Homologous Sequence (Cluster III)	roteasome prosome, macropain) ubunit, beta type 4, roteasome prosome, macropain) subunit, beta type 4, proteasome (prosome, ubunit, beta type, 4   macropain) subunit, beta type, 4   macropain) subunit, beta type, 4	roteasome prosome, macropain) ubunit, beta type 4, proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type 4, proteasome (prosome, macropain) subunit, beta type, 4	(prosome, macropain) EST, Moderately similar to PSB5_RAT Proteasome subunit beta type 5 precursor subunit, beta type 5, (Proteasome epsilon chain) (Macropain epsilon chain) (Multicatalytic endopeptidase proteasome complex epsilon chain) (Proteasome subunit X) (Proteasome chain 6) [R.norvegicus], (prosome, macropain) RIKEN cDNA 5830406J20 gene, proteasome (prosome, macropain) subunit, beta type, 5 5, proteasome (prosome, macropain) subunit, beta type, 5
High Constitution of the Known Genetical Known Genetical Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitution of the Constitut	proteasome (prosome, macropain) subunit, beta type 4, proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit, beta type 4, proteasome (prosome, macropain) subunit, beta type, 4	proteasome (prosome, macropain subunit, beta type 5, proteasome (prosome, macropain subunit, beta type, 5
Model Gode	G, H, X, Y, SSS	חחת	n, rrr
emsenik Age or Raßagi	NM_031629	NM_031629	D45247
13.3		20942	9135
TABL See	3660	3660	2867

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